

OM protein - protein search, using sw model
Run on: August 3, 2006, 09:12:58 ; Search time 84 Seconds
(without alignments)
647.723 Million cell updates/sec

Title: US-10-015-967-2
Perfect score: 644
Sequence: 1 MKVLISLLULLPLMLMSV.....SRACQFLKQCQLRSPALPL 119
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 2589679 seqs, 45716429 residues
Total number of hits satisfying chosen parameters: 2589679
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries

Database : A_Geneseq_8:*
1: Geneseq1980s:*
2: Geneseq1990s:*
3: Geneseq2000s:*
4: Geneseq2001s:*
5: Geneseq2002s:*
6: Geneseq2003ae:*
7: Geneseq2003bs:*
8: Geneseq2004s:*
Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

No.	Score	Match	Length	DB	ID	Description
SUMMARIES						
RESULT 1						
ID	AA66668	standard; protein; 119 AA.				
DE	Membrane-bound protein PRO842.					
PN	WO9963088-A2.					
PD	09-DEC-1999.					
PA	(GETH) GENENTECH INC.					
Query Match	100.0%;	Score 644;	DB 3;	Length 119;		
Best Local Similarity	100.0%;	Pred. No. 3.3e-66;				
RESULT 2						
ID	RAY82453	standard; protein; 119 AA.				
DE	Human TGC-440 secretory protein SEQ ID NO:1.					
PN	WO200014226-A1.					
PD	16-MAR-2000.					
PA	(TAKE) TAKEDA CHEM IND LTD.					
Query Match	100.0%;	Score 644;	DB 3;	Length 119;		
Best Local Similarity	100.0%;	Pred. No. 3.3e-66;				
RESULT 3						
ID	AA87317	standard; protein; 119 AA.				
DE	Human signal peptide containing protein HSPP-94 SEQ ID NO:94.					
PN	WO200000610-A2.					
PD	06-JAN-2000.					
PA	(INCY-) INCYTE PHARM INC.					
Query Match	100.0%;	Score 644;	DB 3;	Length 119;		
Best Local Similarity	100.0%;	Pred. No. 3.3e-66;				
RESULT 4						
ID	AAB34728	standard; protein; 119 AA.				
DE	Human secreted protein encoded by DNA clone vq8 1.					
PN	WO200053375-A1.					
PD	21-SEP-2000.					
PA	(ALPH-) ALPHAGEN INC.					
Query Match	100.0%;	Score 644;	DB 3;	Length 119;		
Best Local Similarity	100.0%;	Pred. No. 3.3e-66;				
RESULT 5						
ID	AAU29093	standard; protein; 119 AA.				
DE	Human PRO polypeptide sequence #70.					
PN	WO200168848-A2.					
PD	20-SEP-2001.					
PA	(GETH) GENENTECH INC.					
Query Match	100.0%;	Score 644;	DB 4;	Length 119;		
Best Local Similarity	100.0%;	Pred. No. 3.3e-66;				
RESULT 6						
ID	AAG63977	standard; protein; 119 AA.				
DE	Amino acid sequence of a human Lng104 polypeptide.					

PN WO200161055-A2.
PD 23-AUG-2001.
PA (DIAD-) DIADEXUS INC.
Query Match 100.0%; Score 644; DB 4; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 7
ID AAB87538 standard; protein; 119 AA.
DE Human PRO842.
PN WO200116318-A2.
PD 08-MAR-2001.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 4; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 8
ID AAB65191 standard; protein; 119 AA.
DE Human PRO842 (UNQ473) protein sequence SEQ ID NO:165.
PN WO200073454-A1.
PD 07-DEC-2000.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 4; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 9
ID ABG95863 standard; protein; 119 AA.
DE Human secreted/transmembrane protein PRO842.
PN US2002119130-A1.
PD 29-AUG-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 5; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 10
ID ABP54931 standard; protein; 119 AA.
DE Human cytokine PRO842 (CK27).
PN WO200270706-A2.
PD 12-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 5; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 11
ID ABUS8469 standard; protein; 119 AA.
DE Human PRO Polypeptide #70.
PN US2003027272-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 12
ID ABUS8017 standard; protein; 119 AA.
DE Novel human secreted and transmembrane protein PRO842.
PN US2003032127-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 13
ID ABUS8432 standard; protein; 119 AA.
DE Human secreted/transmembrane protein (PRO) #70.
PN US2003032112-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 14
ID ABR66206 standard; protein; 119 AA.
DE Human secreted polypeptide PRO842, SEQ ID NO:140.
PN US2003027278-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 15
ID ABR65596 standard; protein; 119 AA.
DE Human secreted polypeptide PRO842, SEQ ID NO:140.
PN US2003036159-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 16
ID AAG63977 standard; protein; 119 AA.
DE Amino acid sequence of a human Lng104 polypeptide.

ID ABU99536 standard; protein; 119 AA.
DE Human secreted/transmembrane protein (PRO) #70.
PN US2003040070-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 644; DB 6; Length 119;
PRED. NO. 3.3e-66;
RESULT 17
ID ABUS8006 standard; protein; 119 AA.
DE Human PRO polypeptide #38.
PN US2003027163-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 644; DB 6; Length 119;
PRED. NO. 3.3e-66;
RESULT 18
ID ABUS9084 standard; protein; 119 AA.
DE Novel human secreted or transmembrane protein PRO842.
PN US2002132252-A1.
PD 19-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 644; DB 6; Length 119;
PRED. NO. 3.3e-66;
RESULT 19
ID ABUS2596 standard; protein; 119 AA.
DE Human secreted/transmembrane protein PRO842.
PN US2003032023-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 644; DB 6; Length 119;
PRED. NO. 3.3e-66;
RESULT 20
ID ABUS2775 standard; protein; 119 AA.
DE Human PRO polypeptide #70.
PN US2003032113-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 644; DB 6; Length 119;
PRED. NO. 3.3e-66;
RESULT 21
ID ABUS9896 standard; protein; 119 AA.
DE Novel human secreted and transmembrane protein PRO842.
PN US2003036147-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 644; DB 6; Length 119;
PRED. NO. 3.3e-66;
RESULT 22
ID ABR68145 standard; protein; 119 AA.
DE Human secreted polypeptide PRO842, SEQ ID NO:140.
PN US2003027264-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 644; DB 6; Length 119;
PRED. NO. 3.3e-66;
RESULT 23
ID ABUS60515 standard; protein; 119 AA.
DE Human secreted/transmembrane protein, #61.
PN US2002160384-A1.
PD 31-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 644; DB 6; Length 119;
PRED. NO. 3.3e-66;
RESULT 24
ID ABUS6198 standard; protein; 119 AA.
DE Novel human secreted and transmembrane protein PRO842.
PN US2003036144-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 644; DB 6; Length 119;
PRED. NO. 3.3e-66;
RESULT 25
ID ABUS2629 standard; protein; 119 AA.
DE Human secreted/transmembrane protein (PRO) #70.
PN US2003036149-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 644; DB 6; Length 119;
PRED. NO. 3.3e-66;
RESULT 26
ID ABO08706 standard; protein; 119 AA.
DE Human secreted/transmembrane protein (PRO) #70.
PN US2003044923-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 644; DB 6; Length 119;
PRED. NO. 3.3e-66;
RESULT 27
ID ABO02758 standard; protein; 119 AA.
DE Human secreted/transmembrane protein (PRO) #70.
PN US2003040062-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 644; DB 6; Length 119;
PRED. NO. 3.3e-66;
RESULT 28
ID ABR74912 standard; protein; 119 AA.
DE Human secreted polypeptide PRO842, SEQ ID NO:140.
PN US2003040056-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 644; DB 6; Length 119;
PRED. NO. 3.3e-66;
RESULT 29
ID ABR94674 standard; protein; 119 AA.
DE Human secreted polypeptide PRO842, SEQ ID NO:140.
PN US2003044926-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 644; DB 6; Length 119;
PRED. NO. 3.3e-66;
RESULT 30
ID ABUL3897 standard; protein; 119 AA.
DE Human PRO842 polypeptide.
PN US2002103125-A1.
PD 01-AUG-2002.
PA (GETH) GENENTECH LTD.
Query Match
Best Local Similarity 100.0%; Score 644; DB 6; Length 119;
PRED. NO. 3.3e-66;
RESULT 31
ID ABUS5647 standard; protein; 119 AA.
DE Human PRO polypeptide #70.
PN US2003036140-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 644; DB 6; Length 119;
PRED. NO. 3.3e-66;
RESULT 32
ID ABUS9807 standard; protein; 119 AA.
DE Novel human secreted and transmembrane protein PRO842.
PN US2003013153-A1.
PD 16-JAN-2003.
Query Match
Best Local Similarity 100.0%; Score 644; DB 6; Length 119;
PRED. NO. 3.3e-66;
RESULT 33
ID ABUS98022 standard; protein; 119 AA.
DE Novel human secreted and transmembrane protein PRO842.
PN US2003017544-A1.
PD 23-JAN-2003.
Query Match
Best Local Similarity 100.0%; Score 644; DB 6; Length 119;
PRED. NO. 3.3e-66;
RESULT 34
ID ABUS1728 standard; protein; 119 AA.
DE Novel human secreted and transmembrane protein PRO842.
PN US2003027277-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 644; DB 6; Length 119;
PRED. NO. 3.3e-66;
RESULT 35
ID ABUS9421 standard; protein; 119 AA.
DE Human PRO polypeptide #70.
PN US2003036141-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 644; DB 6; Length 119;
PRED. NO. 3.3e-66;
RESULT 36
ID ABUS6262 standard; protein; 119 AA.
DE Human secreted/transmembrane protein (PRO) #70.

PN US2003036146-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 37
ID ABU67475 standard; protein; 119 AA.
DE Human secreted/transmembrane protein (PRO) #70.
PN US2003036162-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 38
ID ABU80503 standard; protein; 119 AA.
DE Human PRO protein #70.
PN US2003036137-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 39
ID ABU72482 standard; protein; 119 AA.
DE Novel human secreted and transmembrane protein PRO842.
PN US200303531-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 40
ID ABU90888 standard; protein; 119 AA.
DE Novel human secreted and transmembrane protein PRO842.
PN US2003018173-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 41
ID ABO33947 standard; protein; 119 AA.
DE Human secreted/transmembrane protein PRO842.
PN US2003009013-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 42
ID ABR99421 standard; protein; 119 AA.
DE Human secreted polypeptide PRO842, SEQ ID NO:140.
PN US2003040063-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 43
ID ABR98811 standard; protein; 119 AA.
DE Human secreted polypeptide PRO842, SEQ ID NO:140.
PN US2003040064-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 44
ID ABO16334 standard; protein; 119 AA.
DE Human secreted/transmembrane protein (PRO) #70.
PN US2003027267-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 45
ID ABR92234 standard; protein; 119 AA.
DE Human secreted polypeptide PRO842, SEQ ID NO:140.
PN US2003036160-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 46
ID ABO18875 standard; protein; 119 AA.
DE Human secreted/transmembrane protein (PRO) #70.
PN US2003044925-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 47
ID ABR78296 standard; protein; 119 AA.
DE Human secreted polypeptide PRO842, SEQ ID NO:140.
PN US2003054474-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 48
ID ABU71964 standard; protein; 119 AA.
DE Novel human secreted and transmembrane protein PRO842.
PN US2003018183-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 49
ID ABUS032 standard; protein; 119 AA.
DE Novel human secreted and transmembrane protein PRO842.
PN US2003032114-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 50
ID ABO00171 standard; protein; 119 AA.
DE Novel human secreted and transmembrane protein PRO842.
PN US2003032101-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 51
ID ABO11503 standard; protein; 119 AA.
DE Human secreted/transmembrane protein (PRO) #70.
PN US2003036124-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 52
ID ABO02148 standard; protein; 119 AA.
DE Human secreted/transmembrane protein (PRO) #70.
PN US2003040054-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 53
ID ABU88722 standard; protein; 119 AA.
DE Novel human secreted and transmembrane protein PRO842.
PN US2003036133-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 54
ID ABU83417 standard; protein; 119 AA.
DE Human secreted/transmembrane protein (PRO) #70.
PN US2003036134-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 55
ID ABO06218 standard; protein; 119 AA.
DE Novel human secreted and transmembrane protein PRO842.
PN US2003022294-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 56

ID ABR59254 standard; protein; 119 AA.
DE Human secreted polypeptide PRO842, SEQ ID NO:140.
PN US2003027275-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 57
ID ABO09316 standard; protein; 119 AA.
DE Human secreted/transmembrane protein (PRO) #70.
PN US2003027324-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 58
ID ABO19180 standard; protein; 119 AA.
DE Novel human secreted and transmembrane protein PRO842.
PN US2003036118-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 59
ID ABO11198 standard; protein; 119 AA.
DE Human secreted/transmembrane protein (PRO) #70.
PN US2003036123-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 60
ID ABR66816 standard; protein; 119 AA.
DE Human secreted polypeptide PRO842, SEQ ID NO:140.
PN US2003036148-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 61
ID ABO16029 standard; protein; 119 AA.
DE Human secreted/transmembrane protein (PRO) #70.
PN US2003040060-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 62
ID ABO13735 standard; protein; 119 AA.
DE Human secreted/transmembrane protein (PRO) #70.
PN US2003044916-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 63
ID ABU71518 standard; protein; 119 AA.
DE Human secreted polypeptide PRO842.
PN US2003013855-A1.
PD 16-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 64
ID ABU65638 standard; protein; 119 AA.
DE Human secreted/transmembrane protein, SEQ ID 140.
PN US2003036156-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 65
ID ABO07486 standard; protein; 119 AA.
DE Human PRO polypeptide #70.
PN US2003032117-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 66
ID ABO03673 standard; protein; 119 AA.

DE Human secreted/transmembrane protein (PRO) #70.
PN US2003036128-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 67
ID ABR67121 standard; protein; 119 AA.
DE Human secreted polypeptide PRO842, SEQ ID NO:140.
PN US2003027266-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 68
ID ABO15724 standard; protein; 119 AA.
DE Human secreted/transmembrane protein (PRO) #70.
PN US2003054483-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 69
ID ABU56005 standard; protein; 119 AA.
DE Human secreted/transmembrane protein, PRO842.
PN US2003022298-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 70
ID ABU72299 standard; protein; 119 AA.
DE Human PRO polypeptide #13.
PN US2002182638-A1.
PD 05-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 71
ID ABU65333 standard; protein; 119 AA.
DE Human PRO polypeptide #70.
PN US2003032102-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 72
ID ABU95278 standard; protein; 119 AA.
DE Novel human secreted and transmembrane protein PRO842.
PN US2003036117-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 73
ID ABU71181 standard; protein; 119 AA.
DE Human PRO842 protein.
PN US2003036143-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 74
ID ABO07791 standard; protein; 119 AA.
DE Human PRO polypeptide #70.
PN US2003032130-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 75
ID ABR70032 standard; protein; 119 AA.
DE Human secreted polypeptide PRO842, SEQ ID NO:140.
PN US2003032138-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 76
ID ABR69365 standard; protein; 119 AA.

DE Human secreted polypeptide PRO842, SEQ ID NO:140.
PN US2003036132-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 77
ID ABO01506 standard; protein; 119 AA.
DE Human PRO polypeptide #70.
PN US2003008353-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 78
ID ABU81308 standard; protein; 119 AA.
DE Human PRO polypeptide #70.
PN US2003017542-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 79
ID ABR60105 standard; protein; 119 AA.
DE Human secreted polypeptide PRO842, SEQ ID NO:140.
PN US2003032137-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 80
ID ABU90972 standard; protein; 119 AA.
DE Human PRO polypeptide #13.
PN US2003018168-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 81
ID ABR67840 standard; protein; 119 AA.
DE Human secreted polypeptide PRO842, SEQ ID NO:140.
PN US2003027269-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 82
ID ABR65228 standard; protein; 119 AA.
DE Human secreted polypeptide PRO842, SEQ ID NO:140.
PN US2003027268-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 83
ID ABR68450 standard; protein; 119 AA.
DE Human secreted polypeptide PRO842, SEQ ID NO:140.
PN US2003027274-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 84
ID ABR71862 standard; protein; 119 AA.
DE Human secreted polypeptide PRO842, SEQ ID NO:140.
PN US2003032135-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 85
ID ABU59231 standard; protein; 119 AA.
DE Human secreted/transmembrane protein, #61.
PN US2003027162-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 86
ID ABU85342 standard; protein; 119 AA.

DE Human PRO polypeptide #70.
PN US2003022295-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 87
ID ABU89032 standard; protein; 119 AA.
DE Human secreted/transmembrane protein (PRO) #70.
PN US2003022297-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 88
ID ABU83112 standard; protein; 119 AA.
DE Human secreted/transmembrane protein (PRO) #70.
PN US2003032105-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 89
ID ABU94968 standard; protein; 119 AA.
DE Novel human secreted and transmembrane protein PRO842.
PN US2003032123-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 90
ID ABU90516 standard; protein; 119 AA.
DE Novel human secreted and transmembrane protein PRO842.
PN US2003032108-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 91
ID ABU94027 standard; protein; 119 AA.
DE Human secreted/transmembrane protein (PRO) #70.
PN US2003032111-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 92
ID ABU93678 standard; protein; 119 AA.
DE Novel human secreted and transmembrane protein PRO842.
PN US2003032119-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 93
ID ABO25928 standard; protein; 119 AA.
DE Human PRO842 polypeptide.
PN US2002127576-A1.
PD 12-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 94
ID ABR64923 standard; protein; 119 AA.
DE Human secreted polypeptide PRO842, SEQ ID NO:140.
PN US2003027263-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 95
ID ABO2793 standard; protein; 119 AA.
DE Human secreted/transmembrane polypeptide PRO842.
PN US2003009012-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 96
ID ABR68755 standard; protein; 119 AA.

DE Human secreted polypeptide PRO842, SEQ ID NO:140.
PN US2003027271-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 644; DB 6; Length 119;
RESULT 97
ID ABO06571 standard; protein; 119 AA.
DE Human secreted/transmembrane protein (PRO) #70.
PN US2003036125-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 644; DB 6; Length 119;
RESULT 98
ID ABR99116 standard; protein; 119 AA.
DE Human secreted polypeptide PRO842, SEQ ID NO:140.
PN US2003040068-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 644; DB 6; Length 119;
RESULT 99
ID ABU57000 standard; protein; 119 AA.
DE Human PRO polypeptide #70.
PN US2003027280-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 644; DB 6; Length 119;
RESULT 100
ID ABU85952 standard; protein; 119 AA.
DE Novel human secreted and transmembrane protein PRO842.
PN US2003022300-A1.
PD 30-JAN-2003.
Query Match
Best Local Similarity 100.0%; Score 644; DB 6; Length 119;
RESULT 101
ID ABU82239 standard; protein; 119 AA.
DE Novel human secreted and transmembrane protein PRO842.
PN US2003036136-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 644; DB 6; Length 119;
RESULT 102
ID ABU87250 standard; protein; 119 AA.
DE Human PRO polypeptide #70.
PN US2003036138-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 644; DB 6; Length 119;
RESULT 103
ID ABU83722 standard; protein; 119 AA.
DE Human secreted/transmembrane protein (PRO) #70.
PN US2003032109-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 644; DB 6; Length 119;
RESULT 104
ID ABO08096 standard; protein; 119 AA.
DE Human PRO polypeptide #70.
PN US2003040066-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 644; DB 6; Length 119;
RESULT 105
ID ABU92488 standard; protein; 119 AA.
DE Human secreted/transmembrane protein PRO842.
PN US2003045684-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 644; DB 6; Length 119;
RESULT 106
ID ABU81807 standard; protein; 119 AA.
DE Novel human secreted and transmembrane protein PRO842.
PN US2003032104-A1.

PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 644; DB 6; Length 119;
RESULT 107
ID ABU65971 standard; protein; 119 AA.
DE Novel human secreted and transmembrane protein PRO842.
PN US2003036157-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 644; DB 6; Length 119;
RESULT 108
ID ABU81158 standard; protein; 119 AA.
DE Human secreted polypeptide PRO842.
PN US2003027212-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 644; DB 6; Length 119;
RESULT 109
ID ABR59800 standard; protein; 119 AA.
DE Human secreted polypeptide PRO842, SEQ ID NO:140.
PN US2003032120-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 644; DB 6; Length 119;
RESULT 110
ID ABU93988 standard; protein; 119 AA.
DE Novel human secreted and transmembrane protein PRO842.
PN US2003036155-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 644; DB 6; Length 119;
RESULT 111
ID ABU99841 standard; protein; 119 AA.
DE Novel human secreted and transmembrane protein PRO842.
PN US2003022296-A1.
PD 30-JAN-2003.
Query Match
Best Local Similarity 100.0%; Score 644; DB 6; Length 119;
RESULT 112
ID ABR66511 standard; protein; 119 AA.
DE Human secreted polypeptide PRO842, SEQ ID NO:140.
PN US2003027281-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 644; DB 6; Length 119;
RESULT 113
ID ABR90929 standard; protein; 119 AA.
DE Human secreted polypeptide PRO842, SEQ ID NO:140.
PN US2003040058-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 644; DB 6; Length 119;
RESULT 114
ID AB053273 standard; protein; 119 AA.
DE Novel human secreted and transmembrane protein PRO842.
PN US2003027986-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 644; DB 6; Length 119;
RESULT 115
ID ABU58937 standard; protein; 119 AA.
DE Human secreted/transmembrane protein, #61.
PN US2002142961-A1.
PD 03-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 644; DB 6; Length 119;
RESULT 116
ID ABU94356 standard; protein; 119 AA.
DE Human PRO polypeptide #70.

PN US2003017540-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 117
ID ABU79238 standard; protein; 119 AA.
DE Human PRO polypeptide #70.
PN US2003032106-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 118
ID ABU86567 standard; protein; 119 AA.
DE Human secreted/transmembrane protein (PRO) #70.
PN US2003032129-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 119
ID ABU86872 standard; protein; 119 AA.
DE Novel human secreted and transmembrane protein PRO842.
PN US2003032131-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 120
ID ABU94661 standard; protein; 119 AA.
DE Human PRO polypeptide #70.
PN US2003032103-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 121
ID ABO4588 standard; protein; 119 AA.
DE Human PRO polypeptide #70.
PN US2003032107-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 122
ID ABR70337 standard; protein; 119 AA.
DE Human secreted polypeptide PRO842, SEQ ID NO:140.
PN US2003032139-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 123
ID ABU92315 standard; protein; 119 AA.
DE Novel human secreted and transmembrane protein PRO842.
PN US2003022187-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 124
ID ABU98502 standard; protein; 119 AA.
DE Human PRO polypeptide #70.
PN US2003022301-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 125
ID ABR65901 standard; protein; 119 AA.
DE Human secreted polypeptide PRO842, SEQ ID NO:140.
PN US2003036165-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 126
ID ABR64618 standard; protein; 119 AA.
DE Human secreted polypeptide PRO842, SEQ ID NO:140.
PN US2003027262-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 127
ID ABU59380 standard; protein; 119 AA.
DE Novel human secreted or transmembrane protein PRO839.
PN US2003027985-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 128
ID ABU79543 standard; protein; 119 AA.
DE Human PRO polypeptide #70.
PN US2003032110-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 129
ID ABU92934 standard; protein; 119 AA.
DE Human secreted/transmembrane protein (PRO) #70.
PN US2003036142-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 130
ID ABU95893 standard; protein; 119 AA.
DE Human PRO polypeptide #70.
PN US2003036145-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 131
ID ABU91113 standard; protein; 119 AA.
DE Novel human secreted and transmembrane protein PRO842.
PN US2003036154-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 132
ID ABU90206 standard; protein; 119 AA.
DE Novel human secreted and transmembrane protein PRO842.
PN US2003036153-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 133
ID ABO9621 standard; protein; 119 AA.
DE Human secreted/transmembrane protein (PRO) #70.
PN US2003044931-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 134
ID ABO10893 standard; protein; 119 AA.
DE Human secreted/transmembrane protein (PRO) #70.
PN US2003036150-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 135
ID ABR70947 standard; protein; 119 AA.
DE Human secreted polypeptide PRO842, SEQ ID NO:140.
PN US2003040069-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 136
ID ABU98275 standard; protein; 119 AA.
DE Novel human secreted and transmembrane protein PRO842.
PN US2002183493-A1.
PD 05-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;


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RESULT 137
ID ABU87555 standard; protein; 119 AA.
DE Human secreted/transmembrane protein (PRO) #70.
PN US2003022293-A1.
PD 30-JAN-2003.
Query Match
Best Local Similarity 100.0%; Score 644; DB 6; Length 119;
Pred. No. 3.3e-66;
RESULT 138
ID ABU91423 standard; protein; 119 AA.
DE Human PRO polypeptide #70.
PN US2003032128-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 644; DB 6; Length 119;
Pred. No. 3.3e-66;
RESULT 139
ID ABU89280 standard; protein; 119 AA.
DE Novel human secreted and transmembrane protein PRO842.
PN US2003036634-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 644; DB 6; Length 119;
Pred. No. 3.3e-66;
RESULT 140
ID ABU84637 standard; protein; 119 AA.
DE Human secreted/transmembrane protein (PRO) #70.
PN US2003032116-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 644; DB 6; Length 119;
Pred. No. 3.3e-66;
RESULT 141
ID ABR69727 standard; protein; 119 AA.
DE Human secreted polypeptide PRO842, SEQ ID NO:140.
PN US2003032122-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 644; DB 6; Length 119;
Pred. No. 3.3e-66;
RESULT 142
ID ABU80104 standard; protein; 119 AA.
DE Human PRO protein #70.
PN US2003036139-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 644; DB 6; Length 119;
Pred. No. 3.3e-66;
RESULT 143
ID ABU82487 standard; protein; 119 AA.
DE Novel human secreted and transmembrane protein PRO842.
PN US2002183494-A1.
PD 05-DEC-2002.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 644; DB 6; Length 119;
Pred. No. 3.3e-66;
RESULT 144
ID ABU92146 standard; protein; 119 AA.
DE Novel human secreted and transmembrane protein PRO842.
PN US2003017476-A1.
PD 23-JAN-2003.
Query Match
Best Local Similarity 100.0%; Score 644; DB 6; Length 119;
Pred. No. 3.3e-66;
RESULT 145
ID ABU93373 standard; protein; 119 AA.
DE Human PRO polypeptide #70.
PN US2003017541-A1.
PD 23-JAN-2003.
Query Match
Best Local Similarity 100.0%; Score 644; DB 6; Length 119;
Pred. No. 3.3e-66;
RESULT 146
ID ABO09926 standard; protein; 119 AA.
DE Human secreted/transmembrane protein (PRO) #70.
PN US2003017543-A1.
PD 23-JAN-2003.
Query Match
Best Local Similarity 100.0%; Score 644; DB 6; Length 119;
Pred. No. 3.3e-66;
RESULT 147
ID ABO09011 standard; protein; 119 AA.
DE Human secreted/transmembrane protein (PRO) #70.
PN US2003036152-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 644; DB 6; Length 119;
Pred. No. 3.3e-66;
RESULT 148
ID ABU96451 standard; protein; 119 AA.
DE Human PRO polypeptide #13.
PN US2003027993-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 644; DB 6; Length 119;
Pred. No. 3.3e-66;
RESULT 149
ID ABU10852 standard; protein; 119 AA.
DE Human PRO polypeptide #38.
PN US2002123463-A1.
PD 05-SEP-2002.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 644; DB 6; Length 119;
Pred. No. 3.3e-66;
RESULT 150
ID ABU10579 standard; protein; 119 AA.
DE Human secreted/transmembrane protein #70.
PN US2002127584-A1.
PD 12-SEP-2002.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 644; DB 6; Length 119;
Pred. No. 3.3e-66;
RESULT 151
ID ABU81604 standard; protein; 119 AA.
DE Novel human secreted and transmembrane protein PRO842.
PN US2002177164-A1.
PD 28-NOV-2002.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 644; DB 6; Length 119;
Pred. No. 3.3e-66;
RESULT 152
ID ABU72121 standard; protein; 119 AA.
DE Human PRO polypeptide #13.
PN US2003023042-A1.
PD 30-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 644; DB 6; Length 119;
Pred. No. 3.3e-66;
RESULT 153
ID ABU9588 standard; protein; 119 AA.
DE Human PRO polypeptide #70.
PN US2003032115-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 644; DB 6; Length 119;
Pred. No. 3.3e-66;
RESULT 154
ID ABU96797 standard; protein; 119 AA.
DE Novel human secreted and transmembrane protein PRO842.
PN US2003032140-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 644; DB 6; Length 119;
Pred. No. 3.3e-66;
RESULT 155
ID ABR70642 standard; protein; 119 AA.
DE Human secreted polypeptide PRO842, SEQ ID NO:140.
PN US2003040076-A1.
PD 27-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 644; DB 6; Length 119;
Pred. No. 3.3e-66;
RESULT 156
ID ABO04993 standard; protein; 119 AA.
DE Novel human secreted and transmembrane protein PRO842.
PN US2003008352-A1.
PD 09-JAN-2003.
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PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 157
ID ABO08401 standard; protein; 119 AA.
DE Human secreted/transmembrane protein (PRO) #70.
PN US2003044922-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 158
ID ABO88543 standard; protein; 119 AA.
DE Human secreted and transmembrane polypeptide PRO842.
PN US2002197615-A1.
PD 26-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 159
ID ABO34057 standard; protein; 119 AA.
DE Human PRO842 polypeptide.
PN US2003017981-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 160
ID ABO05608 standard; protein; 119 AA.
DE Human secreted/transmembrane protein (PRO) #70.
PN US2003032118-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 161
ID ABR71997 standard; protein; 119 AA.
DE Human secreted polypeptide PRO842, SEQ ID NO:140.
PN US2003036135-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 162
ID ABR9589 standard; protein; 119 AA.
DE Human secreted polypeptide PRO842, SEQ ID NO:140.
PN US2003054455-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 163
ID ABR80886 standard; protein; 119 AA.
DE Human secreted polypeptide PRO842, SEQ ID NO:140.
PN US2003049741-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 164
ID ABR81191 standard; protein; 119 AA.
DE Human secreted polypeptide PRO842, SEQ ID NO:140.
PN US2003049743-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 165
ID ABO0887 standard; protein; 119 AA.
DE Human secreted polypeptide PRO842, SEQ ID NO:140.
PN US2003049769-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 166
ID ABR88489 standard; protein; 119 AA.
DE Human secreted polypeptide PRO842, SEQ ID NO:140.
PN US2003068743-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 167
ID ABO77310 standard; protein; 119 AA.
DE Human secreted polypeptide PRO842, SEQ ID NO:140.
PN US2003054479-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 168
ID ABO28794 standard; protein; 119 AA.
DE Human secreted/transmembrane protein (PRO) #70.
PN US2003086885-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 169
ID ABO31539 standard; protein; 119 AA.
DE Human secreted/transmembrane protein (PRO) #70.
PN US2003068725-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 170
ID ABO07956 standard; protein; 119 AA.
DE Human secreted polypeptide PRO842, SEQ ID NO:140.
PN US2003068752-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 171
ID ABO40436 standard; protein; 119 AA.
DE Human secreted/transmembrane protein (PRO) #70.
PN US2003068682-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 172
ID ABO35861 standard; protein; 119 AA.
DE Human PRO polypeptide #70.
PN US2003068701-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 173
ID ABO44000 standard; protein; 119 AA.
DE Human PRO polypeptide #70.
PN US2003088755-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 174
ID ADA77892 standard; protein; 119 AA.
DE Human secreted/transmembrane protein (PRO) #70.
PN US2003073180-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 175
ID ABO24795 standard; protein; 119 AA.
DE Human secreted polypeptide PRO842, SEQ ID NO:140.


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PN US2003104539-A1.
PD 05-JUN-2003.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 176
ID ABO03063 standard; protein; 119 AA.
DE Human secreted/transmembrane protein (PRO) #70.
PN US2003036131-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 177
ID ABR90319 standard; protein; 119 AA.
DE Human secreted polypeptide PRO842, SEQ ID NO:140.
PN US2003040075-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 178
ID ABR90319 standard; protein; 119 AA.
DE Human secreted polypeptide PRO842, SEQ ID NO:140.
PN US2003054459-A1.
PD 20-MAR-2003.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 179
ID ABR94979 standard; protein; 119 AA.
DE Human secreted polypeptide PRO842, SEQ ID NO:140.
PN US2003044930-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 180
ID ABR95284 standard; protein; 119 AA.
DE Human secreted polypeptide PRO842, SEQ ID NO:140.
PN US2003040071-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 181
ID ADB17083 standard; protein; 119 AA.
DE Human transmembrane PRO polypeptide (SeqID 26).
PN US2003050462-A1.
PD 13-MAR-2003.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 182
ID ABO21522 standard; protein; 119 AA.
DE Human secreted/transmembrane protein (PRO) #70.
PN US2003054471-A1.
PD 20-MAR-2003.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 183
ID ABR97786 standard; protein; 119 AA.
DE Human secreted polypeptide PRO842, SEQ ID NO:140.
PN US2003064452-A1.
PD 03-APR-2003.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 184
ID ABR87574 standard; protein; 119 AA.
DE Human secreted polypeptide PRO842, SEQ ID NO:140.
PN US2003068705-A1.
PD 10-APR-2003.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
PN US2003104539-A1.
PD 05-JUN-2003.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 185
ID ABW77615 standard; protein; 119 AA.
DE Human secreted polypeptide PRO842, SEQ ID NO:140.
PN US2003054473-A1.
PD 20-MAR-2003.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 186
ID ABM27845 standard; protein; 119 AA.
DE Human secreted polypeptide PRO842, SEQ ID NO:140.
PN US2003064440-A1.
PD 03-APR-2003.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 187
ID ABM06126 standard; protein; 119 AA.
DE Human secreted polypeptide PRO842, SEQ ID NO:140.
PN US2003068704-A1.
PD 10-APR-2003.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 188
ID ABM03632 standard; protein; 119 AA.
DE Human secreted polypeptide PRO842, SEQ ID NO:140.
PN US2003068722-A1.
PD 10-APR-2003.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 189
ID ABM35083 standard; protein; 119 AA.
DE Human secreted polypeptide PRO842, SEQ ID NO:140.
PN US2003073183-A1.
PD 17-APR-2003.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 190
ID ABM26320 standard; protein; 119 AA.
DE Human secreted polypeptide PRO842, SEQ ID NO:140.
PN US2003104549-A1.
PD 05-JUN-2003.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 191
ID ABO48102 standard; protein; 119 AA.
DE Human secreted/transmembrane protein (PRO) #70.
PN US2003049749-A1.
PD 13-MAR-2003.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 192
ID ABR92844 standard; protein; 119 AA.
DE Human secreted polypeptide PRO842, SEQ ID NO:140.
PN US2003064462-A1.
PD 03-APR-2003.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 193
ID ABO24605 standard; protein; 119 AA.
DE Human secreted/transmembrane protein (PRO) #70.
PN US2003065159-A1.
PD 03-APR-2003.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 194
ID ADA37676 standard; protein; 119 AA.
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DE Human secreted/transmembrane protein PRO842.
PN US2003008297-A1.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 195
ID ABM11616 standard; protein; 119 AA.
DE Human secreted polypeptide PRO842, SEQ ID NO:140.
PN US2003064447-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 196
ID ABM02717 standard; protein; 119 AA.
DE Human secreted polypeptide PRO842, SEQ ID NO:140.
PN US2003073184-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 197
ID ABM16013 standard; protein; 119 AA.
DE Human secreted polypeptide PRO842, SEQ ID NO:140.
PN US2003064463-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 198
ID ABO27574 standard; protein; 119 AA.
DE Human secreted/transmembrane protein (PRO) #70.
PN US2003064451-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 199
ID ABM29065 standard; protein; 119 AA.
DE Human secreted polypeptide PRO842, SEQ ID NO:140.
PN US2003068721-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 200
ID ABM07041 standard; protein; 119 AA.
DE Human secreted polypeptide PRO842, SEQ ID NO:140.
PN US2003068699-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 201
ID ABM21135 standard; protein; 119 AA.
DE Human secreted polypeptide PRO842, SEQ ID NO:140.
PN US2003068707-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 202
ID ABM09481 standard; protein; 119 AA.
DE Human secreted polypeptide PRO842, SEQ ID NO:140.
PN US2003073175-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 203
ID ABO41351 standard; protein; 119 AA.
DE Human secreted/transmembrane protein (PRO) #70.
PN US2003068695-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 204
ID ABO36166 standard; protein; 119 AA.
DE Human PRO polypeptide #70.
PN US2003068703-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 205
ID ABO43695 standard; protein; 119 AA.
DE Human PRO polypeptide #70.
PN US2003068732-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 206
ID ABM76395 standard; protein; 119 AA.
DE Human secreted polypeptide PRO842, SEQ ID NO:140.
PN US2003082717-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 207
ID ABM76091 standard; protein; 119 AA.
DE Human secreted polypeptide PRO842, SEQ ID NO:140.
PN US2003104548-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 208
ID ABM25710 standard; protein; 119 AA.
DE Human secreted polypeptide PRO842, SEQ ID NO:140.
PN US2003104542-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 209
ID ABM26015 standard; protein; 119 AA.
DE Human secreted polypeptide PRO842, SEQ ID NO:140.
PN US2003104543-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 210
ID ADA21362 standard; protein; 119 AA.
DE Human secreted/transmembrane polypeptide PRO842.
PN US2003054404-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 211
ID ABO03368 standard; protein; 119 AA.
DE Human secreted/transmembrane protein (PRO) #70.
PN US2003036127-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 212
ID ABO02453 standard; protein; 119 AA.
DE Human secreted/transmembrane protein (PRO) #70.
PN US2003040061-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 213
ID ABO44251 standard; protein; 119 AA.

DE Human secreted/transmembrane polypeptide PRO 842.
PN US2003018172-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 214
ID ABR90624 standard; protein; 119 AA.
DE Human secreted polypeptide PRO842, SEQ ID NO:140.
PN US2003036130-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 215
ID ABR73692 standard; protein; 119 AA.
DE Human secreted polypeptide PRO842, SEQ ID NO:140.
PN US2003054468-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 216
ID ABO16944 standard; protein; 119 AA.
DE Human secreted/transmembrane protein (PRO) #70.
PN US2003054470-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 217
ID ABR94369 standard; protein; 119 AA.
DE Human secreted polypeptide PRO842, SEQ ID NO:140.
PN US2003044917-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 218
ID ABR75876 standard; protein; 119 AA.
DE Human secreted polypeptide PRO842, SEQ ID NO:140.
PN US2003044929-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 219
ID ABR71252 standard; protein; 119 AA.
DE Human secreted polypeptide PRO842, SEQ ID NO:140.
PN US2003059880-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 220
ID ABR93149 standard; protein; 119 AA.
DE Human secreted polypeptide PRO842, SEQ ID NO:140.
PN US2003064465-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 221
ID ABR93454 standard; protein; 119 AA.
DE Human secreted polypeptide PRO842, SEQ ID NO:140.
PN US2003054478-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 222
ID ADA10149 standard; protein; 119 AA.
DE Human secreted/transmembrane protein, PRO842.
PN US2003059831-A1.
PD 27-MAR-2003.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 223
ID ABR87879 standard; protein; 119 AA.
DE Human secreted polypeptide PRO842, SEQ ID NO:140.
PN US2003068718-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 224
ID ABO27879 standard; protein; 119 AA.
DE Human secreted/transmembrane protein (PRO) #70.
PN US2003064454-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 225
ID ABO30014 standard; protein; 119 AA.
DE Human secreted/transmembrane protein (PRO) #70.
PN US2003064461-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 226
ID ABO33223 standard; protein; 119 AA.
DE Human PRO polypeptide #70.
PN US2003068724-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 227
ID ABO4911 standard; protein; 119 AA.
DE Human secreted polypeptide PRO842, SEQ ID NO:140.
PN US2003068727-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 228
ID ABO8871 standard; protein; 119 AA.
DE Human secreted polypeptide PRO842, SEQ ID NO:140.
PN US2003068772-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 229
ID ABO36471 standard; protein; 119 AA.
DE Human secreted/transmembrane protein (PRO) #70.
PN US2003068714-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 230
ID ABO35556 standard; protein; 119 AA.
DE Human PRO polypeptide #70.
PN US2003068758-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 231
ID ABO39521 standard; protein; 119 AA.
DE Human secreted/transmembrane protein (PRO) #70.
PN US2003068776-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;

RESULT 232
ID ABO10396 standard; protein; 119 AA.
DE Human secreted polypeptide PRO842, SEQ ID NO:140.
PN US2003069407-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 233
ID ABO11921 standard; protein; 119 AA.
DE Human secreted polypeptide PRO842, SEQ ID NO:140.
PN US2003104555-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 234
ID ABO52067 standard; protein; 119 AA.
DE Human PRO polypeptide #70.
PN US2003049768-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 235
ID ABO52372 standard; protein; 119 AA.
DE Human PRO polypeptide #70.
PN US2003049771-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 236
ID ADA1988 standard; protein; 119 AA.
DE Novel human secreted and transmembrane protein PRO842.
PN US2003069394-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 237
ID ABO23690 standard; protein; 119 AA.
DE Human secreted/transmembrane protein (PRO) #70.
PN US2003032134-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 238
ID ADB17271 standard; protein; 119 AA.
DE Human transmembrane PRO polypeptide (SeqID 26).
PN US2003050465-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 239
ID ADA17693 standard; protein; 119 AA.
DE Human PRO842 polypeptide.
PN US2003054987-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 240
ID ABR97176 standard; protein; 119 AA.
DE Human secreted polypeptide PRO842, SEQ ID NO:140.
PN US2003054481-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 241
ID ABR86964 standard; protein; 119 AA.
DE Human secreted polypeptide PRO842, SEQ ID NO:140.
PN US2003068684-A1.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 242
ID ABO11006 standard; protein; 119 AA.
DE Human secreted polypeptide PRO842, SEQ ID NO:140.
PN US2003049782-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 243
ID ABO28150 standard; protein; 119 AA.
DE Human secreted polypeptide PRO842, SEQ ID NO:140.
PN US2003054476-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 244
ID ABO32149 standard; protein; 119 AA.
DE Human secreted/transmembrane protein (PRO) #70.
PN US2003068733-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 245
ID ABO15276 standard; protein; 119 AA.
DE Human secreted polypeptide PRO842, SEQ ID NO:140.
PN US2003068692-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 246
ID ABO6431 standard; protein; 119 AA.
DE Human secreted polypeptide PRO842, SEQ ID NO:140.
PN US2003068709-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 247
ID ABO4242 standard; protein; 119 AA.
DE Human secreted polypeptide PRO842, SEQ ID NO:140.
PN US2003068716-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 248
ID ABO22355 standard; protein; 119 AA.
DE Human secreted polypeptide PRO842, SEQ ID NO:140.
PN US2003068740-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 249
ID ABO7651 standard; protein; 119 AA.
DE Human secreted polypeptide PRO842, SEQ ID NO:140.
PN US2003068751-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 250
ID ABO40741 standard; protein; 119 AA.
DE Human secreted/transmembrane protein (PRO) #70.
PN US2003068684-A1.

PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 644; DB 6; Length 119;
RESULT 251
ID ABM35308 standard; protein; 119 AA.
DE Human secreted polypeptide PRO842, SEQ ID NO:140.
PN US2003073179-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 644; DB 6; Length 119;
RESULT 252
ID ABM33151 standard; protein; 119 AA.
DE Human secreted polypeptide PRO842, SEQ ID NO:140.
PN US2003087374-A1.
PD 08-MAY-2003.
Query Match
Best Local Similarity 100.0%; Score 644; DB 6; Length 119;
RESULT 253
ID ABO52677 standard; protein; 119 AA.
DE Human PRO polypeptide #70.
PN US2003049773-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 644; DB 6; Length 119;
RESULT 254
ID ABO50237 standard; protein; 119 AA.
DE Human secreted/transmembrane protein (PRO) #70.
PN US2003049777-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 644; DB 6; Length 119;
RESULT 255
ID ABU99231 standard; protein; 119 AA.
DE Human secreted/transmembrane protein (PRO) #70.
PN US2003040055-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 644; DB 6; Length 119;
RESULT 256
ID ABO04283 standard; protein; 119 AA.
DE Human secreted/transmembrane protein (PRO) #70.
PN US2003036164-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 644; DB 6; Length 119;
RESULT 257
ID ABO05913 standard; protein; 119 AA.
DE Human secreted/transmembrane protein (PRO) #70.
PN US2003040074-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 644; DB 6; Length 119;
RESULT 258
ID ABM18453 standard; protein; 119 AA.
DE Human secreted polypeptide PRO842, SEQ ID NO:140.
PN US2003054480-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 644; DB 6; Length 119;
RESULT 259
ID ADA27801 standard; protein; 119 AA.
DE Human secreted/transmembrane protein PRO842.
PN US2003054359-A1.
PD 20-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 644; DB 6; Length 119;
RESULT 260
ID ABR97481 standard; protein; 119 AA.
DE Human secreted/transmembrane protein (PRO) #70.
PN US2003068773-A1.
DE Human secreted polypeptide PRO842, SEQ ID NO:140.
PN US2003059885-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 644; DB 6; Length 119;
RESULT 261
ID ABR80581 standard; protein; 119 AA.
DE Human secreted polypeptide PRO842, SEQ ID NO:140.
PN US2003049740-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 644; DB 6; Length 119;
RESULT 262
ID ABM01192 standard; protein; 119 AA.
DE Human secreted polypeptide PRO842, SEQ ID NO:140.
PN US2003049770-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 644; DB 6; Length 119;
RESULT 263
ID ABR88794 standard; protein; 119 AA.
DE Human secreted polypeptide PRO842, SEQ ID NO:140.
PN US2003073169-A1.
PD 17-APR-2003.
Query Match
Best Local Similarity 100.0%; Score 644; DB 6; Length 119;
RESULT 264
ID ABM13446 standard; protein; 119 AA.
DE Human secreted polypeptide PRO842, SEQ ID NO:140.
PN US2003064457-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 644; DB 6; Length 119;
RESULT 265
ID ABM20830 standard; protein; 119 AA.
DE Human secreted polypeptide PRO842, SEQ ID NO:140.
PN US2003068711-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 644; DB 6; Length 119;
RESULT 266
ID ABO41961 standard; protein; 119 AA.
DE Human secreted/transmembrane protein (PRO) #70.
PN US2003049745-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 644; DB 6; Length 119;
RESULT 267
ID ABO42571 standard; protein; 119 AA.
DE Human secreted/transmembrane protein (PRO) #70.
PN US2003049751-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 644; DB 6; Length 119;
RESULT 268
ID ABM10091 standard; protein; 119 AA.
DE Human secreted polypeptide PRO842, SEQ ID NO:140.
PN US2003067478-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 644; DB 6; Length 119;
RESULT 269
ID ABO38606 standard; protein; 119 AA.
DE Human secreted/transmembrane protein (PRO) #70.
PN US2003068773-A1.

PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 270
ID ABM32846 standard; protein; 119 AA.
DE Human secreted polypeptide PRO842, SEQ ID NO:140.
PN US2003073185-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 271
ID ABM22660 standard; protein; 119 AA.
DE Human secreted polypeptide PRO842, SEQ ID NO:140.
PN US2003087373-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 272
ID ABM74871 standard; protein; 119 AA.
DE Human secreted polypeptide PRO842, SEQ ID NO:140.
PN US2003096353-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 273
ID ADA79684 standard; protein; 119 AA.
DE Human secreted/transmembrane protein (PRO) #70.
PN US2003073173-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 274
ID ABR96261 standard; protein; 119 AA.
DE Human secreted polypeptide PRO842, SEQ ID NO:140.
PN US2003054458-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 275
ID ABM02412 standard; protein; 119 AA.
DE Human secreted polypeptide PRO842, SEQ ID NO:140.
PN US2003059886-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 276
ID ABR86354 standard; protein; 119 AA.
DE Human secreted polypeptide PRO842, SEQ ID NO:140.
PN US2003049758-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 277
ID ABR86659 standard; protein; 119 AA.
DE Human secreted polypeptide PRO842, SEQ ID NO:140.
PN US2003049772-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 278
ID ABM16623 standard; protein; 119 AA.
DE Human secreted polypeptide PRO842, SEQ ID NO:140.
PN US2003064448-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 279
ID ABM75786 standard; protein; 119 AA.
DE Human secreted polypeptide PRO842, SEQ ID NO:140.
PN US2003104547-A1.

PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 280
ID ABO29099 standard; protein; 119 AA.
DE Human secreted/transmembrane protein (PRO) #70.
PN US2003086693-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 281
ID ABM23980 standard; protein; 119 AA.
DE Human secreted polypeptide PRO842, SEQ ID NO:140.
PN US2003068735-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 282
ID ABM23270 standard; protein; 119 AA.
DE Human secreted polypeptide PRO842, SEQ ID NO:140.
PN US2003068753-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 283
ID ABM22050 standard; protein; 119 AA.
DE Human secreted polypeptide PRO842, SEQ ID NO:140.
PN US2003068742-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 284
ID ABO37691 standard; protein; 119 AA.
DE Human secreted/transmembrane protein (PRO) #70.
PN US2003068756-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 285
ID ABM28455 standard; protein; 119 AA.
DE Human secreted polypeptide PRO842, SEQ ID NO:140.
PN US2003082715-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 286
ID ABM28760 standard; protein; 119 AA.
DE Human secreted polypeptide PRO842, SEQ ID NO:140.
PN US2003082716-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 287
ID ABM66404 standard; protein; 119 AA.
DE Human secreted polypeptide PRO842, SEQ ID NO:140.
PN US2003068737-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 288
ID ABM75786 standard; protein; 119 AA.
DE Human secreted polypeptide PRO842, SEQ ID NO:140.
PN US2003104547-A1.

PN US2003104557-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 308
ID ADA81411 standard; protein; 119 AA.
DE Human secreted/transmembrane protein (PRO) #70.
PN US2003092121-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 309
ID ABO16639 standard; protein; 119 AA.
DE Human secreted/transmembrane protein (PRO) #70.
PN US2003027276-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 310
ID ABO18265 standard; protein; 119 AA.
DE Human secreted/transmembrane protein (PRO) #70.
PN US2003044920-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 311
ID ABO22692 standard; protein; 119 AA.
DE Human PRO polypeptide #70.
PN US2003027285-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 312
ID ABO22997 standard; protein; 119 AA.
DE Human PRO polypeptide #70.
PN US2003054461-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 313
ID ABR92539 standard; protein; 119 AA.
DE Human secreted polypeptide PRO842, SEQ ID NO:140.
PN US2003084446-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 314
ID ABR81496 standard; protein; 119 AA.
DE Human secreted polypeptide PRO842, SEQ ID NO:140.
PN US2003049744-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 315
ID ABR77920 standard; protein; 119 AA.
DE Human secreted polypeptide PRO842, SEQ ID NO:140.
PN US2003049783-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 316
ID ABR89709 standard; protein; 119 AA.
DE Human secreted polypeptide PRO842, SEQ ID NO:140.
PN US2003073171-A1.
PD 17-APR-2003.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;

RESULT 317
ID ABM26625 standard; protein; 119 AA.
DE Human secreted polypeptide PRO842, SEQ ID NO:140.
PN US2003032121-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 318
ID ABM13751 standard; protein; 119 AA.
DE Human secreted polypeptide PRO842, SEQ ID NO:140.
PN US2003084458-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 319
ID ABO28489 standard; protein; 119 AA.
DE Human secreted/transmembrane protein (PRO) #70.
PN US2003064460-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 320
ID ABO30319 standard; protein; 119 AA.
DE Human secreted/transmembrane protein (PRO) #70.
PN US2003064464-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 321
ID ABM07346 standard; protein; 119 AA.
DE Human secreted polypeptide PRO842, SEQ ID NO:140.
PN US2003088702-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 322
ID ABM03937 standard; protein; 119 AA.
DE Human secreted polypeptide PRO842, SEQ ID NO:140.
PN US2003068734-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 323
ID ABO37081 standard; protein; 119 AA.
DE Human secreted/transmembrane protein (PRO) #70.
PN US2003068719-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 324
ID ABO41656 standard; protein; 119 AA.
DE Human secreted/transmembrane protein (PRO) #70.
PN US2003068729-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 325
ID ABO35251 standard; protein; 119 AA.
DE Human PRO polypeptide #70.
PN US2003068738-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 326
ID ABM25100 standard; protein; 119 AA.

DE Human secreted polypeptide PRO842, SEQ ID NO:140.
PN US2003104540-A1.
PD 05-JUN-2003.
Query Match
Best Local Similarity 100.0%; Score 644; DB 6; Length 119;
RESULT 336
ID ABO20912 standard; protein; 119 AA.
DE Human secreted/transmembrane protein (PRO) #70.
PN US2003032132-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 644; DB 6; Length 119;
RESULT 337
ID ABR96871 standard; protein; 119 AA.
DE Human secreted polypeptide PRO842, SEQ ID NO:140.
PN US2003054462-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 644; DB 6; Length 119;
RESULT 338
ID ADA38606 standard; protein; 119 AA.
DE Human secreted/transmembrane protein PRO842.
PN US2003059780-A1.
PD 27-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 644; DB 6; Length 119;
RESULT 339
ID ABM12226 standard; protein; 119 AA.
DE Human secreted polypeptide PRO842, SEQ ID NO:140.
PN US2003064445-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 644; DB 6; Length 119;
RESULT 340
ID ABU62090 standard; protein; 119 AA.
DE Human PRO842 polypeptide.
PN US2003065154-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 644; DB 6; Length 119;
RESULT 341
ID ABM16318 standard; protein; 119 AA.
DE Human secreted polypeptide PRO842, SEQ ID NO:140.
PN US2003064449-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 644; DB 6; Length 119;
RESULT 342
ID ABM24185 standard; protein; 119 AA.
DE Human secreted polypeptide PRO842, SEQ ID NO:140.
PN US2003064441-A1.
PD 03-APR-2003.
Query Match
Best Local Similarity 100.0%; Score 644; DB 6; Length 119;
RESULT 343
ID ABM14666 standard; protein; 119 AA.
DE Human secreted polypeptide PRO842, SEQ ID NO:140.
PN US2003068596-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 644; DB 6; Length 119;
RESULT 344
ID ABM04547 standard; protein; 119 AA.
DE Human secreted polypeptide PRO842, SEQ ID NO:140.
PN US2003068712-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 644; DB 6; Length 119;
RESULT 345
ID ABM06736 standard; protein; 119 AA.

DE Human secreted polypeptide PRO842, SEQ ID NO:140.
PN US2003104540-A1.
PD 05-JUN-2003.
Query Match
Best Local Similarity 100.0%; Score 644; DB 6; Length 119;
RESULT 327
ID ABO47492 standard; protein; 119 AA.
DE Human secreted/transmembrane protein (PRO) #70.
PN US2003049742-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 644; DB 6; Length 119;
RESULT 328
ID ABO47797 standard; protein; 119 AA.
DE Human secreted/transmembrane protein (PRO) #70.
PN US2003049747-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 644; DB 6; Length 119;
RESULT 329
ID ABO48407 standard; protein; 119 AA.
DE Human secreted/transmembrane protein (PRO) #70.
PN US2003049750-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 644; DB 6; Length 119;
RESULT 330
ID ABO51457 standard; protein; 119 AA.
DE Human PRO polypeptide #70.
PN US2003049766-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 644; DB 6; Length 119;
RESULT 331
ID ABO51762 standard; protein; 119 AA.
DE Human PRO polypeptide #70.
PN US2003049767-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 644; DB 6; Length 119;
RESULT 332
ID ABO50542 standard; protein; 119 AA.
DE Human secreted/transmembrane protein (PRO) #70.
PN US2003049779-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 644; DB 6; Length 119;
RESULT 333
ID ABR79666 standard; protein; 119 AA.
DE Human secreted polypeptide PRO842, SEQ ID NO:140.
PN US2003040059-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 644; DB 6; Length 119;
RESULT 334
ID ABM16928 standard; protein; 119 AA.
DE Human secreted polypeptide PRO842, SEQ ID NO:140.
PN US2003040078-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 644; DB 6; Length 119;
RESULT 335
ID ABO17960 standard; protein; 119 AA.
DE Human secreted/transmembrane protein (PRO) #70.
PN US2003044918-A1.
PD 06-MAR-2003.

Query Match	100.0%;	Score 644;	DB 6;	Length 119;
Best Local Similarity	100.0%;	Pred. No. 3.3e-66;		
RESULT 355				
ID ABR72167 standard; protein; 119 AA.				
DE Human secreted polypeptide PRO842, SEQ ID NO:140.				
PN US2003032136-A1.				
PD 13-FEB-2003.				
Query Match	100.0%;	Score 644;	DB 6;	Length 119;
Best Local Similarity	100.0%;	Pred. No. 3.3e-66;		
RESULT 356				
ID ABR98506 standard; protein; 119 AA.				
DE Human secreted polypeptide PRO842, SEQ ID NO:140.				
PN US2003036129-A1.				
PD 20-FEB-2003.				
Query Match	100.0%;	Score 644;	DB 6;	Length 119;
Best Local Similarity	100.0%;	Pred. No. 3.3e-66;		
RESULT 357				
ID ABO06876 standard; protein; 119 AA.				
DE Human secreted/transmembrane protein (PRO) #70.				
PN US2003040053-A1.				
PD 27-FEB-2003.				
Query Match	100.0%;	Score 644;	DB 6;	Length 119;
Best Local Similarity	100.0%;	Pred. No. 3.3e-66;		
RESULT 358				
ID ABR84829 standard; protein; 119 AA.				
DE Human secreted polypeptide PRO842, SEQ ID NO:140.				
PN US2003040057-A1.				
PD 27-FEB-2003.				
Query Match	100.0%;	Score 644;	DB 6;	Length 119;
Best Local Similarity	100.0%;	Pred. No. 3.3e-66;		
RESULT 359				
ID ABR73387 standard; protein; 119 AA.				
DE Human secreted polypeptide PRO842, SEQ ID NO:140.				
PN US2003054467-A1.				
PD 20-MAR-2003.				
PA (GETH) GENENTECH INC.				
Query Match	100.0%;	Score 644;	DB 6;	Length 119;
Best Local Similarity	100.0%;	Pred. No. 3.3e-66;		
RESULT 360				
ID ABR76481 standard; protein; 119 AA.				
DE Human secreted polypeptide PRO842, SEQ ID NO:140.				
PN US2003044932-A1.				
PD 06-MAR-2003.				
Query Match	100.0%;	Score 644;	DB 6;	Length 119;
Best Local Similarity	100.0%;	Pred. No. 3.3e-66;		
RESULT 361				
ID ABR73082 standard; protein; 119 AA.				
DE Human secreted polypeptide PRO842, SEQ ID NO:140.				
PN US2003027270-A1.				
PD 06-FEB-2003.				
Query Match	100.0%;	Score 644;	DB 6;	Length 119;
Best Local Similarity	100.0%;	Pred. No. 3.3e-66;		
RESULT 362				
ID ABR18148 standard; protein; 119 AA.				
DE Human secreted polypeptide PRO842, SEQ ID NO:140.				
PN US2003054469-A1.				
PD 20-MAR-2003.				
PA (GETH) GENENTECH INC.				
Query Match	100.0%;	Score 644;	DB 6;	Length 119;
Best Local Similarity	100.0%;	Pred. No. 3.3e-66;		
RESULT 363				
ID ABO20607 standard; protein; 119 AA.				
DE Human secreted/transmembrane protein (PRO) #70.				
PN US2003032126-A1.				
PD 13-FEB-2003.				
Query Match	100.0%;	Score 644;	DB 6;	Length 119;
Best Local Similarity	100.0%;	Pred. No. 3.3e-66;		
RESULT 364				
ID ABO25350 standard; protein; 119 AA.				
DE Human PRO polypeptide #70.				
PN US2003054463-A1.				
PD 20-MAR-2003.				
PA (GETH) GENENTECH INC.				

Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 365
ID ABO25655 standard; protein; 119 AA.
DE Human PRO polypeptide #70.
PN US2003054466-A1.
PD 20-NAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 366
ID ABR94064 standard; protein; 119 AA.
DE Human secreted polypeptide PRO842, SEQ ID NO:140.
PN US2003059879-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 367
ID ADA32727 standard; protein; 119 AA.
DE Human secreted/transmembrane protein PRO842.
PN US2003060407-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 368
ID ABR79971 standard; protein; 119 AA.
DE Human secreted polypeptide PRO842, SEQ ID NO:140.
PN US2003049738-A1.
PD 13-NAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 369
ID ABM11311 standard; protein; 119 AA.
DE Human secreted polypeptide PRO842, SEQ ID NO:140.
PN US2003064466-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 370
ID ABO32918 standard; protein; 119 AA.
DE Human PRO polypeptide #70.
PN US2003064453-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 371
ID ABO30624 standard; protein; 119 AA.
DE Human secreted/transmembrane protein (PRO) #70.
PN US2003064466-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 372
ID ABO30929 standard; protein; 119 AA.
DE Human secreted/transmembrane protein (PRO) #70.
PN US2003064468-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 373
ID ABM27235 standard; protein; 119 AA.
DE Human secreted polypeptide PRO842, SEQ ID NO:140.
PN US2003068760-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 374
ID ABM19610 standard; protein; 119 AA.
DE Human secreted polypeptide PRO842, SEQ ID NO:140.

ID ABM29980 standard; protein; 119 AA.
DE Human secreted polypeptide PRO842, SEQ ID NO:140.
PN US2003068769-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 375
ID ABM05516 standard; protein; 119 AA.
DE Human secreted polypeptide PRO842, SEQ ID NO:140.
PN US2003045700-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 376
ID ABM15581 standard; protein; 119 AA.
DE Human secreted polypeptide PRO842, SEQ ID NO:140.
PN US2003068698-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 377
ID ABM08566 standard; protein; 119 AA.
DE Human secreted polypeptide PRO842, SEQ ID NO:140.
PN US2003068759-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 378
ID ABO42266 standard; protein; 119 AA.
DE Human secreted/transmembrane protein (PRO) #70.
PN US2003049748-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 379
ID ABO37996 standard; protein; 119 AA.
DE Human secreted/transmembrane protein (PRO) #70.
PN US2003068765-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 380
ID ABO45906 standard; protein; 119 AA.
DE Human PRO polypeptide #70.
PN US2003049754-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 381
ID ABM66709 standard; protein; 119 AA.
DE Human secreted polypeptide PRO842, SEQ ID NO:140.
PN US2003068688-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 382
ID ADB20252 standard; protein; 119 AA.
DE Human secreted/transmembrane protein (PRO) #70.
PN US2003082767-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 383
ID ABM19610 standard; protein; 119 AA.
DE Human secreted polypeptide PRO842, SEQ ID NO:140.

PD 13-MAR-2003.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 7; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 393

ID ABO50847 standard; protein; 119 AA.
DE Human secreted/transmembrane protein (PRO) #70.
PN US2003049780-A1.
PD 13-MAR-2003.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 7; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 394

ID ABO05303 standard; protein; 119 AA.
DE Human secreted/transmembrane protein (PRO) #70.
PN US2003036126-A1.
PD 20-FEB-2003.

Query Match 100.0%; Score 644; DB 7; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 395

ID ABR74607 standard; protein; 119 AA.
DE Human secreted polypeptide PRO842, SEQ ID NO:140.
PN US2003044924-A1.
PD 06-MAR-2003.

Query Match 100.0%; Score 644; DB 7; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 396

ID ABR77086 standard; protein; 119 AA.
DE Human secreted polypeptide PRO842, SEQ ID NO:140.
PN US2003044927-A1.
PD 06-MAR-2003.

Query Match 100.0%; Score 644; DB 7; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 397

ID ASW17843 standard; protein; 119 AA.
DE Human secreted polypeptide PRO842, SEQ ID NO:140.
PN US2003040072-A1.
PD 27-FEB-2003.

Query Match 100.0%; Score 644; DB 7; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 398

ID ABR95894 standard; protein; 119 AA.
DE Human secreted polypeptide PRO842, SEQ ID NO:140.
PN US2003040073-A1.
PD 27-FEB-2003.

Query Match 100.0%; Score 644; DB 7; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 399

ID ABO21827 standard; protein; 119 AA.
DE Human secreted/transmembrane protein (PRO) #70.
PN US2003054475-A1.
PD 20-MAR-2003.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 7; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 400

ID ABO19997 standard; protein; 119 AA.
DE Human secreted/transmembrane protein (PRO) #70.
PN US2003032124-A1.
PD 13-FEB-2003.

Query Match 100.0%; Score 644; DB 7; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 401

ID ABO24300 standard; protein; 119 AA.
DE Human secreted/transmembrane protein (PRO) #70.
PN US2003064467-A1.
PD 03-APR-2003.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 7; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 402

ID ABR86049 standard; protein; 119 AA.
DE Human secreted polypeptide PRO842, SEQ ID NO:140.


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PA  US2003049759-A1.
PD  13-MAR-2003.
PA  (GETH ) GENENTECH INC.
Query Match 100.0%; Score 644; DB 7; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 403
ID  ABM10701 standard; protein; 119 AA.
DE  Human secreted polypeptide PRO842, SEQ ID NO:140.
PN  US2003064455-A1.
PD  03-APR-2003.
PA  (GETH ) GENENTECH INC.
Query Match 100.0%; Score 644; DB 7; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 404
ID  ABM76700 standard; protein; 119 AA.
DE  Human secreted polypeptide PRO842, SEQ ID NO:140.
PN  US2003054465-A1.
PD  20-NAR-2003.
PA  (GETH ) GENENTECH INC.
Query Match 100.0%; Score 644; DB 7; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 405
ID  ABR89404 standard; protein; 119 AA.
DE  Human secreted polypeptide PRO842, SEQ ID NO:140.
PN  US2003073170-A1.
PD  17-APR-2003.
PA  (GETH ) GENENTECH INC.
Query Match 100.0%; Score 644; DB 7; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 406
ID  ABM12531 standard; protein; 119 AA.
DE  Human secreted polypeptide PRO842, SEQ ID NO:140.
PN  US2003073176-A1.
PD  17-APR-2003.
PA  (GETH ) GENENTECH INC.
Query Match 100.0%; Score 644; DB 7; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 407
ID  ABM05821 standard; protein; 119 AA.
DE  Human secreted polypeptide PRO842, SEQ ID NO:140.
PN  US2003068717-A1.
PD  10-APR-2003.
PA  (GETH ) GENENTECH INC.
Query Match 100.0%; Score 644; DB 7; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 408
ID  ABO34946 standard; protein; 119 AA.
DE  Human PRO polypeptide #70.
PN  US2003068728-A1.
PD  10-APR-2003.
PA  (GETH ) GENENTECH INC.
Query Match 100.0%; Score 644; DB 7; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 409
ID  ABM03022 standard; protein; 119 AA.
DE  Human secreted polypeptide PRO842, SEQ ID NO:140.
PN  US2003068764-A1.
PD  10-APR-2003.
PA  (GETH ) GENENTECH INC.
Query Match 100.0%; Score 644; DB 7; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 410
ID  ABM19000 standard; protein; 119 AA.
DE  Human secreted polypeptide PRO842, SEQ ID NO:140.
PN  US2003104550-A1.
PD  05-JUN-2003.
PA  (GETH ) GENENTECH INC.
Query Match 100.0%; Score 644; DB 7; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 411
ID  ABM19305 standard; protein; 119 AA.
DE  Human secreted polypeptide PRO842, SEQ ID NO:140.
PN  US2003104551-A1.
PD  05-JUN-2003.
PA  (GETH ) GENENTECH INC.
Query Match 100.0%; Score 644; DB 7; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 412
ID  ABO46516 standard; protein; 119 AA.
DE  Human PRO polypeptide #70.
PN  US2003049761-A1.
PD  13-MAR-2003.
PA  (GETH ) GENENTECH INC.
Query Match 100.0%; Score 644; DB 7; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 413
ID  ABO49017 standard; protein; 119 AA.
DE  Human secreted/transmembrane protein (PRO) #70.
PN  US2003049757-A1.
PD  13-MAR-2003.
PA  (GETH ) GENENTECH INC.
Query Match 100.0%; Score 644; DB 7; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 414
ID  ABR69060 standard; protein; 119 AA.
DE  Human secreted polypeptide PRO842, SEQ ID NO:140.
PN  US2003027273-A1.
PD  06-FEB-2003.
PA  (GETH ) GENENTECH INC.
Query Match 100.0%; Score 644; DB 7; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 415
ID  ABR89099 standard; protein; 119 AA.
DE  Human secreted polypeptide PRO842, SEQ ID NO:140.
PN  US2003036119-A1.
PD  20-FEB-2003.
PA  (GETH ) GENENTECH INC.
Query Match 100.0%; Score 644; DB 7; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 416
ID  ABR72472 standard; protein; 119 AA.
DE  Human secreted polypeptide PRO842, SEQ ID NO:140.
PN  US2003036120-A1.
PD  20-FEB-2003.
PA  (GETH ) GENENTECH INC.
Query Match 100.0%; Score 644; DB 7; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 417
ID  ABR74302 standard; protein; 119 AA.
DE  Human secreted polypeptide PRO842, SEQ ID NO:140.
PN  US2003036161-A1.
PD  20-FEB-2003.
PA  (GETH ) GENENTECH INC.
Query Match 100.0%; Score 644; DB 7; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 418
ID  ABO18570 standard; protein; 119 AA.
DE  Human secreted/transmembrane protein (PRO) #70.
PN  US2003044921-A1.
PD  06-MAR-2003.
PA  (GETH ) GENENTECH INC.
Query Match 100.0%; Score 644; DB 7; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 419
ID  ABR80276 standard; protein; 119 AA.
DE  Human secreted polypeptide PRO842, SEQ ID NO:140.
PN  US2003049739-A1.
PD  13-MAR-2003.
PA  (GETH ) GENENTECH INC.
Query Match 100.0%; Score 644; DB 7; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 420
ID  ABM01497 standard; protein; 119 AA.
DE  Human secreted polypeptide PRO842, SEQ ID NO:140.
PN  US2003059882-A1.
PD  27-MAR-2003.
PA  (GETH ) GENENTECH INC.
Query Match 100.0%; Score 644; DB 7; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 421
ID  ABM02107 standard; protein; 119 AA.
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DE Human secreted polypeptide PRO842, SEQ ID NO:140.
PN US2003059884-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 7; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 422
ID ABR87269 standard; protein; 119 AA.
DE Human secreted polypeptide PRO842, SEQ ID NO:140.
PN US2003068687-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 7; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 423
ID ABR12836 standard; protein; 119 AA.
DE Human secreted polypeptide PRO842, SEQ ID NO:140.
PN US2003073186-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 7; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 424
ID ABR30590 standard; protein; 119 AA.
DE Human secreted polypeptide PRO842, SEQ ID NO:140.
PN US2003064443-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 7; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 425
ID ABR24490 standard; protein; 119 AA.
DE Human secreted polypeptide PRO842, SEQ ID NO:140.
PN US2003064444-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 7; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 426
ID ABR29404 standard; protein; 119 AA.
DE Human secreted/transmembrane protein (PRO) #70.
PN US2003068697-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 7; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 427
ID ABR31234 standard; protein; 119 AA.
DE Human secreted/transmembrane protein (PRO) #70.
PN US2003068710-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 7; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 428
ID ABR14361 standard; protein; 119 AA.
DE Human secreted polypeptide PRO842, SEQ ID NO:140.
PN US2003068686-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 7; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 429
ID ABR09786 standard; protein; 119 AA.
DE Human secreted polypeptide PRO842, SEQ ID NO:140.
PN US2003073178-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 7; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 430
ID ABR38911 standard; protein; 119 AA.
DE Human secreted/transmembrane protein (PRO) #70.

PN US2003068774-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 7; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 431
ID ABR34676 standard; protein; 119 AA.
DE Human secreted polypeptide PRO842, SEQ ID NO:140.
PN US2003104538-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 7; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 432
ID ABR051152 standard; protein; 119 AA.
DE Human secreted/transmembrane protein (PRO) #70.
PN US2003049781-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 7; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 433
ID ABR03978 standard; protein; 119 AA.
DE Human secreted/transmembrane protein (PRO) #70.
PN US2003036158-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 7; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 434
ID ABR010448 standard; protein; 119 AA.
DE Human PRO polypeptide #70.
PN US2003036151-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 7; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 435
ID ABR053143 standard; protein; 119 AA.
DE Human secreted/transmembrane protein PRO842.
PN US2003044806-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 7; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 436
ID ABR77691 standard; protein; 119 AA.
DE Human secreted polypeptide PRO842, SEQ ID NO:140.
PN US2003040067-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 7; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 437
ID ABR78901 standard; protein; 119 AA.
DE Human secreted polypeptide PRO842, SEQ ID NO:140.
PN US2003054456-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 7; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 438
ID ABR023995 standard; protein; 119 AA.
DE Human secreted/transmembrane protein (PRO) #70.
PN US2003054482-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 7; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 439
ID ABR93759 standard; protein; 119 AA.
DE Human secreted polypeptide PRO842, SEQ ID NO:140.
PN US2003054457-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 7; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 440
ID ABR01802 standard; protein; 119 AA.

DE Human secreted polypeptide PRO842, SEQ ID NO:140.
PN US2003059883-A1.
PD 27-NAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 644; DB 7; Length 119;
RESULT 441
ID ABM78225 standard; protein; 119 AA.
DE Human secreted polypeptide PRO842, SEQ ID NO:140.
PN US2003049764-A1.
PD 13-NAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 644; DB 7; Length 119;
RESULT 442
ID ABR90014 standard; protein; 119 AA.
DE Human secreted polypeptide PRO842, SEQ ID NO:140.
PN US2003073177-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 644; DB 7; Length 119;
RESULT 443
ID ADA22288 standard; protein; 119 AA.
DE Human secreted/transmembrane polypeptide PRO842.
PN US2003040473-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 644; DB 7; Length 119;
RESULT 444
ID ABM27540 standard; protein; 119 AA.
DE Human secreted polypeptide PRO842, SEQ ID NO:140.
PN US2003064442-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 644; DB 7; Length 119;
RESULT 445
ID ABM13141 standard; protein; 119 AA.
DE Human secreted polypeptide PRO842, SEQ ID NO:140.
PN US2003064450-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 644; DB 7; Length 119;
RESULT 446
ID ABO31844 standard; protein; 119 AA.
DE Human secreted/transmembrane protein (PRO) #70.
PN US2003068731-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 644; DB 7; Length 119;
RESULT 447
ID ABM14056 standard; protein; 119 AA.
DE Human secreted polypeptide PRO842, SEQ ID NO:140.
PN US2003068683-A1.
PD 10-APR-2003.
Query Match
Best Local Similarity 100.0%; Score 644; DB 7; Length 119;
RESULT 448
ID ABM08261 standard; protein; 119 AA.
DE Human secreted polypeptide PRO842, SEQ ID NO:140.
PN US2003068754-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 644; DB 7; Length 119;
RESULT 449
ID ABO40131 standard; protein; 119 AA.
DE Human secreted/transmembrane protein (PRO) #70.
PN US2003068681-A1.
PD 10-APR-2003.

Query Match
Best Local Similarity 100.0%; Score 644; DB 7; Length 119;
RESULT 450
ID ABM74566 standard; protein; 119 AA.
DE Human secreted polypeptide PRO842, SEQ ID NO:140.
PN US2003096351-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 644; DB 7; Length 119;
RESULT 451
ID ABM33761 standard; protein; 119 AA.
DE Human secreted polypeptide PRO842, SEQ ID NO:140.
PN US2003096358-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 644; DB 7; Length 119;
RESULT 452
ID ABM20220 standard; protein; 119 AA.
DE Human secreted polypeptide PRO842, SEQ ID NO:140.
PN US2003104556-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 644; DB 7; Length 119;
RESULT 453
ID ABO48712 standard; protein; 119 AA.
DE Human secreted/transmembrane protein (PRO) #70.
PN US2003049756-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 644; DB 7; Length 119;
RESULT 454
ID ABO22513 standard; protein; 119 AA.
DE Human secreted/transmembrane protein PRO842.
PN US2003017982-A1.
PD 23-JAN-2003.
Query Match
Best Local Similarity 100.0%; Score 644; DB 7; Length 119;
RESULT 455
ID ABR72777 standard; protein; 119 AA.
DE Human secreted polypeptide PRO842, SEQ ID NO:140.
PN US2003036122-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 644; DB 7; Length 119;
RESULT 456
ID ABO15419 standard; protein; 119 AA.
DE Human secreted/transmembrane protein (PRO) #70.
PN US2003036121-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 644; DB 7; Length 119;
RESULT 457
ID ABR85134 standard; protein; 119 AA.
DE Human secreted polypeptide PRO842, SEQ ID NO:140.
PN US2003040065-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 644; DB 7; Length 119;
RESULT 458
ID ABO15114 standard; protein; 119 AA.
DE Human secreted/transmembrane protein (PRO) #70.
PN US2003044919-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 644; DB 7; Length 119;
RESULT 459
ID ABO17249 standard; protein; 119 AA.
DE Human secreted/transmembrane protein (PRO) #70.

PN US2003040077-A1.
Query Match 100.0%; Score 644; DB 7; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 460
ID ABM17538 standard; protein; 119 AA.
DE Human secreted polypeptide PRO842, SEQ ID NO:140.
PN US2003044928-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 644; DB 7; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 461
ID ADA06454 standard; protein; 119 AA.
DE Human secreted/transmembrane PRO polypeptide #38.
PN US2003049638-A1.
PD 13-MAR-2003.
Query Match 100.0%; Score 644; DB 7; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 462
ID ADA39147 standard; protein; 119 AA.
DE Human secreted/transmembrane protein PRO842.
PN US2003059782-A1.
PD 27-MAR-2003.
Query Match 100.0%; Score 644; DB 7; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 463
ID ABR85439 standard; protein; 119 AA.
DE Human secreted polypeptide PRO842, SEQ ID NO:140.
PN US2003049746-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 7; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 464
ID ABM77005 standard; protein; 119 AA.
DE Human secreted polypeptide PRO842, SEQ ID NO:140.
PN US2003054464-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 7; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 465
ID ABO28184 standard; protein; 119 AA.
DE Human secreted/transmembrane protein (PRO) #70.
PN US2003064459-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 7; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 466
ID ABM22965 standard; protein; 119 AA.
DE Human secreted polypeptide PRO842, SEQ ID NO:140.
PN US2003068757-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 7; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 467
ID ABM30285 standard; protein; 119 AA.
DE Human secreted polypeptide PRO842, SEQ ID NO:140.
PN US2003068723-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 7; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 468
ID ABM21745 standard; protein; 119 AA.
DE Human secreted polypeptide PRO842, SEQ ID NO:140.
PN US2003068741-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 7; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;

RESULT 469
ID ABM21440 standard; protein; 119 AA.
DE Human secreted polypeptide PRO842, SEQ ID NO:140.
PN US2003068744-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 7; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 470
ID ABM14971 standard; protein; 119 AA.
DE Human secreted polypeptide PRO842, SEQ ID NO:140.
PN US2003068766-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 7; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 471
ID ABO41046 standard; protein; 119 AA.
DE Human secreted/transmembrane protein (PRO) #70.
PN US2003068694-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 7; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 472
ID ABO36776 standard; protein; 119 AA.
DE Human secreted/transmembrane protein (PRO) #70.
PN US2003068715-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 7; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 473
ID ABO37386 standard; protein; 119 AA.
DE Human secreted/transmembrane protein (PRO) #70.
PN US2003068726-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 7; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 474
ID ABM75176 standard; protein; 119 AA.
DE Human secreted polypeptide PRO842, SEQ ID NO:140.
PN US2003104544-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 7; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 475
ID ABM33456 standard; protein; 119 AA.
DE Human secreted polypeptide PRO842, SEQ ID NO:140.
PN US2003096357-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 7; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 476
ID ABO46211 standard; protein; 119 AA.
DE Human PRO polypeptide #70.
PN US2003049760-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 7; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 477
ID ADA82575 standard; protein; 119 AA.
DE Human secreted/transmembrane protein (PRO) #70.
PN US2003049755-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 7; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 478
ID ADA82575 standard; protein; 119 AA.
DE Human secreted/transmembrane protein (PRO) #70.
PN US2003049755-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 7; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;


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ID ADB85599 standard; protein; 119 AA.
DE Novel human secreted and transmembrane protein PRO842.
PN US2003049735-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 644; DB 7; Length 119;
RESULT 479
ID ADB96173 standard; protein; 119 AA.
DE Human PRO polypeptide #38.
PN US2003054403-A1.
PD 20-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 644; DB 7; Length 119;
RESULT 480
ID ADB31810 standard; protein; 119 AA.
DE Human secreted polypeptide PRO842, SEQ ID NO:140.
PN US2003068680-A1.
PD 10-APR-2003.
Query Match
Best Local Similarity 100.0%; Score 644; DB 7; Length 119;
RESULT 481
ID ADB31200 standard; protein; 119 AA.
DE Human secreted polypeptide PRO842, SEQ ID NO:140.
PN US2003068762-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 644; DB 7; Length 119;
RESULT 482
ID ADB85893 standard; protein; 119 AA.
DE Human secreted/transmembrane protein (PRO) #70.
PN US2003054472-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 644; DB 7; Length 119;
RESULT 483
ID ADB32115 standard; protein; 119 AA.
DE Human secreted polypeptide PRO842, SEQ ID NO:140.
PN US2003068708-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 644; DB 7; Length 119;
RESULT 484
ID ADB32420 standard; protein; 119 AA.
DE Human secreted polypeptide PRO842, SEQ ID NO:140.
PN US2003068713-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 644; DB 7; Length 119;
RESULT 485
ID ADB68278 standard; protein; 119 AA.
DE Human PRO842 protein.
PN US2003065161-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 644; DB 7; Length 119;
RESULT 486
ID ADB68085 standard; protein; 119 AA.
DE Human PRO842 protein.
PN US2003060600-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 644; DB 7; Length 119;
RESULT 487
ID ADB31505 standard; protein; 119 AA.
DE Human secreted polypeptide PRO842, SEQ ID NO:140.
PN US2003068761-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 644; DB 7; Length 119;
RESULT 488
ID ADB30895 standard; protein; 119 AA.
DE Human secreted polypeptide PRO842, SEQ ID NO:140.
PN US2003068771-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 644; DB 7; Length 119;
RESULT 489
ID ADB90902 standard; protein; 119 AA.
DE Novel human secreted and transmembrane protein PRO842.
PN US2003083473-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 644; DB 7; Length 119;
RESULT 490
ID ADC57645 standard; protein; 119 AA.
DE Human PRO polypeptide #38.
PN US2003027754-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 644; DB 7; Length 119;
RESULT 491
ID ADC55009 standard; protein; 119 AA.
DE Human PRO polypeptide #38.
PN US2003045463-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 644; DB 7; Length 119;
RESULT 492
ID ADC11876 standard; protein; 119 AA.
DE Human secreted/transmembrane protein PRO842.
PN US2003049681-A1.
PD 13-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 644; DB 7; Length 119;
RESULT 493
ID ADC06982 standard; protein; 119 AA.
DE Human PRO842 protein.
PN US2003060602-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 644; DB 7; Length 119;
RESULT 494
ID ADC56298 standard; protein; 119 AA.
DE Human PRO polypeptide #38.
PN US2003064375-A1.
PD 03-APR-2003.
Query Match
Best Local Similarity 100.0%; Score 644; DB 7; Length 119;
RESULT 495
ID ADC17161 standard; protein; 119 AA.
DE Mammalian PRO polypeptide (SeqID 26).
PN US2003065143-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 644; DB 7; Length 119;
RESULT 496
ID ADC07353 standard; protein; 119 AA.
DE Human secreted/transmembrane protein PRO842.
PN US2003068647-A1.
PD 10-APR-2003.
Query Match
Best Local Similarity 100.0%; Score 644; DB 7; Length 119;
RESULT 497
ID ADC11343 standard; protein; 119 AA.
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DE Human secreted/transmembrane protein PRO842.
PN US2003069403-A1.
PD 10-APR-2003.
Query Match 100.0%; Score 644; DB 7; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 498
ID ADC14859 standard; protein; 119 AA.
DE Novel human secreted and transmembrane protein PRO842.
PN US2003073208-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 7; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 499
ID ADC52354 standard; protein; 119 AA.
DE Novel human secreted and transmembrane protein PRO842.
PN US2003138882-A1.
PD 24-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 7; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 500
ID ADC14465 standard; protein; 119 AA.
DE Novel human secreted and transmembrane protein PRO842.
PN US2003082546-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 7; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 501
ID ADD07997 standard; protein; 119 AA.
DE Novel human secreted and transmembrane protein PRO842.
PN US2003068623-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 7; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 502
ID ADC81822 standard; protein; 119 AA.
DE Human PRO polypeptide #38.
PN US2003083461-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 7; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 503
ID ADD07464 standard; protein; 119 AA.
DE Novel human secreted and transmembrane protein PRO842.
PN US2002193299-A1.
PD 19-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 7; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 504
ID ADC82355 standard; protein; 119 AA.
DE Human PRO polypeptide #38.
PN US2003059833-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 7; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 505
ID ADD05613 standard; protein; 119 AA.
DE Human secreted/transmembrane protein (PRO) #70.
PN US2003087376-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 7; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 506
ID ADD06535 standard; protein; 119 AA.
DE Novel human secreted and transmembrane protein PRO842.
PN US2003073090-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 7; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 507
ID ADD06784 standard; protein; 119 AA.
DE Novel human secreted and transmembrane protein PRO842.
PN US2002193300-A1.
PD 19-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 7; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 508
ID ADC83031 standard; protein; 119 AA.
DE Human PRO polypeptide #38.
PN US2003059783-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 7; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 509
ID ABR61571 standard; protein; 119 AA.
DE Human VCC-1 polypeptide.
PN WO2003087157-A2.
PD 23-OCT-2003.
PA (PHAA) PHARMACIA CORP.
Query Match 100.0%; Score 644; DB 7; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 510
ID ADD55138 standard; protein; 119 AA.
DE Human PRO polypeptide #38.
PN US2003077593-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 7; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 511
ID ADD36030 standard; protein; 119 AA.
DE Novel human secreted and transmembrane protein PRO842.
PN US2003105298-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 7; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 512
ID ADD56096 standard; protein; 119 AA.
DE Human PRO polypeptide #38.
PN US2003077594-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 7; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 513
ID ADD54534 standard; protein; 119 AA.
DE Human PRO polypeptide #38.
PN US2002132253-A1.
PD 19-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 7; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 514
ID ADE26688 standard; protein; 119 AA.
DE Novel human secreted and transmembrane protein PRO842.
PN US2003087304-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 7; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 515
ID ADE26155 standard; protein; 119 AA.
DE Novel human secreted and transmembrane protein PRO842.
PN US2003087305-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 7; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 516
ID ADF67092 standard; protein; 119 AA.
DE Human PRO842 amino acid sequence SEQ ID NO:165.
PN US2002198148-A1.
PD 26-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 7; Length 119;

Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 517
ID ADG01031 standard; protein; 119 AA.
DE Novel human secreted and transmembrane protein PRO842.
PN US2003078387-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 7; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 518
ID ADG08584 standard; protein; 119 AA.
DE Novel human secreted and transmembrane protein PRO842.
PN US2003180793-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 7; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 519
ID ADG02608 standard; protein; 119 AA.
DE Novel human secreted and transmembrane protein PRO842.
PN US2003207397-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 7; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 520
ID ADG01315 standard; protein; 119 AA.
DE Novel human secreted and transmembrane protein PRO842.
PN US2003207399-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 7; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 521
ID ADF95490 standard; protein; 119 AA.
DE Novel human secreted and transmembrane protein PRO842.
PN US2003207398-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 7; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 522
ID ADF95205 standard; protein; 119 AA.
DE Novel human secreted and transmembrane protein PRO842.
PN US2003180795-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 7; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 523
ID ADG12305 standard; protein; 119 AA.
DE Novel human secreted and transmembrane protein PRO842.
PN US2003207392-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 7; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 524
ID ADH24058 standard; protein; 119 AA.
DE Novel human secreted and transmembrane protein PRO842.
PN US2003180918-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 7; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 525
ID ADH34084 standard; protein; 119 AA.
DE Novel human secreted and transmembrane protein PRO842.
PN US2003180858-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 7; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 526
ID ADH24228 standard; protein; 119 AA.
DE Novel human secreted and transmembrane protein PRO842.
PN US2003180905-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 7; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 527
ID ADH29917 standard; protein; 119 AA.
DE Novel human secreted and transmembrane protein PRO842.
PN US2003180859-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 7; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 528
ID ADH23888 standard; protein; 119 AA.
DE Novel human secreted and transmembrane protein PRO842.
PN US2003180919-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 7; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 529
ID ADH08965 standard; protein; 119 AA.
DE Human PRO polypeptide #70.
PN US2003207395-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 7; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 530
ID ADH24568 standard; protein; 119 AA.
DE Novel human secreted and transmembrane protein PRO842.
PN US2003180904-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 7; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 531
ID ADH37424 standard; protein; 119 AA.
DE Human secreted and transmembrane protein PRO842.
PN US2003181646-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 7; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 532
ID ADH02013 standard; protein; 119 AA.
DE Human PRO polypeptide #13.
PN US2003180837-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 7; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 533
ID ADH37594 standard; protein; 119 AA.
DE Human secreted and transmembrane protein PRO842.
PN US2003181648-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 7; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 534
ID ADG85632 standard; protein; 119 AA.
DE Novel human secreted and transmembrane protein PRO842.
PN US2003180905-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 7; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 535
ID ADH24228 standard; protein; 119 AA.
DE Novel human secreted and transmembrane protein PRO842.
PN US2003180905-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 7; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 536
ID ADH24228 standard; protein; 119 AA.


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DE Novel human secreted and transmembrane protein PRO842.
PN US2003180914-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 644; DB 7; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 536
ID ADH38522 standard; protein; 119 AA.
DE Novel human secreted and transmembrane protein PRO842.
PN US2003181643-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 644; DB 7; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 537
ID ADG83643 standard; protein; 119 AA.
DE Human PRO polypeptide #13.
PN US2003180794-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 644; DB 7; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 538
ID ADH29451 standard; protein; 119 AA.
DE Novel human secreted and transmembrane protein PRO842.
PN US2003180860-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 644; DB 7; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 539
ID ADH27567 standard; protein; 119 AA.
DE Novel human secreted and transmembrane protein PRO842.
PN US2003180906-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 644; DB 7; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 540
ID ADH37764 standard; protein; 119 AA.
DE Novel human secreted and transmembrane protein PRO842.
PN US2003181647-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 644; DB 7; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 541
ID ADH37941 standard; protein; 119 AA.
DE Human secreted and transmembrane protein PRO842.
PN US2003181649-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 644; DB 7; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 542
ID ADH57361 standard; protein; 119 AA.
DE Novel human secreted and transmembrane protein PRO842.
PN US2003180920-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 644; DB 7; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 543
ID ADH53503 standard; protein; 119 AA.
DE Novel human secreted and transmembrane protein PRO842.
PN US2003181636-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 644; DB 7; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 544
ID ADH53673 standard; protein; 119 AA.
DE Novel human secreted and transmembrane protein PRO842.
PN US2003180914-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 644; DB 7; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 545
ID ADH52009 standard; protein; 119 AA.
DE Novel human secreted and transmembrane protein PRO842.
PN US2003181638-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 644; DB 7; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 546
ID ADH49864 standard; protein; 119 AA.
DE Novel human secreted and transmembrane protein PRO842.
PN US2003181639-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 644; DB 7; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 547
ID ADI25374 standard; protein; 119 AA.
DE Novel human secreted and transmembrane protein PRO842.
PN US2003181696-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 644; DB 7; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 548
ID ADH90167 standard; protein; 119 AA.
DE Novel human secreted and transmembrane protein PRO842.
PN US2003181698-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 644; DB 7; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 549
ID ADI25544 standard; protein; 119 AA.
DE Novel human secreted and transmembrane protein PRO842.
PN US2003181669-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 644; DB 7; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 550
ID ADH97718 standard; protein; 119 AA.
DE Novel human secreted and transmembrane protein PRO842.
PN US2003181672-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 644; DB 7; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 551
ID ADI35346 standard; protein; 119 AA.
DE Human PRO polypeptide #38.
PN US2003050457-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 644; DB 7; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 552
ID ADI03566 standard; protein; 119 AA.
DE Novel human secreted and transmembrane protein PRO842.
PN US2003181656-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 644; DB 7; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 553
ID ADI11923 standard; protein; 119 AA.
DE Human PRO polypeptide #13.
PN US2003181686-A1.
PD 25-SEP-2003.
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PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 644; DB 7; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 554
ID ADH99997 standard; protein; 119 AA.
DE Novel human secreted and transmembrane protein PRO842.
PN US2003181697-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 644; DB 7; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 555
ID ADH99838 standard; protein; 119 AA.
DE Novel human secreted and transmembrane protein PRO842.
PN US2003049682-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 644; DB 7; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 556
ID ADH98398 standard; protein; 119 AA.
DE Novel human secreted and transmembrane protein PRO842.
PN US2003181707-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 644; DB 7; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 557
ID ADI11073 standard; protein; 119 AA.
DE Human PRO polypeptide #13.
PN US2003181682-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 644; DB 7; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 558
ID ADI11583 standard; protein; 119 AA.
DE Human PRO polypeptide #13.
PN US2003181684-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 644; DB 7; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 559
ID ADH98228 standard; protein; 119 AA.
DE Novel human secreted and transmembrane protein PRO842.
PN US2003181709-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 644; DB 7; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 560
ID ADH98568 standard; protein; 119 AA.
DE Novel human secreted and transmembrane protein PRO842.
PN US2003181708-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 644; DB 7; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 561
ID ADH98058 standard; protein; 119 AA.
DE Novel human secreted and transmembrane protein PRO842.
PN US2003181673-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 644; DB 7; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 562
ID ADI05046 standard; protein; 119 AA.
DE Novel human secreted and transmembrane protein PRO842.
PN US2003180848-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 644; DB 7; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 563
ID ADI03396 standard; protein; 119 AA.
DE Novel human secreted and transmembrane protein PRO842.
PN US2003181654-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 644; DB 7; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 564
ID ADI04791 standard; protein; 119 AA.
DE Novel human secreted and transmembrane protein PRO842.
PN US2003181657-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 644; DB 7; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 565
ID ADH78245 standard; protein; 119 AA.
DE Human PRO polypeptide #13.
PN US2003181668-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 644; DB 7; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 566
ID ADI19589 standard; protein; 119 AA.
DE Novel human secreted and transmembrane protein PRO842.
PN US2003181676-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 644; DB 7; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 567
ID ADH90337 standard; protein; 119 AA.
DE Novel human secreted and transmembrane protein PRO842.
PN US2003181699-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 644; DB 7; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 568
ID ADI03056 standard; protein; 119 AA.
DE Novel human secreted and transmembrane protein PRO842.
PN US2003181653-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 644; DB 7; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 569
ID ADH77905 standard; protein; 119 AA.
DE Human PRO polypeptide #13.
PN US2003181666-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 644; DB 7; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 570
ID ADH97888 standard; protein; 119 AA.
DE Novel human secreted and transmembrane protein PRO842.
PN US2003181674-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 644; DB 7; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 571
ID ADI01273 standard; protein; 119 AA.
DE Novel human secreted and transmembrane protein PRO842.
PN US2003190669-A1.
PD 09-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 644; DB 7; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
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ID ADH79632 standard; protein; 119 AA.
DE Novel human secreted and transmembrane protein PRO842.
FN US2003191288-A1.
PA 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 7; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 582
ID ADI01458 standard; protein; 119 AA.
DE Novel human secreted and transmembrane protein PRO842.
FN US2003181678-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 7; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 583
ID ADI01628 standard; protein; 119 AA.
DE Novel human secreted and transmembrane protein PRO842.
FN US2003181679-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 7; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 584
ID ADI01798 standard; protein; 119 AA.
DE Novel human secreted and transmembrane protein PRO842.
FN US2003181680-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 7; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 585
ID ADH79802 standard; protein; 119 AA.
DE Novel human secreted and transmembrane protein PRO842.
FN US2003191289-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 7; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 586
ID ADI04620 standard; protein; 119 AA.
DE Novel human secreted and transmembrane protein PRO842.
FN US2003171550-A1.
PD 11-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 7; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 587
ID ADI02756 standard; protein; 119 AA.
DE Novel human secreted and transmembrane protein PRO842.
FN US2003181651-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 7; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 588
ID ADH78075 standard; protein; 119 AA.
DE Human PRO polypeptide #13.
FN US2003181667-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 7; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 589
ID ADH78075 standard; protein; 119 AA.
DE Human PRO polypeptide #13.
FN US2003181667-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 7; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 590
ID ADI25714 standard; protein; 119 AA.
DE Novel human secreted and transmembrane protein PRO842.
FN US2003181670-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 7; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 591
ID ADI25984 standard; protein; 119 AA.

DE Novel human secreted and transmembrane protein PRO842.
PN US2003181671-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 7; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 591
ID ADK65396 standard; protein; 119 AA.
DE Novel human secreted and transmembrane protein PRO842.
PN US2003073821-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 7; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 592
ID ADH98738 standard; protein; 119 AA.
DE Novel human secreted and transmembrane protein PRO842.
PN US2003191284-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 7; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 593
ID ADH79979 standard; protein; 119 AA.
DE Novel human secreted and transmembrane protein PRO842.
PN US2003191287-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 7; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 594
ID ADH32746 standard; protein; 119 AA.
DE Novel human secreted and transmembrane protein PRO842.
PN US2003207396-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 7; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 595
ID ADM30280 standard; protein; 119 AA.
DE Novel human secreted and transmembrane protein PRO842.
PN US2003073813-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 7; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 596
ID ADL93710 standard; protein; 119 AA.
DE Novel human secreted and transmembrane protein PRO842.
PN US2003040013-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 7; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 597
ID ADC52164 standard; protein; 119 AA.
DE Novel human secreted and transmembrane protein PRO842.
PN US2003130483-A1.
PD 10-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 7; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 598
ID ADE74277 standard; protein; 119 AA.
DE Human secreted/transmembrane protein (PRO) #70.
PN US2003211572-A1.
PD 13-NOV-2003.
Query Match 100.0%; Score 644; DB 8; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 599
ID ADE74899 standard; protein; 119 AA.
DE Human secreted/transmembrane protein (PRO) #70.
PN US2003211574-A1.

PD 13-NOV-2003.
Query Match 100.0%; Score 644; DB 8; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 600
ID ADF35291 standard; protein; 119 AA.
DE Human PRO842 polypeptide.
PN US2003194760-A1.
PD 16-OCT-2003.
Query Match 100.0%; Score 644; DB 8; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 601
ID ADG11541 standard; protein; 119 AA.
DE Human PRO842 polypeptide.
PN US2003228655-A1.
PD 11-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 8; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 602
ID ADF96102 standard; protein; 119 AA.
DE Novel human secreted and transmembrane protein PRO842.
PN US2003215909-A1.
PD 20-NOV-2003.
Query Match 100.0%; Score 644; DB 8; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 603
ID ADG04373 standard; protein; 119 AA.
DE Novel human secreted and transmembrane protein PRO842.
PN US2003215912-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 8; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 604
ID ADG00533 standard; protein; 119 AA.
DE Novel human secreted and transmembrane protein PRO842.
PN US2003215911-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 8; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 605
ID ADH06596 standard; protein; 119 AA.
DE Novel human secreted and transmembrane protein PRO842.
PN US2003180852-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 8; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 606
ID ADH06426 standard; protein; 119 AA.
DE Novel human secreted and transmembrane protein PRO842.
PN US2003180853-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 8; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 607
ID ADG68847 standard; protein; 119 AA.
DE Novel human secreted and transmembrane protein PRO842.
PN US2003180855-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 8; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 608
ID ADH27737 standard; protein; 119 AA.
DE Novel human secreted and transmembrane protein PRO842.
PN US2003180912-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 8; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;


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RESULT 609
ID ADH25078 standard; protein; 119 AA.
DE Novel human secreted and transmembrane protein PRO842.
PN US2003180913-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 644; DB 8; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 610
ID ADH33710 standard; protein; 119 AA.
DE Human PRO polypeptide #13.
PN US2003181645-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 644; DB 8; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 611
ID ADG82789 standard; protein; 119 AA.
DE Human PRO polypeptide #70.
PN US2003215910-A1.
PD 20-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 644; DB 8; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 612
ID ADH02353 standard; protein; 119 AA.
DE Human PRO polypeptide #13.
PN US2003180839-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 644; DB 8; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 613
ID ADH07960 standard; protein; 119 AA.
DE Novel human secreted and transmembrane protein PRO842.
PN US2003180845-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 644; DB 8; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 614
ID ADG69357 standard; protein; 119 AA.
DE Novel human secreted and transmembrane protein PRO842.
PN US2003180846-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 644; DB 8; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 615
ID ADH39178 standard; protein; 119 AA.
DE Novel human secreted and transmembrane protein PRO842.
PN US2003180917-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 644; DB 8; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 616
ID ADH26070 standard; protein; 119 AA.
DE Novel human secreted and transmembrane protein PRO842.
PN US2003068770-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 644; DB 8; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 617
ID ADG83918 standard; protein; 119 AA.
DE Human PRO polypeptide #13.
PN US2003180842-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 644; DB 8; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 618
ID ADH39348 standard; protein; 119 AA.
DE Novel human secreted and transmembrane protein PRO842.
PN US2003180861-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 644; DB 8; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 619
ID ADH19411 standard; protein; 119 AA.
DE Human secreted/transmembrane protein PRO842.
PN US2003228656-A1.
PD 11-DEC-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 644; DB 8; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 620
ID ADG85462 standard; protein; 119 AA.
DE Novel human secreted and transmembrane protein PRO842.
PN US2003186848-A1.
PD 04-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 644; DB 8; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 621
ID ADH30086 standard; protein; 119 AA.
DE Novel human secreted and transmembrane protein PRO842.
PN US2003180856-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 644; DB 8; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 622
ID ADH24398 standard; protein; 119 AA.
DE Novel human secreted and transmembrane protein PRO842.
PN US2003180910-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 644; DB 8; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 623
ID ADH33039 standard; protein; 119 AA.
DE Human PRO polypeptide #70.
PN US2003068768-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 644; DB 8; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 624
ID ADG69527 standard; protein; 119 AA.
DE Novel human secreted and transmembrane protein PRO842.
PN US2003180844-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 644; DB 8; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 625
ID ADH07790 standard; protein; 119 AA.
DE Novel human secreted and transmembrane protein PRO842.
PN US2003180851-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 644; DB 8; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 626
ID ADG85802 standard; protein; 119 AA.
DE Novel human secreted and transmembrane protein PRO842.
PN US2003180861-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 644; DB 8; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 627
ID ADH39348 standard; protein; 119 AA.
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DE Novel human secreted and transmembrane protein PRO842.
PN US2003180916-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 644; DB 8; Length 119;
RESULT 628
ID ADH33540 standard; protein; 119 AA.
DE Human PRO polypeptide #13.
PN US2003181637-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 644; DB 8; Length 119;
RESULT 629
ID ADH33880 standard; protein; 119 AA.
DE Human PRO polypeptide #13.
PN US2003181644-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 644; DB 8; Length 119;
RESULT 630
ID ADH01090 standard; protein; 119 AA.
DE Human PRO polypeptide #13.
PN US2003180838-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 644; DB 8; Length 119;
RESULT 631
ID ADG69697 standard; protein; 119 AA.
DE Novel human secreted and transmembrane protein PRO842.
PN US2003180843-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 644; DB 8; Length 119;
RESULT 632
ID ADH20904 standard; protein; 119 AA.
DE Human secreted/transmembrane protein PRO842.
PN US2003224358-A1.
PD 04-DEC-2003.
Query Match
Best Local Similarity 100.0%; Score 644; DB 8; Length 119;
RESULT 633
ID ADH02183 standard; protein; 119 AA.
DE Human PRO polypeptide #13.
PN US2003180841-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 644; DB 8; Length 119;
RESULT 634
ID ADG69187 standard; protein; 119 AA.
DE Novel human secreted and transmembrane protein PRO842.
PN US2003180847-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 644; DB 8; Length 119;
RESULT 635
ID ADG85972 standard; protein; 119 AA.
DE Novel human secreted and transmembrane protein PRO842.
PN US2003180862-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 644; DB 8; Length 119;
RESULT 636
ID ADH24908 standard; protein; 119 AA.
DE Novel human secreted and transmembrane protein PRO842.
PN US2003180909-A1.

PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 644; DB 8; Length 119;
RESULT 637
ID ADH3925 standard; protein; 119 AA.
DE Novel human secreted and transmembrane protein PRO842.
PN US2003180915-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 644; DB 8; Length 119;
RESULT 638
ID ADH1944 standard; protein; 119 AA.
DE Human secreted/transmembrane protein PRO842.
PN US2003219856-A1.
PD 27-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 644; DB 8; Length 119;
RESULT 639
ID ADH02523 standard; protein; 119 AA.
DE Human PRO polypeptide #13.
PN US2003180840-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 644; DB 8; Length 119;
RESULT 640
ID ADG69017 standard; protein; 119 AA.
DE Novel human secreted and transmembrane protein PRO842.
PN US2003180849-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 644; DB 8; Length 119;
RESULT 641
ID ADH07620 standard; protein; 119 AA.
DE Novel human secreted and transmembrane protein PRO842.
PN US2003180850-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 644; DB 8; Length 119;
RESULT 642
ID ADG86142 standard; protein; 119 AA.
DE Novel human secreted and transmembrane protein PRO842.
PN US2003180863-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 644; DB 8; Length 119;
RESULT 643
ID ADH24738 standard; protein; 119 AA.
DE Novel human secreted and transmembrane protein PRO842.
PN US2003180908-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 644; DB 8; Length 119;
RESULT 644
ID ADH25786 standard; protein; 119 AA.
DE Novel human secreted and transmembrane protein PRO842.
PN US2003180911-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 644; DB 8; Length 119;
RESULT 645
ID ADH38352 standard; protein; 119 AA.
DE Novel human secreted and transmembrane protein PRO842.
PN US2003180922-A1.
PD 25-SEP-2003.
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PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 8; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 646
ID ADH57191 standard; protein; 119 AA.
DE Novel human secreted and transmembrane protein PRO842.
PN US2003181642-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 8; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 647
ID ADH52179 standard; protein; 119 AA.
DE Novel human secreted and transmembrane protein PRO842.
PN US2003180921-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 8; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 648
ID ADH49545 standard; protein; 119 AA.
DE Novel human secreted and transmembrane protein PRO842.
PN US2003180857-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 8; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 649
ID ADH90507 standard; protein; 119 AA.
DE Novel human secreted and transmembrane protein PRO842.
PN US2003181700-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 8; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 650
ID ADI11243 standard; protein; 119 AA.
DE Human PRO polypeptide #13.
PN US2003181683-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 8; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 651
ID ADH98908 standard; protein; 119 AA.
DE Novel human secreted and transmembrane protein PRO842.
PN US2003190698-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 8; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 652
ID ADI02138 standard; protein; 119 AA.
DE Novel human secreted and transmembrane protein PRO842.
PN US2003190699-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 8; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 653
ID ADH90677 standard; protein; 119 AA.
DE Novel human secreted and transmembrane protein PRO842.
PN US2003181701-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 8; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 654
ID ADK70554 standard; protein; 119 AA.
DE Respiratory disease differentially expressed protein #120.
PN WO2003101283-A2.
PD 11-DEC-2003.
PA (INCY-) INCYTE CORP.

Query Match 100.0%; Score 644; DB 8; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 655
ID ADJ54778 standard; protein; 119 AA.
DE Human PRO polypeptide #70.
PN US2004023321-A1.
PD 05-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 8; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 656
ID ADJ98552 standard; protein; 119 AA.
DE Novel human secreted and transmembrane protein PRO842.
PN US2003187197-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 8; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 657
ID ADJ98722 standard; protein; 119 AA.
DE Novel human secreted and transmembrane protein PRO842.
PN US2003187228-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 8; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 658
ID ADH78881 standard; protein; 119 AA.
DE Novel human secreted and transmembrane protein PRO842.
PN US2003181703-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 8; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 659
ID ADJ99115 standard; protein; 119 AA.
DE Novel human secreted and transmembrane protein PRO842.
PN US2003186408-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 8; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 660
ID ADJ9285 standard; protein; 119 AA.
DE Novel human secreted and transmembrane protein PRO842.
PN US2003187196-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 8; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 661
ID ADJ98903 standard; protein; 119 AA.
DE Novel human secreted and transmembrane protein PRO842.
PN US2003187242-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 8; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 662
ID ADH79051 standard; protein; 119 AA.
DE Novel human secreted and transmembrane protein PRO842.
PN US2003181702-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 8; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 663
ID ADK00911 standard; protein; 119 AA.
DE Human PRO polypeptide #13.
PN US2003186407-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 644; DB 8; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;


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Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 664
ID ADK14432 standard; protein; 119 AA.
DE Novel human secreted and transmembrane protein PRO842.
PN US2003187229-A1.
PD 02-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 644; DB 8; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 665
ID ADL01573 standard; protein; 119 AA.
DE Human VEGF co-regulated chemokine-1 (VCC-1) polypeptide.
PN WO2004016224-A2.
PD 26-FEB-2004.
PA (PHAA ) PHARMACIA CORP.
Query Match 100.0%; Score 644; DB 8; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 666
ID ADJ64549 standard; protein; 119 AA.
DE Human PRO polypeptide #70.
PN US2004038337-A1.
PD 26-FEB-2004.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 644; DB 8; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 667
ID ADM31445 standard; protein; 119 AA.
DE Novel human secreted and transmembrane protein PRO842.
PN US2004048334-A1.
PD 11-MAR-2004.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 644; DB 8; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 668
ID ADM36492 standard; protein; 119 AA.
DE Novel human secreted and transmembrane protein PRO842.
PN US2004053358-A1.
PD 18-MAR-2004.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 644; DB 8; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 669
ID ADM40297 standard; protein; 119 AA.
DE Novel human secreted and transmembrane protein PRO842.
PN US2004048335-A1.
PD 11-MAR-2004.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 644; DB 8; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 670
ID ADM80881 standard; protein; 119 AA.
DE Human PRO polypeptide #13.
PN US2004058411-A1.
PD 25-MAR-2004.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 644; DB 8; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 671
ID ADN37905 standard; protein; 119 AA.
DE Novel human secreted and transmembrane protein PRO842.
PN US2004091959-A1.
PD 13-MAY-2004.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 644; DB 8; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 672
ID ADP07801 standard; protein; 119 AA.
DE Human secreted protein, seq id 284.
PN WO2004042000-A2.
PD 21-MAY-2004.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 100.0%; Score 644; DB 8; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 673
ID ADP07856 standard; protein; 119 AA.
DE Human secreted protein, seq id 339.
PN WO2004042000-A2.
PD 21-MAY-2004.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 100.0%; Score 644; DB 8; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 674
ID ADP07780 standard; protein; 119 AA.
DE Human secreted protein, seq id 263.
PN WO2004042000-A2.
PD 21-MAY-2004.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 100.0%; Score 644; DB 8; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 675
ID ADP07879 standard; protein; 119 AA.
DE Human secreted protein, seq id 362.
PN WO2004042000-A2.
PD 21-MAY-2004.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 100.0%; Score 644; DB 8; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 676
ID ADP07807 standard; protein; 119 AA.
DE Human secreted protein, seq id 290.
PN WO2004042000-A2.
PD 21-MAY-2004.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 100.0%; Score 644; DB 8; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 677
ID ADP07852 standard; protein; 119 AA.
DE Human secreted protein, seq id 335.
PN WO2004042000-A2.
PD 21-MAY-2004.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 100.0%; Score 644; DB 8; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 678
ID ADV7721 standard; protein; 119 AA.
DE Neoplastic disease detection protein PRO842.
PN US2005059102-A1.
PD 17-MAR-2005.
PA (EATO//) EATON D L.
PA (FILV//) FILVAROFF E.
PA (GERR//) GERRITSEN M E.
PA (GODD//) GODDARD A.
PA (GODO//) GODOWSKI P J.
PA (GRIM//) GRIMALDI J C.
PA (GURN//) GURNEY A L.
PA (WATA//) WATANABE C K.
PA (WOOD//) WOOD W I.
Query Match 100.0%; Score 644; DB 9; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 679
ID ADZ45057 standard; protein; 119 AA.
DE Human PRO842 encoding SEQ ID NO:2.
PN US2005100544-A1.
PD 12-MAY-2005.
PA (EATO//) EATON D L.
PA (PISA//) PISABARRO M T.
PA (SCHM//) SCHMIDT K N.
PA (VAND//) VANDLEN R.
PA (CHIA//) CHIANG N.
PA (DIEH//) DIEHL L.
Query Match 100.0%; Score 644; DB 9; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 680
ID AEA38434 standard; protein; 119 AA.
DE Human secreted/transmembrane protein, #106.
PN US2005112725-A1.
```


Query Match 85.1%; Score 548; DB 7; Length 97;
Best Local Similarity 100.0%; Pred. No. 3.3e-55;
RESULT 689
ID AAW83953 standard; protein; 93 AA.
DE Polypeptide encoded by gene 7 clone HJPDJ64.
PN W09845712-A2.
PD 15-OCT-1998.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 81.8%; Score 527; DB 2; Length 93;
Best Local Similarity 100.0%; Pred. No. 8.5e-53;
RESULT 690
ID ADT50870 standard; protein; 118 AA.
DE Cancer related protein sequence #33.
PN W02004092338-A2.
PD 28-OCT-2004.
PA (DIAD-) DIADEXUS INC.
Query Match 81.8%; Score 537; DB 8; Length 118;
Best Local Similarity 100.0%; Pred. No. 1.1e-52;
RESULT 691
ID ADT50869 standard; protein; 94 AA.
DE Cancer related protein sequence #32.
PN W02004092338-A2.
PD 28-OCT-2004.
PA (DIAD-) DIADEXUS INC.
Query Match 80.9%; Score 521; DB 8; Length 94;
Best Local Similarity 100.0%; Pred. No. 4.3e-52;
RESULT 692
ID ADT50871 standard; protein; 100 AA.
DE Cancer related protein sequence #34.
PN W02004092338-A2.
PD 28-OCT-2004.
PA (DIAD-) DIADEXUS INC.
Query Match 80.9%; Score 521; DB 8; Length 100;
Best Local Similarity 100.0%; Pred. No. 4.6e-52;
RESULT 693
ID AYR82457 standard; protein; 119 AA.
DE Mouse TGC-440 secretory protein SEQ ID NO:3.
PN W0200014226-A1.
PD 16-MAR-2000.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 70.8%; Score 456; DB 3; Length 119;
Best Local Similarity 71.4%; Pred. No. 1.9e-44;
RESULT 694
ID ABR61573 standard; protein; 119 AA.
DE Mouse VCC-1 polypeptide.
PN W02003087157-A2.
PD 23-OCT-2003.
PA (PHAA) PHARMACIA CORP.
Query Match 70.8%; Score 456; DB 7; Length 119;
Best Local Similarity 71.4%; Pred. No. 1.9e-44;
RESULT 695
ID ADT50873 standard; protein; 84 AA.
DE Cancer related protein sequence #36.
PN W02004092338-A2.
PD 28-OCT-2004.
PA (DIAD-) DIADEXUS INC.
Query Match 64.4%; Score 415; DB 8; Length 84;
Best Local Similarity 80.9%; Pred. No. 6.8e-40;
RESULT 696
ID AYR82458 standard; protein; 97 AA.
DE Mature mouse TGC-440 secretory protein SEQ ID NO:9.
PN W0200014226-A1.
PD 16-MAR-2000.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 59.9%; Score 386; DB 3; Length 97;
Best Local Similarity 71.1%; Pred. No. 1.8e-36;
RESULT 697
ID ABR61574 standard; protein; 97 AA.
DE Mouse VCC-1 mature polypeptide.
PN W02003087157-A2.
PD 23-OCT-2003.
PA (PHAA) PHARMACIA CORP.
Query Match 59.9%; Score 386; DB 7; Length 97;

Best Local Similarity 71.1%; Pred. No. 1.8e-36;
RESULT 698
ID AAY82455 standard; protein; 119 AA.
DE Rat TGC-440 secretory protein SEQ ID NO:2.
PN WO200014226-A1.
PD 16-MAR-2000.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 59.9%; Score 386; DB 3; Length 119;
Best Local Similarity 63.0%; Pred. No. 2.3e-36;
RESULT 699
ID AAY11732 standard; protein; 69 AA.
DE Human 5' EST secreted protein SEQ ID No: 332.
PN WO9906550-A2.
PD 11-FEB-1999.
PA (GEST) GENSET.
Query Match 55.6%; Score 358; DB 2; Length 69;
Best Local Similarity 100.0%; Pred. No. 2.1e-33;
RESULT 700
ID AAY82456 standard; protein; 97 AA.
DE Mature rat TGC-440 secretory protein SEQ ID NO:8.
PN WO200014226-A1.
PD 16-MAR-2000.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 53.1%; Score 342; DB 3; Length 97;
Best Local Similarity 64.9%; Pred. No. 2.3e-31;
RESULT 701
ID AAW83938 standard; protein; 64 AA.
DE Human secreted protein from gene 8 clone HLHCM89.
PN WO9845712-A2.
PD 15-OCT-1998.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 46.0%; Score 296; DB 2; Length 64;
Best Local Similarity 96.6%; Pred. No. 2.9e-26;
RESULT 702
ID AAY11731 standard; protein; 48 AA.
DE Human 5' EST secreted protein SEQ ID No: 331.
PN WO9906550-A2.
PD 11-FEB-1999.
PA (GEST) GENSET.
Query Match 34.9%; Score 225; DB 2; Length 48;
Best Local Similarity 97.9%; Pred. No. 3.4e-18;
RESULT 703
ID ADY30565 standard; protein; 57 AA.
DE Human splice variant protein expressed in ovary cells DEX0487_006.aa.1.
PN WO2005017102-A2.
PD 24-FEB-2005.
PA (DIAD-) DIADEXUS INC.
Query Match 18.6%; Score 119.5; DB 9; Length 57;
Best Local Similarity 61.2%; Pred. No. 6.6e-06;
RESULT 704
ID ADY30567 standard; protein; 98 AA.
DE Human splice variant protein expressed in ovary cells DEX0487_006.aa.2.
PN WO2005017102-A2.
PD 24-FEB-2005.
PA (DIAD-) DIADEXUS INC.
Query Match 18.6%; Score 119.5; DB 9; Length 98;
Best Local Similarity 61.2%; Pred. No. 1.3e-05;
RESULT 705
ID ABO68555 standard; protein; 620 AA.
DE Pseudomonas aeruginosa polypeptide #730.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 13.1%; Score 84.5; DB 7; Length 620;
Best Local Similarity 30.7%; Pred. No. 1.3;
RESULT 706
ID AAU66308 standard; protein; 191 AA.
DE Propionibacterium acnes immunogenic protein #27204.
PN WO200181581-A2.
PD 01-NOV-2001.
PA (CORI-) CORIXA CORP.
Query Match 12.2%; Score 78.5; DB 4; Length 191;
Best Local Similarity 22.4%; Pred. No. 1.6;

RESULT 707
ID ABM62827 standard; protein; 191 AA.
DE Propionibacterium acnes predicted ORF-encoded polypeptide #27503.
PN WO2003033515-A1.
PD 24-APR-2003.
PA (CORI-) CORIXA CORP.
Query Match 12.2%; Score 78.5; DB 6; Length 191;
Best Local Similarity 22.4%; Pred. No. 1.6;
RESULT 708
ID ABO68031 standard; protein; 629 AA.
DE Pseudomonas aeruginosa polypeptide #206.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 11.5%; Score 74; DB 7; Length 629;
Best Local Similarity 30.2%; Pred. No. 21;
RESULT 709
ID AAP91996 standard; protein; 70 AA.
DE Part of chick vitamin D receptor.
PN WO9909223-A.
PD 05-OCT-1989.
PA (ARCH-) ARCH DEV CORP.
Query Match 11.4%; Score 73.5; DB 1; Length 70;
Best Local Similarity 35.5%; Pred. No. 1.8;
RESULT 710
ID AAR43657 standard; protein; 70 AA.
DE Chicken vitamin D receptor.
PN US5260199-A.
PD 09-NOV-1993.
PA (WISC) WISCONSIN ALUMNI RES FOUND.
Query Match 11.4%; Score 73.5; DB 2; Length 70;
Best Local Similarity 35.5%; Pred. No. 1.8;
RESULT 711
ID ABO79771 standard; protein; 724 AA.
DE Pseudomonas aeruginosa polypeptide #11946.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 11.3%; Score 72.5; DB 7; Length 724;
Best Local Similarity 28.4%; Pred. No. 38;
RESULT 712
ID ADB64837 standard; protein; 752 AA.
DE Human protein encoded by clone OCBF20166900.
PN EPI308459-A2.
PD 07-MAY-2003.
PA (HELI-) HELIX RES INST.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 11.3%; Score 72.5; DB 7; Length 752;
Best Local Similarity 28.0%; Pred. No. 39;
RESULT 713
ID ADE54405 standard; protein; 3313 AA.
DE Rat Protein BAA32459, SEQ ID NO 208.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 11.3%; Score 72.5; DB 7; Length 3313;
Best Local Similarity 27.6%; Pred. No. 2.3e+02;
RESULT 714
ID ADE54409 standard; protein; 3313 AA.
DE Rat Protein BAA32459, SEQ ID NO 212.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 11.3%; Score 72.5; DB 7; Length 3313;
Best Local Similarity 27.6%; Pred. No. 2.3e+02;
RESULT 715
ID ADN49433 standard; protein; 3313 AA.
DE Rat seven-pass transmembrane receptor protein.
PN US2004086931-A1.
PD 06-MAY-2004.
PA (SPAD/) SPADERNA S K.

PA (QUIN/) QUINN K E.
PA (SHIM/) SHIMKETS R A.
PA (PADI/) PADIGARU M.
PA (SPYT/) SPYTEK K A.
Query Match 11.3%; Score 72.5; DB 8; Length 3313;
Best Local Similarity 27.6%; Pred. No. 2.3e+02;
RESULT 716
ID ABO70512 standard; protein; 689 AA.
DE Pseudomonas aeruginosa polypeptide #2687.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 11.2%; Score 72; DB 7; Length 689;
Best Local Similarity 40.5%; Pred. No. 41;
RESULT 717
ID AAO21337 standard; protein; 108 AA.
DE Arabidopsis thaliana KCP-like protein, SEQ ID NO 92.
PN WO200222821-A2.
PD 21-MAR-2002.
PA (PION-) PIONEER HI-BRED INT INC.
Query Match 11.1%; Score 71.5; DB 5; Length 108;
Best Local Similarity 25.9%; Pred. No. 5.1;
RESULT 718
ID ADG74889 standard; protein; 108 AA.
DE Plant developmental pathway modulation-related RKS/ELS ligand protein 10.
PN EPI382682-A2.
PD 21-JAN-2004.
PA (EXPR-) EXPRESSIVE RES BV.
Query Match 11.1%; Score 71.5; DB 8; Length 108;
Best Local Similarity 25.9%; Pred. No. 5.1;
RESULT 719
ID AEA49162 standard; protein; 651 AA.
DE L. rhamosus polypeptide #26.
PN WO2005036801-A1.
PD 23-JUN-2005.
PA (GENE-) GENESIS RES & DEV CORP LTD.
PA (FONT-) FONTERRA COOP GROUP LTD.
Query Match 11.1%; Score 71.5; DB 9; Length 651;
Best Local Similarity 23.8%; Pred. No. 43;
RESULT 720
ID AED03570 standard; protein; 651 AA.
DE L. rhamosus HexB protein SEQ ID NO:106.
PN US2005020437-A1.
PD 15-SEP-2005.
PA (GENE-) GENESIS RES & DEV CORP LTD.
PA (VIAL-) VIALACTIA BIOSCIENCES NZ LTD.
Query Match 11.1%; Score 71.5; DB 9; Length 651;
Best Local Similarity 23.8%; Pred. No. 43;
RESULT 721
ID ADX69288 standard; protein; 188 AA.
DE Human VEGF-B.
PN WO2005016963-A2.
PD 24-FEB-2005.
PA (LUDW-) LUDWIG INST CANCER RES.
PA (LICN) LICENTIA LTD.
Query Match 11.0%; Score 71; DB 9; Length 188;
Best Local Similarity 29.7%; Pred. No. 11;
RESULT 722
ID ADX68179 standard; protein; 249 AA.
DE Plant full length insert polypeptide seqid 39022.
PN US2004034888-A1.
PD 19-FEB-2004.
PA (LIUJ/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABA/) TABASKA J E.
PA (CAOY/) CAO Y.
Query Match 11.0%; Score 71; DB 8; Length 249;
Best Local Similarity 29.9%; Pred. No. 16;
RESULT 723
ID ABG25331 standard; protein; 330 AA.
DE Novel human diagnostic protein #25322.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 11.0%; Score 71; DB 4; Length 330;
Best Local Similarity 29.8%; Pred. No. 22;
RESULT 724
ID ADX89286 standard; protein; 330 AA.
DE Plant full length insert polypeptide seqid 51950.
PN US2004034888-A1.
PD 19-FEB-2004.
PA (LIUJ/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABA/) TABASKA J E.
PA (CAOY/) CAO Y.
Query Match 11.0%; Score 71; DB 8; Length 330;
Best Local Similarity 29.9%; Pred. No. 22;
RESULT 725
ID ADY04494 standard; protein; 330 AA.
DE Plant full length insert polypeptide seqid 60309.
PN US2004034888-A1.
PD 19-FEB-2004.
PA (LIUJ/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABA/) TABASKA J E.
PA (CAOY/) CAO Y.
Query Match 11.0%; Score 71; DB 8; Length 330;
Best Local Similarity 29.9%; Pred. No. 22;
RESULT 726
ID ADY06784 standard; protein; 351 AA.
DE Plant full length insert polypeptide seqid 62599.
PN US2004034888-A1.
PD 19-FEB-2004.
PA (LIUJ/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABA/) TABASKA J E.
PA (CAOY/) CAO Y.
Query Match 11.0%; Score 71; DB 8; Length 351;
Best Local Similarity 29.9%; Pred. No. 24;
RESULT 727
ID ADX77174 standard; protein; 356 AA.
DE Plant full length insert polypeptide seqid 46540.
PN US2004034888-A1.
PD 19-FEB-2004.
PA (LIUJ/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABA/) TABASKA J E.
PA (CAOY/) CAO Y.
Query Match 11.0%; Score 71; DB 8; Length 356;
Best Local Similarity 29.9%; Pred. No. 24;
RESULT 728
ID ADX68580 standard; protein; 604 AA.
DE Plant full length insert polypeptide seqid 39423.
PN US2004034888-A1.
PD 19-FEB-2004.
PA (LIUJ/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABA/) TABASKA J E.
PA (CAOY/) CAO Y.
Query Match 11.0%; Score 71; DB 8; Length 604;
Best Local Similarity 33.3%; Pred. No. 45;
RESULT 729
ID ADX95182 standard; protein; 777 AA.
DE Plant full length insert polypeptide seqid 57846.

PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 10.9%; Score 70.5; DB 7; Length 420;
Best Local Similarity 24.8%; Pred. No. 34;
RESULT 738
ID ABG61841 standard; protein; 117 AA.
DE Prostate cancer-associated protein #42.
PN WO200230268-A2.
PD 18-APR-2002.
PA (CAOY/) CAO Y.
Query Match 11.0%; Score 71; DB 8; Length 777;
Best Local Similarity 33.3%; Pred. No. 61;
RESULT 739
ID AAM50896 standard; protein; 1798 AA.
DE Human laminin B2 chain.
PN WO9815179-A1.
PD 16-APR-1998.
PA (UNIW) UNIV WASHINGTON.
Query Match 11.0%; Score 71; DB 2; Length 1798;
Best Local Similarity 28.4%; Pred. No. 1.7e+02;
RESULT 731
ID ADE60385 standard; protein; 1798 AA.
DE Human protein P55268, SEQ ID NO 6294.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 11.0%; Score 71; DB 7; Length 1798;
Best Local Similarity 28.4%; Pred. No. 1.7e+02;
RESULT 732
ID AAB84634 standard; protein; 3190 AA.
DE Amino acid sequence of CBP protein of Drosophila.
PN WO200147981-A1.
PD 05-JUL-2001.
PA (INSR) INST ROUSSY GUSTAVE.
PA (CNRS) CENT NAT RECH SCI.
Query Match 11.0%; Score 71; DB 4; Length 3190;
Best Local Similarity 26.7%; Pred. No. 3.3e+02;
RESULT 733
ID ABB70437 standard; protein; 3275 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 38103.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 11.0%; Score 71; DB 4; Length 3275;
Best Local Similarity 26.7%; Pred. No. 3.4e+02;
RESULT 734
ID ADK11301 standard; protein; 3275 AA.
DE Drosophila CREB binding protein (p300/CBP) protein.
PN WO2003040301-A2.
PD 15-MAY-2003.
PA (CYCL-) CYCLACEL LTD.
Query Match 11.0%; Score 71; DB 7; Length 3275;
Best Local Similarity 26.7%; Pred. No. 3.4e+02;
RESULT 735
ID AAU83095 standard; protein; 146 AA.
DE Novel secreted protein Z3038GIP.
PN WO200202621-A2.
PD 10-JAN-2002.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 10.9%; Score 70.5; DB 5; Length 146;
Best Local Similarity 32.5%; Pred. No. 9.5;
RESULT 736
ID AED54309 standard; protein; 160 AA.
DE Peanut conglutinin-like allergen.
PN WO2005100995-A2.
PD 27-OCT-2005.
PA (MOUN) MOUNT SINAI SCHOOL MEDICINE.
Query Match 10.9%; Score 70.5; DB 9; Length 160;
Best Local Similarity 22.1%; Pred. No. 11;
RESULT 737
ID ABO78864 standard; protein; 420 AA.
DE Pseudomonas aeruginosa polypeptide #11039.
PN US651795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 10.9%; Score 70.5; DB 7; Length 420;
Best Local Similarity 24.8%; Pred. No. 34;
RESULT 738
ID ABG61841 standard; protein; 117 AA.
DE Prostate cancer-associated protein #42.
PN WO200230268-A2.
PD 18-APR-2002.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 10.9%; Score 70; DB 5; Length 117;
Best Local Similarity 29.5%; Pred. No. 8.4;
RESULT 739
ID ABM82165 standard; protein; 117 AA.
DE Tumour-associated antigenic target (TAT) polypeptide PRO23238, SEQ.5589.
PN WO2004030615-A2.
PD 15-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 10.9%; Score 70; DB 8; Length 117;
Best Local Similarity 29.5%; Pred. No. 8.4;
RESULT 740
ID ADY20193 standard; protein; 117 AA.
DE PRO polypeptide SEQ ID NO 5993.
PN WO2005016962-A2.
PD 24-FEB-2005.
PA (GETH) GENENTECH INC.
Query Match 10.9%; Score 70; DB 9; Length 117;
Best Local Similarity 29.5%; Pred. No. 8.4;
RESULT 741
ID AAY66165 standard; protein; 121 AA.
DE Human bladder tumour EST encoded protein 23.
PN DE19818619-A1.
PD 28-OCT-1999.
PA (META-) METAGEN GES GENOMFORSCHUNG MBH.
Query Match 10.9%; Score 70; DB 2; Length 121;
Best Local Similarity 29.5%; Pred. No. 8.7;
RESULT 742
ID AAS56893 standard; protein; 121 AA.
DE Human prostate cancer antigen protein sequence SEQ ID NO.1471.
PN WO200055174-A1.
PD 21-SEP-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 10.9%; Score 70; DB 3; Length 121;
Best Local Similarity 29.5%; Pred. No. 8.7;
RESULT 743
ID ADR66888 standard; protein; 121 AA.
DE Human prostatic carcinoma derived DNA SEQ ID 186 #4.
PN WO2004076614-A2.
PD 10-SEP-2004.
PA (HINZ/) HINZMANN B.
PA (DAHL/) DAHL E.
PA (ROSE/) ROSENTHAL A.
PA (HERM/) HERMANN K.
PA (PILA/) PILARSKY C.
Query Match 10.9%; Score 70; DB 8; Length 121;
Best Local Similarity 29.5%; Pred. No. 8.7;
RESULT 744
ID ADR65990 standard; protein; 121 AA.
DE Human prostatic carcinoma derived protein SEQ ID 186 #1.
PN WO2004076614-A2.
PD 10-SEP-2004.
PA (HINZ/) HINZMANN B.
PA (DAHL/) DAHL E.
PA (ROSE/) ROSENTHAL A.
PA (HERM/) HERMANN K.
PA (PILA/) PILARSKY C.
Query Match 10.9%; Score 70; DB 8; Length 121;
Best Local Similarity 29.5%; Pred. No. 8.7;
RESULT 745
ID AAY08283 standard; protein; 167 AA.
DE Human growth factor protein fragment VEGF-B167.
PN DE19748734-A1.
PD 06-MAY-1999.

PA (GBFB) GES BIOTECHNOLOGISCHE FORSCHUNG MBH.
 Query Match 10.9%; Score 70; DB 2; Length 167;
 Best Local Similarity 28.4%; Pred. No. 13;
 RESULT 746
 ID AAB24082 standard; protein; 167 AA.
 DE Human PRO834 mature VEGF-B protein sequence SEQ ID NO:69.
 PN WO200053755-A2.
 PD 14-SEP-2000.
 PA (GETH) GENENTECH INC.
 Query Match 10.9%; Score 70; DB 3; Length 167;
 Best Local Similarity 28.4%; Pred. No. 13;
 RESULT 747
 ID AAW00726 standard; protein; 188 AA.
 DE Vascular endothelial growth factor-like protein SOM175-e6.
 PN WO9627007-A1.
 PD 06-SEP-1996.
 PA (AMRA-) AMRAD OPERATIONS PTY LTD.
 Query Match 10.9%; Score 70; DB 2; Length 188;
 Best Local Similarity 28.4%; Pred. No. 15;
 RESULT 748
 ID AAW04829 standard; protein; 188 AA.
 DE Fibrosarcoma vascular endothelial growth factor-B167.
 PN WO9626736-A1.
 PD 06-SEP-1996.
 PA (LUDW-) LUDWIG INST CANCER RES.
 PA (UYHE-) UNIV HELSINKI LICENSING LTD OY.
 Query Match 10.9%; Score 70; DB 2; Length 188;
 Best Local Similarity 28.4%; Pred. No. 15;
 RESULT 749
 ID AAY33442 standard; protein; 188 AA.
 DE Parapox virus VEGF growth factor homologue protein fragment 9.
 PN DE19813774-A1.
 PD 30-SEP-1999.
 PA (PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
 Query Match 10.9%; Score 70; DB 2; Length 188;
 Best Local Similarity 28.4%; Pred. No. 15;
 RESULT 750
 ID AAW80493 standard; protein; 188 AA.
 DE Human vascular endothelial growth factor (VEGF)-B167.
 PN US5840693-A.
 PD 24-NOV-1998.
 PA (LUDW-) LUDWIG INST CANCER RES.
 PA (UYHE-) UNIV HELSINKI LICENSING LTD OY.
 Query Match 10.9%; Score 70; DB 2; Length 188;
 Best Local Similarity 28.4%; Pred. No. 15;
 RESULT 751
 ID AAB10647 standard; protein; 188 AA.
 DE Human VEGF protein.
 PN WO200037641-A2.
 PD 29-JUN-2000.
 PA (JANC) JANSSEN PHARM NV.
 Query Match 10.9%; Score 70; DB 3; Length 188;
 Best Local Similarity 28.4%; Pred. No. 15;
 RESULT 752
 ID AAB24083 standard; protein; 188 AA.
 DE Human PRO834 proVEGF-b protein sequence SEQ ID NO:69.
 PN WO200053755-A2.
 PD 14-SEP-2000.
 PA (GETH) GENENTECH INC.
 Query Match 10.9%; Score 70; DB 3; Length 188;
 Best Local Similarity 28.4%; Pred. No. 15;
 RESULT 753
 ID AAU08440 standard; protein; 188 AA.
 DE Polypeptide for human VEGF-B.
 PN WO200162942-A2.
 PD 30-AUG-2001.
 PA (LUDW-) LUDWIG INST CANCER RES.
 PA (LICN) LICENTIA LTD.
 Query Match 10.9%; Score 70; DB 4; Length 188;
 Best Local Similarity 28.4%; Pred. No. 15;
 RESULT 754
 ID AAG77791 standard; protein; 188 AA.
 DE Human vascular endothelial growth factor B-167 protein (VEGFB-167).

PN WO200164233-A1.
 PD 07-SEP-2001.
 PA (AMRA-) AMRAD OPERATIONS PTY LTD.
 Query Match 10.9%; Score 70; DB 4; Length 188;
 Best Local Similarity 28.4%; Pred. No. 15;
 RESULT 755
 ID AAU83407 standard; protein; 188 AA.
 DE Human vascular endothelial growth factor VEGF-B167.
 PN US6331301-B1.
 PD 18-DEC-2001.
 PA (LUDW-) LUDWIG INST CANCER RES.
 PA (UYHE-) UNIV HELSINKI LICENSING LTD OY.
 Query Match 10.9%; Score 70; DB 5; Length 188;
 Best Local Similarity 28.4%; Pred. No. 15;
 RESULT 756
 ID ABB07952 standard; protein; 188 AA.
 DE Human VEGF-B167 protein.
 PN WO200207514-A2.
 PD 31-JAN-2002.
 PA (LUDW-) LUDWIG INST CANCER RES.
 PA (LICN) LICENTIA LTD.
 Query Match 10.9%; Score 70; DB 5; Length 188;
 Best Local Similarity 28.4%; Pred. No. 15;
 RESULT 757
 ID ADH53391 standard; protein; 188 AA.
 DE Human VEGF-B167 protein.
 PN US2003170253-A1.
 PD 11-SEP-2003.
 PA (UYHE-) UNIV HELSINKI LICENSING LTD.
 Query Match 10.9%; Score 70; DB 7; Length 188;
 Best Local Similarity 28.4%; Pred. No. 15;
 RESULT 758
 ID ADR31420 standard; protein; 188 AA.
 DE Human vascular endothelial growth factor B (VEGF-B) protein #1.
 PN WO2004070018-A2.
 PD 19-AUG-2004.
 PA (LUDW-) LUDWIG INST CANCER RES.
 PA (UYFL-) FLANDERS INTERUNIVERSITY INST BIOTECHNOL.
 Query Match 10.9%; Score 70; DB 8; Length 188;
 Best Local Similarity 28.4%; Pred. No. 15;
 RESULT 759
 ID ADY86488 standard; protein; 188 AA.
 DE Human VEGF - B167 protein, SEQ ID NO: 11.
 PN US2005064493-A1.
 PD 24-MAR-2005.
 PA (LICN) LICENTIA LTD.
 Query Match 10.9%; Score 70; DB 9; Length 188;
 Best Local Similarity 28.4%; Pred. No. 15;
 RESULT 760
 ID AED26693 standard; protein; 188 AA.
 DE Human VEGF-B isoform 1.
 PN WO2005087808-A2.
 PD 22-SEP-2005.
 PA (LUDW-) LUDWIG INST CANCER RES.
 PA (LICN) LICENTIA LTD.
 Query Match 10.9%; Score 70; DB 9; Length 188;
 Best Local Similarity 28.4%; Pred. No. 15;
 RESULT 761
 ID AEF19782 standard; protein; 188 AA.
 DE Human vascular endothelial growth factor B (VEGF-B) isoform 2 protein.
 PN WO2006001888-A2.
 PD 05-JAN-2006.
 PA (ACUI-) ACUIITY PHARM INC.
 Query Match 10.9%; Score 70; DB 10; Length 188;
 Best Local Similarity 28.4%; Pred. No. 15;
 RESULT 762
 ID AAE09217 standard; protein; 189 AA.
 DE Hexa-His-tagged human VEGF-B167 protein.
 PN WO200160861-A1.
 PD 23-AUG-2001.
 PA (AMRA-) AMRAD OPERATIONS PTY LTD.
 Query Match 10.9%; Score 70; DB 4; Length 189;

Best Local Similarity 28.4%; Pred. No. 15;
RESULT 763
ID AEF19783 standard; protein; 192 AA.
DE Human VEGF-B isoform 2 protein with KDEL signal.
PN WO2006001898-A2.
PD 05-JAN-2006.
PA (ACUI-) ACUTY PHARM INC.
Query Match 10.9%; Score 70; DB 10; Length 192;
Best Local Similarity 28.4%; Pred. No. 15;
RESULT 764
ID ABP41889 standard; protein; 216 AA.
DE Human ovarian antigen HHA7P38, SEQ ID NO:3021.
PN WO200200677-A1.
PD 03-JAN-2002.
PA (HUNA-) HUMAN GENOME SCI INC.
Query Match 10.9%; Score 70; DB 5; Length 216;
Best Local Similarity 28.4%; Pred. No. 17;
RESULT 765
ID AAB99889 standard; protein; 491 AA.
DE Physcomitrella patens 78_pproti_092_e12-260rev protein.
PN WO200144276-A2.
PD 21-JUN-2001.
PA (BADI) BASF PLANT SCI GMBH.
Query Match 10.9%; Score 70; DB 4; Length 491;
Best Local Similarity 24.8%; Pred. No. 46;
RESULT 766
ID ABB71263 standard; protein; 543 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 40581.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 10.9%; Score 70; DB 4; Length 543;
Best Local Similarity 26.7%; Pred. No. 52;
RESULT 767
ID ABO81764 standard; protein; 626 AA.
DE Pseudomonas aeruginosa polypeptide #13939.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 10.9%; Score 70; DB 7; Length 626;
Best Local Similarity 29.6%; Pred. No. 62;
RESULT 768
ID AAU29777 standard; protein; 795 AA.
DE Novel human secreted protein #268.
PN WO200179449-A2.
PD 25-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 10.9%; Score 70; DB 4; Length 795;
Best Local Similarity 28.4%; Pred. No. 82;
RESULT 769
ID ADE08948 standard; protein; 935 AA.
DE Novel protein-related contig polypeptide sequence #14.
PN WO2003054152-A2.
PD 03-JUL-2003
PA (HYSE-) HYSEQ INC.
Query Match 10.9%; Score 70; DB 7; Length 935;
Best Local Similarity 28.4%; Pred. No. 1e+02;
RESULT 770
ID ADY09512 standard; protein; 204 AA.
DE Plant full length insert polypeptide seqid 65327.
PN US2004034888-A1.
PD 19-FEB-2004.
PA (LIUJ/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABAS/) TABASKA J E.
PA (CAOY/) CAO Y.
Query Match 10.8%; Score 69.5; DB 8; Length 204;
Best Local Similarity 27.0%; Pred. No. 19;
RESULT 771
ID AAU4571 standard; protein; 361 AA.
DE Propionibacterium acnes immunogenic protein #25467.
PN WO2000181581-A2.
PD 01-NOV-2001.
PA (CORI-) CORIXA CORP.
Query Match 10.8%; Score 69.5; DB 4; Length 361;
Best Local Similarity 28.0%; Pred. No. 37;
RESULT 772
ID ABM61090 standard; protein; 361 AA.
DE Propionibacterium acnes predicted ORF-encoded polypeptide #25766.
PN WO2003033515-A1.
PD 24-APR-2003.
PA (CORI-) CORIXA CORP.
Query Match 10.8%; Score 69.5; DB 6; Length 361;
Best Local Similarity 28.0%; Pred. No. 37;
RESULT 773
ID AAR45335 standard; protein; 461 AA.
DE Thrombomodulin analogue Q336N, Q365E.
PN WO9325675-A1.
PD 23-DEC-1993.
PA (SCHD) SCHERING AG.
Query Match 10.8%; Score 69.5; DB 2; Length 461;
Best Local Similarity 23.5%; Pred. No. 49;
RESULT 774
ID AAR45347 standard; protein; 462 AA.
DE Thrombomodulin analogue 398-417X.
PN WO9325675-A1.
PD 23-DEC-1993.
PA (SCHD) SCHERING AG.
Query Match 10.8%; Score 69.5; DB 2; Length 462;
Best Local Similarity 23.5%; Pred. No. 49;
RESULT 775
ID AAR45349 standard; protein; 462 AA.
DE Thrombomodulin analogue 423-461X.
PN WO9325675-A1.
PD 23-DEC-1993.
PA (SCHD) SCHERING AG.
Query Match 10.8%; Score 69.5; DB 2; Length 462;
Best Local Similarity 23.5%; Pred. No. 49;
RESULT 776
ID AAR45337 standard; protein; 462 AA.
DE Thrombomodulin analogue R456X, H457X.
PN WO9325675-A1.
PD 23-DEC-1993.
PA (SCHD) SCHERING AG.
Query Match 10.8%; Score 69.5; DB 2; Length 462;
Best Local Similarity 23.5%; Pred. No. 49;
RESULT 777
ID AAR45339 standard; protein; 462 AA.
DE Thrombomodulin analogue Q365X, L369X, M388X, R456X, H457X.
PN WO9325675-A1.
PD 23-DEC-1993.
PA (SCHD) SCHERING AG.
Query Match 10.8%; Score 69.5; DB 2; Length 462;
Best Local Similarity 23.5%; Pred. No. 49;
RESULT 778
ID AAR45343 standard; protein; 462 AA.
DE Thrombomodulin analogue D349N.
PN WO9325675-A1.
PD 23-DEC-1993.
PA (SCHD) SCHERING AG.
Query Match 10.8%; Score 69.5; DB 2; Length 462;
Best Local Similarity 23.5%; Pred. No. 49;
RESULT 779
ID AAR45355 standard; protein; 462 AA.
DE Thrombomodulin analogue 408-461X.
PN WO9325675-A1.
PD 23-DEC-1993.
PA (SCHD) SCHERING AG.
Query Match 10.8%; Score 69.5; DB 2; Length 462;
Best Local Similarity 23.5%; Pred. No. 49;
RESULT 780
ID AAR45341 standard; protein; 462 AA.
DE Thrombomodulin analogue 349-461X.
PN WO9325675-A1.

PA	(SCHD) SCHERING AG.
Query Match	10.8%; Score 69.5; DB 2; Length 462;
Best Local Similarity	23.5%; Pred. No. 49;
RESULT 790	
ID	AAR45344 standard; protein; 462 AA.
DE	Thrombomodulin analogue.
PN	WO9325675-A1.
PD	23-DEC-1993.
PA	(SCHD) SCHERING AG.
Query Match	10.8%; Score 69.5; DB 2; Length 462;
Best Local Similarity	23.5%; Pred. No. 49;
RESULT 791	
ID	AAR45340 standard; protein; 463 AA.
DE	Thrombomodulin analogue 336-461X.
PN	WO9325675-A1.
PD	23-DEC-1993.
PA	(SCHD) SCHERING AG.
Query Match	10.8%; Score 69.5; DB 2; Length 463;
Best Local Similarity	23.5%; Pred. No. 49;
RESULT 792	
ID	AAR22032 standard; protein; 475 AA.
DE	Truncated human urinary thrombomodulin.
PN	WO9200325-A.
PD	03-JAN-1992.
PA	(MOCH) MOCHIDA PHARM CO LTD.
Query Match	10.8%; Score 69.5; DB 2; Length 475;
Best Local Similarity	23.5%; Pred. No. 51;
RESULT 793	
ID	AAR78725 standard; protein; 476 AA.
DE	Mature thrombomodulin.
PN	JPO7165796-A.
PD	27-JUN-1995.
PA	(KOWA) KOWA CO LTD.
Query Match	10.8%; Score 69.5; DB 2; Length 476;
Best Local Similarity	23.5%; Pred. No. 51;
RESULT 794	
ID	AAR86377 standard; protein; 476 AA.
DE	Modified thrombomodulin, lacking sialic acid.
PN	JPO7224100-A.
PD	22-AUG-1995.
PA	(KOWA) KOWA CO LTD.
Query Match	10.8%; Score 69.5; DB 2; Length 476;
Best Local Similarity	23.5%; Pred. No. 51;
RESULT 795	
ID	AAR86376 standard; protein; 476 AA.
DE	Modified thrombomodulin, GAG-UTM, lacking sialic acid.
PN	JPO7224100-A.
PD	22-AUG-1995.
PA	(KOWA) KOWA CO LTD.
Query Match	10.8%; Score 69.5; DB 2; Length 476;
Best Local Similarity	23.5%; Pred. No. 51;
RESULT 796	
ID	AAR22013 standard; protein; 480 AA.
DE	Truncated human thrombomodulin encoded by plasmid M13TWD3.
PN	EP474273-A.
PD	11-MAR-1992.
PA	(ASAHI) ASAHI KASEI KOGYO KK.
Query Match	10.8%; Score 69.5; DB 2; Length 480;
Best Local Similarity	23.5%; Pred. No. 51;
RESULT 797	
ID	AAR13877 standard; protein; 486 AA.
DE	Thrombin-binding substances (A) and (B).
PN	EP445681-A.
PD	11-SEP-1991.
PA	(KOWA) KOWA CO LTD.
Query Match	10.8%; Score 69.5; DB 2; Length 486;
Best Local Similarity	23.5%; Pred. No. 52;
RESULT 798	
ID	AAR17531 standard; protein; 490 AA.
DE	Human thrombomodulin (TM) deletion mutant, P490.
PN	WO200198352-A2.
PD	27-DEC-2001.
PA	(SCHD) SCHERING AG.

Query Match 10.8%; Score 69.5; DB 5; Length 490;
Best Local Similarity 23.5%; Pred. No. 53;
RESULT 799
ID AAE23032 standard; protein; 490 AA.
DE Human thrombomodulin deletion mutant #2.
PN WO200217953-A2.
PD 07-MAR-2002.
PA (SCHD) SCHERING AG.
Query Match 10.8%; Score 69.5; DB 5; Length 490;
Best Local Similarity 23.5%; Pred. No. 53;
RESULT 800
ID AAR24400 standard; protein; 494 AA.
DE Recombinant thrombin-binding gene.
PN EP488317-A2.
PD 03-JUN-1992.
PA (KOWA) KOWA CO LTD.
Query Match 10.8%; Score 69.5; DB 2; Length 494;
Best Local Similarity 23.5%; Pred. No. 53;
RESULT 801
ID AAR78727 standard; protein; 494 AA.
DE Thrombomodulin with non-native signal peptide.
PN JP07165796-A.
PD 27-JUN-1995.
PA (KOWA) KOWA CO LTD.
Query Match 10.8%; Score 69.5; DB 2; Length 494;
Best Local Similarity 23.5%; Pred. No. 53;
RESULT 802
ID AAR78726 standard; protein; 494 AA.
DE Thrombomodulin with wild-type signal peptide.
PN JP07165796-A.
PD 27-JUN-1995.
PA (KOWA) KOWA CO LTD.
Query Match 10.8%; Score 69.5; DB 2; Length 494;
Best Local Similarity 23.5%; Pred. No. 53;
RESULT 803
ID AAV67401 standard; protein; 494 AA.
DE Novel sugar chain-bonded thrombomodulin-like peptide #1.
PN WO200000516-A1.
PD 06-JAN-2000.
PA (MOCH) MOCHIDA PHARM CO LTD.
Query Match 10.8%; Score 69.5; DB 3; Length 494;
Best Local Similarity 23.5%; Pred. No. 53;
RESULT 804
ID AAR94607 standard; protein; 497 AA.
DE Human recombinant soluble thrombomodulin for autoantibody detection.
PN WO9610180-A1.
PD 04-APR-1996.
PA (OKLA-) OKLAHOMA MED RES FOUND.
Query Match 10.8%; Score 69.5; DB 2; Length 497;
Best Local Similarity 23.5%; Pred. No. 54;
RESULT 805
ID AAW69520 standard; protein; 497 AA.
DE rSTM protein SEQ ID NO:4 from WO9829453 Claim 14.
PN WO9829453-A1.
PD 09-JUL-1998.
PA (MOCH) MOCHIDA PHARM CO LTD.
Query Match 10.8%; Score 69.5; DB 2; Length 497;
Best Local Similarity 23.5%; Pred. No. 54;
RESULT 806
ID AAR84185 standard; protein; 498 AA.
DE Human derived thrombomodulin.
PN WO9528953-A1.
PD 02-NOV-1995.
PA (ASAH) ASAH KASEI KOGYO KK.
Query Match 10.8%; Score 69.5; DB 2; Length 498;
Best Local Similarity 23.5%; Pred. No. 54;
RESULT 807
ID AAW01600 standard; protein; 498 AA.
DE Thrombomodulin TME456 protein.
PN JP08283174-A.
PD 29-OCT-1996.
PA (ASAH) ASAH KASEI KOGYO KK.
Query Match 10.8%; Score 69.5; DB 2; Length 498;

Best Local Similarity 23.5%; Pred. No. 54;
RESULT 808
ID AAY67402 standard; protein; 498 AA.
DE Novel sugar chain-bonded thrombomodulin-like peptide #2.
PN WO200000516-A1.
PD 06-JAN-2000.
PA (MOCH) MOCHIDA PHARM CO LTD.
Query Match 10.8%; Score 69.5; DB 3; Length 498;
Best Local Similarity 23.5%; Pred. No. 54;
RESULT 809
ID AAY69530 standard; protein; 500 AA.
DE Human thrombomodulin variant, SEQ ID NO:4.
PN JP11341990-A.
PD 14-DEC-1999.
PA (ASAH) ASAH KASEI KOGYO KK.
Query Match 10.8%; Score 69.5; DB 3; Length 500;
Best Local Similarity 23.5%; Pred. No. 54;
RESULT 810
ID AEF31119 standard; protein; 505 AA.
DE Solulin.
PN WO2006005362-A1.
PD 19-JAN-2006.
PA (FRAU) FRAUNHOFER GES FOERDERUNG ANGEWANDTEN EV.
PA (PAIO-) PAION DEUT GMBH.
Query Match 10.8%; Score 69.5; DB 10; Length 505;
Best Local Similarity 23.5%; Pred. No. 55;
RESULT 811
ID AAR10617 standard; protein; 515 AA.
DE Soluble thrombomodulin deriv.
PN EP412841-A.
PD 13-FEB-1991.
PA (ELIL) LILLY & CO ELI.
Query Match 10.8%; Score 69.5; DB 2; Length 515;
Best Local Similarity 23.5%; Pred. No. 56;
RESULT 812
ID AAR22017 standard; protein; 516 AA.
DE Human thrombomodulin (1-516) with Asp367 substituted by Ala.
PN EP474273-A.
PD 11-MAR-1992.
PA (ASAH) ASAH KASEI KOGYO KK.
Query Match 10.8%; Score 69.5; DB 2; Length 516;
Best Local Similarity 23.5%; Pred. No. 56;
RESULT 813
ID AAR22016 standard; protein; 516 AA.
DE Truncated human thrombomodulin encoded by plasmid pSV2TMD1.
PN EP474273-A.
PD 11-MAR-1992.
PA (ASAH) ASAH KASEI KOGYO KK.
Query Match 10.8%; Score 69.5; DB 2; Length 516;
Best Local Similarity 23.5%; Pred. No. 56;
RESULT 814
ID AAR22018 standard; protein; 516 AA.
DE Human thrombomodulin (1-516) with Asp367 substituted by Glu.
PN EP474273-A.
PD 11-MAR-1992.
PA (ASAH) ASAH KASEI KOGYO KK.
Query Match 10.8%; Score 69.5; DB 2; Length 516;
Best Local Similarity 23.5%; Pred. No. 56;
RESULT 815
ID AAY09347 standard; protein; 516 AA.
DE Human thrombomodulin SEQ ID NO:1.
PN WO9918994-A1.
PD 22-APR-1999.
PA (ASAH) ASAH KASEI KOGYO KK.
Query Match 10.8%; Score 69.5; DB 2; Length 516;
Best Local Similarity 23.5%; Pred. No. 56;
RESULT 816
ID AAY09348 standard; protein; 516 AA.
DE Human thrombomodulin SEQ ID NO:2.
PN WO9918994-A1.
PD 22-APR-1999.
PA (ASAH) ASAH KASEI KOGYO KK.
Query Match 10.8%; Score 69.5; DB 2; Length 516;


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ID AAE17596 standard; protein; 557 AA.
DE Human thrombomodulin (TM) mutant, L339A.
PN WO200198352-A2.
PD 27-DEC-2001.
PA (SCHD ) SCHERING AG.
Query Match 10.8%; Score 69.5; DB 5; Length 557;
Best Local Similarity 23.5%; Pred. No. 61;
RESULT 836
ID AAE17591 standard; protein; 557 AA.
DE Human thrombomodulin (TM) mutant, Y358A.
PN WO200198352-A2.
PD 27-DEC-2001.
PA (SCHD ) SCHERING AG.
Query Match 10.8%; Score 69.5; DB 5; Length 557;
Best Local Similarity 23.5%; Pred. No. 61;
RESULT 837
ID AAE17595 standard; protein; 557 AA.
DE Human thrombomodulin (TM) mutant, D338A.
PN WO200198352-A2.
PD 27-DEC-2001.
PA (SCHD ) SCHERING AG.
Query Match 10.8%; Score 69.5; DB 5; Length 557;
Best Local Similarity 23.5%; Pred. No. 61;
RESULT 838
ID AAE17597 standard; protein; 557 AA.
DE Human thrombomodulin (TM) mutant, D349A.
PN WO200198352-A2.
PD 27-DEC-2001.
PA (SCHD ) SCHERING AG.
Query Match 10.8%; Score 69.5; DB 5; Length 557;
Best Local Similarity 23.5%; Pred. No. 61;
RESULT 839
ID AAE17525 standard; protein; 557 AA.
DE Human thrombomodulin (TM) mutant, M388L.
PN WO200198352-A2.
PD 27-DEC-2001.
PA (SCHD ) SCHERING AG.
Query Match 10.8%; Score 69.5; DB 5; Length 557;
Best Local Similarity 23.5%; Pred. No. 61;
RESULT 840
ID AAE17529 standard; protein; 557 AA.
DE Human thrombomodulin (TM) mutant, D341A.
PN WO200198352-A2.
PD 27-DEC-2001.
PA (SCHD ) SCHERING AG.
Query Match 10.8%; Score 69.5; DB 5; Length 557;
Best Local Similarity 23.5%; Pred. No. 61;
RESULT 841
ID AAE17530 standard; protein; 557 AA.
DE Human thrombomodulin (TM) mutant, E343A.
PN WO200198352-A2.
PD 27-DEC-2001.
PA (SCHD ) SCHERING AG.
Query Match 10.8%; Score 69.5; DB 5; Length 557;
Best Local Similarity 23.5%; Pred. No. 61;
RESULT 842
ID AAE17598 standard; protein; 557 AA.
DE Human thrombomodulin (TM) mutant, E357A.
PN WO200198352-A2.
PD 27-DEC-2001.
PA (SCHD ) SCHERING AG.
Query Match 10.8%; Score 69.5; DB 5; Length 557;
Best Local Similarity 23.5%; Pred. No. 61;
RESULT 843
ID AAE17527 standard; protein; 557 AA.
DE Human thrombomodulin (TM) mutant, H457Q.
PN WO200198352-A2.
PD 27-DEC-2001.
PA (SCHD ) SCHERING AG.
Query Match 10.8%; Score 69.5; DB 5; Length 557;
Best Local Similarity 23.5%; Pred. No. 61;
RESULT 844
ID AAE23031 standard; protein; 557 AA.
DE Human thrombomodulin mutant, S474A.
PN WO200217953-A2.
PD 07-MAR-2002.
PA (SCHD ) SCHERING AG.
Query Match 10.8%; Score 69.5; DB 5; Length 557;
Best Local Similarity 23.5%; Pred. No. 61;
RESULT 845
ID AAE23029 standard; protein; 557 AA.
DE Human thrombomodulin mutant, R456G.
PN WO200217953-A2.
PD 07-MAR-2002.
PA (SCHD ) SCHERING AG.
Query Match 10.8%; Score 69.5; DB 5; Length 557;
Best Local Similarity 23.5%; Pred. No. 61;
RESULT 846
ID AAE23030 standard; protein; 557 AA.
DE Human thrombomodulin mutant, H457Q.
PN WO200217953-A2.
PD 07-MAR-2002.
PA (SCHD ) SCHERING AG.
Query Match 10.8%; Score 69.5; DB 5; Length 557;
Best Local Similarity 23.5%; Pred. No. 61;
RESULT 847
ID AAE23028 standard; protein; 557 AA.
DE Human thrombomodulin mutant, M388L.
PN WO200217953-A2.
PD 07-MAR-2002.
PA (SCHD ) SCHERING AG.
Query Match 10.8%; Score 69.5; DB 5; Length 557;
Best Local Similarity 23.5%; Pred. No. 61;
RESULT 848
ID AD065702 standard; protein; 557 AA.
DE Novel human protein sequence #675.
PN EP1440981-A2.
PD 28-JUL-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 10.8%; Score 69.5; DB 8; Length 557;
Best Local Similarity 23.5%; Pred. No. 61;
RESULT 849
ID AB078293 standard; protein; 568 AA.
DE Pseudomonas aeruginosa polypeptide #10468.
PN US6551795-R1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 10.8%; Score 69.5; DB 7; Length 568;
Best Local Similarity 28.8%; Pred. No. 63;
RESULT 850
ID AAP82070 standard; protein; 575 AA.
DE Human thrombomodulin encoded by plasmid p2.1.
PN WO8809811-A.
PD 15-DEC-1988.
PA (NOVO ) NOVO IND AS.
Query Match 10.8%; Score 69.5; DB 1; Length 575;
Best Local Similarity 23.5%; Pred. No. 64;
RESULT 851
ID AAR11534 standard; protein; 575 AA.
DE Human thrombomodulin type II polypeptide.
PN WO9104276-A.
PD 04-APR-1991.
PA (ASAH ) ASahi Kasei Kogyo KK.
Query Match 10.8%; Score 69.5; DB 2; Length 575;
Best Local Similarity 23.5%; Pred. No. 64;
RESULT 852
ID AAR14341 standard; protein; 575 AA.
DE Human thrombomodulin.
PN WO9115514-A.
PD 17-OCT-1991.
PA (SCHD ) SCHERING AG.
Query Match 10.8%; Score 69.5; DB 2; Length 575;
Best Local Similarity 23.5%; Pred. No. 64;
RESULT 853
ID AAR20639 standard; protein; 575 AA.
DE Human urinary thrombomodulin.
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PN WO9200325-A.
PD 09-JAN-1992.
PA (MOCH) MOCHIDA PHARM CO LTD.
Query Match 10.8%; Score 69.5; DB 2; Length 575;
Best Local Similarity 23.5%; Pred. No. 64;
RESULT 854
ID AAR22189 standard; protein; 575 AA.
DE Sequence of thrombomodulin.
PN WO9203149-A.
PD 05-MAR-1992.
PA (BERL-) BERLEX LAB INC.
Query Match 10.8%; Score 69.5; DB 2; Length 575;
Best Local Similarity 23.5%; Pred. No. 64;
RESULT 855
ID AAR31572 standard; protein; 575 AA.
DE Human thrombomodulin.
PN WO9301282-A1.
PD 21-JAN-1993.
PA (BERL-) BERLEX LAB INC.
Query Match 10.8%; Score 69.5; DB 2; Length 575;
Best Local Similarity 23.5%; Pred. No. 64;
RESULT 856
ID AAR41806 standard; peptide; 575 AA.
DE Thrombomodulin.
PN JP05213998-A.
PD 24-AUG-1993.
PA (ASAH) ASAH CHEM IND CO LTD.
Query Match 10.8%; Score 69.5; DB 2; Length 575;
Best Local Similarity 23.5%; Pred. No. 64;
RESULT 857
ID AAR43031 standard; protein; 575 AA.
DE Human thrombomodulin.
PN WO9322447-A1.
PD 11-NOV-1993.
PA (ASAH) ASAH KASRI KOGYO KK.
Query Match 10.8%; Score 69.5; DB 2; Length 575;
Best Local Similarity 23.5%; Pred. No. 64;
RESULT 858
ID AAW73970 standard; protein; 575 AA.
DE Human thrombomodulin protein sequence.
PN US5863760-A.
PD 26-JAN-1999.
PA (SCHD) SCHERING AG.
Query Match 10.8%; Score 69.5; DB 2; Length 575;
Best Local Similarity 23.5%; Pred. No. 64;
RESULT 859
ID AAE17521 standard; protein; 575 AA.
DE Human full-length native thrombomodulin (TM).
PN WO200198352-A2.
PD 27-DEC-2001.
PA (SCHD) SCHERING AG.
Query Match 10.8%; Score 69.5; DB 5; Length 575;
Best Local Similarity 23.5%; Pred. No. 64;
RESULT 860
ID AAE23026 standard; protein; 575 AA.
DE Human thrombomodulin protein.
PN WO200217953-A2.
PD 07-MAR-2002.
PA (SCHD) SCHERING AG.
Query Match 10.8%; Score 69.5; DB 5; Length 575;
Best Local Similarity 23.5%; Pred. No. 64;
RESULT 861
ID ABG72575 standard; protein; 575 AA.
DE Human thrombomodulin protein #2 (CD141).
PN WO200293172-A1.
PD 21-NOV-2002.
PA (MILT-) MILTENY BIOTEC INC.
Query Match 10.8%; Score 69.5; DB 6; Length 575;
Best Local Similarity 23.5%; Pred. No. 64;
RESULT 862
ID ABUS2408 standard; protein; 575 AA.
DE Human GPCR related protein NOV44a.
PN WO200279398-A2.

PD 10-OCT-2002.
PA (CURA-) CURAGEN CORP.
Query Match 10.8%; Score 69.5; DB 6; Length 575;
Best Local Similarity 23.5%; Pred. No. 64;
RESULT 863
ID ABM78950 standard; protein; 575 AA.
DE Breast cancer specific marker under-expressed in breast cancer.
PN WO2003073911-A2.
PD 12-SEP-2003.
PA (GEOU) UNIV GEORGETOWN.
Query Match 10.8%; Score 69.5; DB 7; Length 575;
Best Local Similarity 23.5%; Pred. No. 64;
RESULT 864
ID ADE54760 standard; protein; 575 AA.
DE Human Protein P07204, SEQ ID NO 565.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 10.8%; Score 69.5; DB 7; Length 575;
Best Local Similarity 23.5%; Pred. No. 64;
RESULT 865
ID ADD48168 standard; protein; 575 AA.
DE Human Protein NP_000352, SEQ ID NO 13866.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 10.8%; Score 69.5; DB 7; Length 575;
Best Local Similarity 23.5%; Pred. No. 64;
RESULT 866
ID ADL24151 standard; protein; 575 AA.
DE Human NOVX polypeptide #98.
PN US2004002120-A1.
PD 01-JAN-2004.
PA (TCHE/) TCHERNEV V T.
PA (KEKU/) KEKUDA R.
PA (LIUX/) LIU X.
PA (SPYT/) SPYTEK K A.
PA (PATT/) PATTURAJAN M.
PA (BURG/) BURGESS C E.
PA (VERN/) VERNET C A M.
PA (LILL/) LI L.
PA (GORM/) GORMAN L.
PA (MALX/) MALYANKAR U M.
PA (BOLD/) BOLDOG F L.
PA (GUOX/) GUO X.
PA (SHEN/) SHENOY S G.
PA (PADI/) PADIGARU M.
PA (TAUP/) TAUPIER R J.
PA (MILL/) MILLER C E.
PA (CASN/) CASMAN S J.
PA (PENA/) PENA C E A.
PA (GANG/) GANGOLLI E A.
PA (GUSE/) GUSEV V Y.
PA (SMIT/) SMITHSON G.
PA (ZERR/) ZERRHUSEN B D.
PA (GERL/) GERLACH V.
PA (POCH/) POCHART P F.
PA (FERN/) FERNANDES E R.
PA (SHIM/) SHIMKETS R A.
PA (RASP/) RASTELLI L.
PA (SPAD/) SPADERNA S K.
PA (LARO/) LAROCHELLE W J.
PA (ZHON/) ZHONG M.
PA (KHRA/) KHRAMTSOV N V.
PA (VOSS/) VOSS E Z.
PA (HERR/) HERRMANN J L.
Query Match 10.8%; Score 69.5; DB 8; Length 575;
Best Local Similarity 23.5%; Pred. No. 64;
RESULT 867
ID ADN04006 standard; protein; 575 AA.
DE Antipsoriatic protein sequence #198.

PN WO2004028479-A2.
PD 08-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 69.5; DB 8; Length 575;
Best Local Similarity 23.5%; Pred. No. 64;
RESULT 868
ID ADP12616 standard; protein; 575 AA.
DE Protein encoded by mRNA of the invention #226.
PN WO2004042346-A2.
PD 21-MAY-2004.
PA (EXPR-) EXPRESSION DIAGNOSTICS INC.
Query Match 10.8%; Score 69.5; DB 8; Length 575;
Best Local Similarity 23.5%; Pred. No. 64;
RESULT 869
ID ADO28681 standard; protein; 575 AA.
DE Human thrombomodulin protein SEQ ID NO:110.
PN WO2004044178-A2.
PD 27-MAY-2004.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 69.5; DB 8; Length 575;
Best Local Similarity 23.5%; Pred. No. 64;
RESULT 870
ID ADP79506 standard; protein; 575 AA.
DE Human thrombomodulin.
PN WO2004050844-A2.
PD 17-JUN-2004.
PA (BIOV-) BIOVEC LLC.
Query Match 10.8%; Score 69.5; DB 8; Length 575;
Best Local Similarity 23.5%; Pred. No. 64;
RESULT 871
ID ADR32191 standard; protein; 575 AA.
DE Human thrombomodulin SEQ ID NO:2.
PN WO2004076635-A2.
PD 10-SEP-2004.
PA (BIOV-) BIOVEC BV.
Query Match 10.8%; Score 69.5; DB 8; Length 575;
Best Local Similarity 23.5%; Pred. No. 64;
RESULT 872
ID ADU06321 standard; protein; 575 AA.
DE Novel bronchial cancer-associated human protein seqID545.
PN DE10316701-A1.
PD 04-NOV-2004.
PA (HINZ/) HINZMANN B.
PA (HERM/) HERMANN K.
PA (CAST/) HEIDEN CASTANOS-VELEZ E.
Query Match 10.8%; Score 69.5; DB 8; Length 575;
Best Local Similarity 23.5%; Pred. No. 64;
RESULT 873
ID AEC90400 standard; protein; 575 AA.
DE Human thrombomodulin SEQ ID NO 4.
PN WO2005081926-A2.
PD 09-SEP-2005.
PA (UYEM-) UNIV EMORY.
Query Match 10.8%; Score 69.5; DB 9; Length 575;
Best Local Similarity 23.5%; Pred. No. 64;
RESULT 874
ID ABG72572 standard; protein; 631 AA.
DE Human thrombomodulin protein #1 (CD141).
PN WO200293172-A1.
PD 21-NOV-2002.
PA (MILT-) MILTENYI BIOTECH INC.
Query Match 10.8%; Score 69.5; DB 6; Length 631;
Best Local Similarity 23.5%; Pred. No. 71;
RESULT 875
ID ADN05602 standard; protein; 681 AA.
DE Antipsoriatic protein sequence #966.
PN WO2004028479-A2.
PD 08-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 69.5; DB 8; Length 681;
Best Local Similarity 23.5%; Pred. No. 78;
RESULT 876
ID AAU33693 standard; protein; 200 AA.

DE Pseudomonas aeruginosa cellular proliferation protein #137.
PN WO200170955-A2.
PD 27-SEP-2001.
PA (ELIT-) ELITRA PHARM INC.
Query Match 10.7%; Score 69; DB 4; Length 200;
Best Local Similarity 25.8%; Pred. No. 21;
RESULT 877
ID ABU15655 standard; protein; 200 AA.
DE Protein encoded by Prokaryotic essential gene #1182.
PN WO20027183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 10.7%; Score 69; DB 6; Length 200;
Best Local Similarity 25.8%; Pred. No. 21;
RESULT 878
ID AAG23831 standard; protein; 214 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 27282.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 10.7%; Score 69; DB 3; Length 214;
Best Local Similarity 35.7%; Pred. No. 22;
RESULT 879
ID ABO76121 standard; protein; 229 AA.
DE Pseudomonas aeruginosa polypeptide #8296.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 10.7%; Score 69; DB 7; Length 229;
Best Local Similarity 25.8%; Pred. No. 24;
RESULT 880
ID ABG29324 standard; protein; 234 AA.
DE Novel human diagnostic protein #29315.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 10.7%; Score 69; DB 4; Length 234;
Best Local Similarity 29.1%; Pred. No. 25;
RESULT 881
ID ADC33348 standard; protein; 234 AA.
DE Human novel contig-encoded polypeptide sequence, SEQ ID NO:3430.
PN WO2003029271-A2.
PD 10-APR-2003.
PA (HYSE-) HYSEQ INC.
Query Match 10.7%; Score 69; DB 7; Length 234;
Best Local Similarity 29.1%; Pred. No. 25;
RESULT 882
ID AAG50626 standard; protein; 252 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 64177.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 10.7%; Score 69; DB 3; Length 252;
Best Local Similarity 35.7%; Pred. No. 27;
RESULT 883
ID ABO72740 standard; protein; 261 AA.
DE Pseudomonas aeruginosa polypeptide #4915.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 10.7%; Score 69; DB 7; Length 261;
Best Local Similarity 24.8%; Pred. No. 28;
RESULT 884
ID AAU72792 standard; protein; 271 AA.
DE Human anticancer protein #5.
PN CN1313298-A.
PD 19-SEP-2001.
PA (SHAN-) SHANGHAI INST ONCOLOGY.
Query Match 10.7%; Score 69; DB 5; Length 271;
Best Local Similarity 31.9%; Pred. No. 30;
RESULT 885
ID AAG50625 standard; protein; 293 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 64176.
PN EP1033405-A2.
PD 06-SEP-2000.

Query Match 10.7%; Score 69; DB 3; Length 293;
Best Local Similarity 35.7%; Pred. No. 33;
RESULT 886
ID AAG21634 standard; protein; 299 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 24260.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 10.7%; Score 69; DB 3; Length 299;
Best Local Similarity 31.0%; Pred. No. 33;
RESULT 887
ID AAG50624 standard; protein; 299 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 64175.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 10.7%; Score 69; DB 3; Length 299;
Best Local Similarity 35.7%; Pred. No. 33;
RESULT 888
ID AAG50623 standard; protein; 400 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 64173.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 10.7%; Score 69; DB 3; Length 400;
Best Local Similarity 35.7%; Pred. No. 47;
RESULT 889
ID AAG21633 standard; protein; 400 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 24259.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 10.7%; Score 69; DB 3; Length 400;
Best Local Similarity 31.0%; Pred. No. 47;
RESULT 890
ID AAG21632 standard; protein; 418 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 24258.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 10.7%; Score 69; DB 3; Length 418;
Best Local Similarity 31.0%; Pred. No. 50;
RESULT 891
ID AAG50622 standard; protein; 418 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 64172.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 10.7%; Score 69; DB 3; Length 418;
Best Local Similarity 35.7%; Pred. No. 50;
RESULT 892
ID AAG50621 standard; protein; 420 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 64171.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 10.7%; Score 69; DB 3; Length 420;
Best Local Similarity 35.7%; Pred. No. 50;
RESULT 893
ID ADT55510 standard; protein; 430 AA.
DE Plant polypeptide, SEQ ID 5587.
PN US2004216190-A1.
PD 28-OCT-2004.
PA (KOVA/) KOVALIC D K.
Query Match 10.7%; Score 69; DB 8; Length 430;
Best Local Similarity 35.7%; Pred. No. 52;
RESULT 894
ID AED19037 standard; protein; 454 AA.
DE Cherry salmon fatty acid desaturase gene, SEQ ID NO:2.
PN WO2005094570-A1.
PD 13-OCT-2005.
PA (NISC-) JAPAN SCI & TECHNOLOGY AGENCY.
Query Match 10.7%; Score 69; DB 9; Length 454;
Best Local Similarity 29.3%; Pred. No. 55;
RESULT 895
ID ADB64137 standard; protein; 1077 AA.
DE Human protein encoded by clone CTONG20020950.
PN EP13084459-A2.
PD 07-MAY-2003.
PA (HELI-) HELIX RES INST.

PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 10.7%; Score 69; DB 7; Length 1077;
Best Local Similarity 28.1%; Pred. No. 1.5e+02;
RESULT 896
ID ADD01192 standard; protein; 1081 AA.
DE Human nucleic acid-associated protein NAAP-30 SEQ ID NO:30.
PN WO2003054219-A2.
PD 03-JUL-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 10.7%; Score 69; DB 7; Length 1081;
Best Local Similarity 28.1%; Pred. No. 1.5e+02;
RESULT 897
ID ADX73027 standard; protein; 326 AA.
DE Plant full length insert polypeptide seqid 42393.
PN US2004034888-A1.
PD 19-FEB-2004.
PA (LIUJ/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABA/) TABASKA J E.
PA (CAOY/) CAO Y.
Query Match 10.6%; Score 68.5; DB 8; Length 326;
Best Local Similarity 29.9%; Pred. No. 42;
RESULT 898
ID AAW37261 standard; protein; 356 AA.
DE Rat vitamin D receptor isoform protein (VDR1).
PN WO9747172-A1.
PD 18-DEC-1997.
PA (CHUS) CHUGAI SEIYAKU KK.
Query Match 10.6%; Score 68.5; DB 2; Length 356;
Best Local Similarity 30.1%; Pred. No. 47;
RESULT 899
ID AAW94622 standard; protein; 356 AA.
DE Rat vitamin D receptor isoform protein VDR1.
PN WO9856908-A1.
PD 17-DEC-1998.
PA (CHUS) CHUGAI SEIYAKU KK.
Query Match 10.6%; Score 68.5; DB 2; Length 356;
Best Local Similarity 30.1%; Pred. No. 47;
RESULT 900
ID AAB84255 standard; protein; 376 AA.
DE Amino acid sequence of a human nuclear vitamin D receptor mutant.
PN WO200138393-A1.
PD 31-MAY-2001.
PA (CNRS) CENT NAT RECH SCI.
Query Match 10.6%; Score 68.5; DB 4; Length 376;
Best Local Similarity 30.1%; Pred. No. 50;
RESULT 901
ID ADP05823 standard; protein; 422 AA.
DE Mouse nuclear receptor protein SeqID197.
PN WO2004045369-A2.
PD 03-JUN-2004.
PA (NURA-) NURA INC.
Query Match 10.6%; Score 68.5; DB 8; Length 422;
Best Local Similarity 30.1%; Pred. No. 58;
RESULT 902
ID AAW47509 standard; protein; 423 AA.
DE Rat vitamin D receptor (VDR0).
PN WO9747172-A1.
PD 18-DEC-1997.
PA (CHUS) CHUGAI SEIYAKU KK.
Query Match 10.6%; Score 68.5; DB 2; Length 423;
Best Local Similarity 30.1%; Pred. No. 58;
RESULT 903
ID AAW94623 standard; protein; 423 AA.
DE Rat vitamin D receptor protein VDR0.
PN WO9856908-A1.
PD 17-DEC-1998.
PA (CHUS) CHUGAI SEIYAKU KK.
Query Match 10.6%; Score 68.5; DB 2; Length 423;
Best Local Similarity 30.1%; Pred. No. 58;
RESULT 904

ID AAW68156 standard; protein; 427 AA.
DE Human vitamin D receptor.
PN WO9831835-A1.
PD 23-JUL-1998.
PA (UYNA-) UNIV MARYLAND BALTIMORE.
PA (UYPI-) UNIV PITTSBURGH.
Query Match 10.6%; Score 68.5; DB 2; Length 427;
Best Local Similarity 30.1%; Pred. No. 58;
RESULT 905
ID AAY09064 standard; protein; 427 AA.
DE Human vitamin D receptor (VDR) gene transcript 11 amino acid sequence.
PN WO9916872-A1.
PD 08-APR-1999.
PA (GARV-) GARVAN INST MEDICAL RES.
Query Match 10.6%; Score 68.5; DB 2; Length 427;
Best Local Similarity 30.1%; Pred. No. 58;
RESULT 906
ID AAB84254 standard; protein; 427 AA.
DE Amino acid sequence of a human nuclear vitamin D receptor (VDR).
PN WO200138393-A1.
PD 31-MAY-2001.
PA (CNRS) CENT NAT RECH SCI.
Query Match 10.6%; Score 68.5; DB 4; Length 427;
Best Local Similarity 30.1%; Pred. No. 58;
RESULT 907
ID ADB99956 standard; protein; 427 AA.
DE Human vitamin D nuclear receptor.
PN WO2003041657-A2.
PD 22-MAY-2003.
PA (ISIS-) ISIS PHARM INC.
Query Match 10.6%; Score 68.5; DB 7; Length 427;
Best Local Similarity 30.1%; Pred. No. 58;
RESULT 908
ID ADL63243 standard; protein; 427 AA.
DE Human PRO4854, SEQ ID 445.
PN WO2004024097-A2.
PD 25-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 68.5; DB 8; Length 427;
Best Local Similarity 30.1%; Pred. No. 58;
RESULT 909
ID ADP05821 standard; protein; 427 AA.
DE Human nuclear receptor protein seqId195.
PN WO2004045369-A2.
PD 03-JUN-2004.
PA (NURA-) NURA INC.
Query Match 10.6%; Score 68.5; DB 8; Length 427;
Best Local Similarity 30.1%; Pred. No. 58;
RESULT 910
ID ADP54492 standard; protein; 427 AA.
DE Human PRO protein sequence SEQ ID NO:468.
PN WO2004039956-A2.
PD 13-MAY-2004.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 68.5; DB 8; Length 427;
Best Local Similarity 30.1%; Pred. No. 58;
RESULT 911
ID ADX05510 standard; protein; 427 AA.
DE Cyclin-dependent kinase modulation biomarker SEQ ID NO 75.
PN WO2005012875-A2.
PD 10-FEB-2005.
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
Query Match 10.6%; Score 68.5; DB 9; Length 427;
Best Local Similarity 30.1%; Pred. No. 58;
RESULT 912
ID ADY15298 standard; protein; 427 AA.
DE PRO polypeptide SEQ ID NO 1104.
PN WO2005016962-A2.
PD 24-FEB-2005.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 68.5; DB 9; Length 427;
Best Local Similarity 30.1%; Pred. No. 58;
RESULT 913
ID ADX77856 standard; protein; 849 AA.
DE PRO polypeptide SEQ ID NO 1106.
PN WO2005016962-A2.
PD 24-FEB-2005.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 68.5; DB 9; Length 427;
Best Local Similarity 30.1%; Pred. No. 58;
RESULT 914
ID ADZ21386 standard; protein; 427 AA.
DE Vitamin D receptor.
PN WO2005033291-A2.
PD 14-APR-2005.
PA (UYRP) UNIV ROCHESTER.
Query Match 10.6%; Score 68.5; DB 9; Length 427;
Best Local Similarity 30.1%; Pred. No. 58;
RESULT 915
ID AEC92031 standard; protein; 427 AA.
DE Human vitamin D3 receptor (VDR) protein, SEQ ID: 2.
PN US2005202515-A1.
PD 15-SEP-2005.
PA (AMHP) WYETH.
Query Match 10.6%; Score 68.5; DB 9; Length 427;
Best Local Similarity 30.1%; Pred. No. 58;
RESULT 916
ID AED54296 standard; protein; 427 AA.
DE Human VDR1 receptor polypeptide.
PN WO2005101022-A2.
PD 27-OCT-2005.
PA (FARB) BAYER HEALTHCARE AG.
Query Match 10.6%; Score 68.5; DB 9; Length 427;
Best Local Similarity 30.1%; Pred. No. 58;
RESULT 917
ID AAY09036 standard; protein; 450 AA.
DE Human vitamin D receptor (VDR) gene transcript 9 amino acid sequence.
PN WO9916872-A1.
PD 08-APR-1999.
PA (GARV-) GARVAN INST MEDICAL RES.
Query Match 10.6%; Score 68.5; DB 2; Length 450;
Best Local Similarity 30.1%; Pred. No. 62;
RESULT 918
ID AAY09035 standard; protein; 477 AA.
DE Human vitamin D receptor (VDR) gene transcript 6 amino acid sequence.
PN WO9916872-A1.
PD 08-APR-1999.
PA (GARV-) GARVAN INST MEDICAL RES.
Query Match 10.6%; Score 68.5; DB 2; Length 477;
Best Local Similarity 30.1%; Pred. No. 67;
RESULT 919
ID ADJ33699 standard; protein; 213 AA.
DE Protein of the invention SEQ ID NO:676.
PN WO200187917-A1.
PD 22-NOV-2001.
PA (HYSE-) HYSEQ INC.
Query Match 10.6%; Score 68; DB 5; Length 213;
Best Local Similarity 24.4%; Pred. No. 29;
RESULT 920
ID ABO77058 standard; protein; 451 AA.
DE Pseudomonas aeruginosa polypeptide #9233.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 10.6%; Score 68; DB 7; Length 451;
Best Local Similarity 28.8%; Pred. No. 71;
RESULT 921
ID ABO73678 standard; protein; 613 AA.
DE Pseudomonas aeruginosa polypeptide #5853.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 10.6%; Score 68; DB 7; Length 613;
Best Local Similarity 31.0%; Pred. No. 1e+02;
RESULT 922
ID ADX77856 standard; protein; 849 AA.

DE Plant full length insert polypeptide seqid 47222.
PN US2004034888-A1.
PD 19-FEB-2004.
PA (LIUJ/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABA/) TABASKA J E.
PA (CAOV/) CAO Y.
Query Match 10.6%; Score 68; DB 8; Length 849;
Best Local Similarity 25.0%; Pred. No. 1.5e+02;
RESULT 923
ID ABO73085 standard; protein; 863 AA.
DE Pseudomonas aeruginosa polypeptide #5260.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 10.6%; Score 68; DB 7; Length 863;
Best Local Similarity 27.1%; Pred. No. 1.5e+02;
RESULT 924
ID ADZ21348 standard; protein; 70 AA.
DE Vitamin D receptor DNA binding domain.
PN WO2005033291-A2.
PD 14-APR-2005.
PA (UYRP) UNIV ROCHESTER.
Query Match 10.5%; Score 67.5; DB 9; Length 70;
Best Local Similarity 32.3%; Pred. No. 8.8;
RESULT 925
ID ABO76684 standard; protein; 521 AA.
DE Pseudomonas aeruginosa polypeptide #8859.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 10.5%; Score 67.5; DB 7; Length 521;
Best Local Similarity 28.3%; Pred. No. 97;
RESULT 926
ID ABO67969 standard; protein; 690 AA.
DE Pseudomonas aeruginosa polypeptide #144.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 10.5%; Score 67.5; DB 7; Length 690;
Best Local Similarity 28.7%; Pred. No. 1.4e+02;
RESULT 927
ID ABM89053 standard; protein; 1076 AA.
DE Rice abiotic stress responsive polypeptide SEQ ID NO:7299.
PN WO2003008540-A2.
PD 30-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 10.5%; Score 67.5; DB 7; Length 1076;
Best Local Similarity 22.6%; Pred. No. 2.3e+02;
RESULT 928
ID ABO69387 standard; protein; 285 AA.
DE Pseudomonas aeruginosa polypeptide #1562.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 10.4%; Score 67; DB 7; Length 285;
Best Local Similarity 24.2%; Pred. No. 54;
RESULT 929
ID RAO16407 standard; protein; 426 AA.
DE Human nucleic acid-associated protein (NAAP) - SEQ ID NO 4.
PN WO2003000864-A2.
PD 03-JAN-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 10.4%; Score 67; DB 6; Length 426;
Best Local Similarity 26.8%; Pred. No. 87;
RESULT 930
ID ABE85564 standard; protein; 454 AA.
DE PUFa pathway enzyme delta-5 desaturase SEQ ID NO 106.
PN WO2005118814-A2.
PD 15-DEC-2005.
PA (FLUX-) FLUXOME SCI AS.

Query Match 10.4%; Score 67; DB 10; Length 454;
Best Local Similarity 29.5%; Pred. No. 94;
RESULT 931
ID ADS44937 standard; protein; 475 AA.
DE Bacterial polypeptide #23367.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOV/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 10.4%; Score 67; DB 8; Length 475;
Best Local Similarity 22.5%; Pred. No. 99;
RESULT 932
ID AAU28084 standard; protein; 529 AA.
DE Novel human secretory protein, Seq ID No 253.
PN WO200166689-A2.
PD 13-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 10.4%; Score 67; DB 4; Length 529;
Best Local Similarity 26.8%; Pred. No. 1.1e+02;
RESULT 933
ID ABO73410 standard; protein; 209 AA.
DE Pseudomonas aeruginosa polypeptide #5585.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 10.3%; Score 66.5; DB 7; Length 209;
Best Local Similarity 31.6%; Pred. No. 42;
RESULT 934
ID ABO69685 standard; protein; 333 AA.
DE Pseudomonas aeruginosa polypeptide #1860.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 10.3%; Score 66.5; DB 7; Length 333;
Best Local Similarity 22.8%; Pred. No. 74;
RESULT 935
ID AAR07294 standard; protein; 418 AA.
DE Chicken ovalbumin upstream promoter transcription factor.
PN EP32691-A.
PD 17-OCT-1990.
PA (BAYU) BAYLOR COLLEGE MEDICINE.
PA (OMAL/) OMALLEY B W.
Query Match 10.3%; Score 66.5; DB 2; Length 418;
Best Local Similarity 26.5%; Pred. No. 97;
RESULT 936
ID ADE62161 standard; protein; 419 AA.
DE Rat Protein AAA83437, SEQ ID NO 8090.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 10.3%; Score 66.5; DB 7; Length 419;
Best Local Similarity 26.5%; Pred. No. 97;
RESULT 937
ID ADE62157 standard; protein; 419 AA.
DE Rat Protein AAA83437, SEQ ID NO 8086.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 10.3%; Score 66.5; DB 7; Length 419;
Best Local Similarity 26.5%; Pred. No. 97;
RESULT 938
ID ADP05633 standard; protein; 422 AA.
DE Mouse nuclear receptor protein SeqID7.
PN WO2004045369-A2.
PD 03-JUN-2004.
PA (NURA-) NURA INC.
Query Match 10.3%; Score 66.5; DB 8; Length 422;
Best Local Similarity 26.5%; Pred. No. 98;

RESULT 939
ID AAU84296 standard; protein; 423 AA.
DE Human endometrial cancer related protein, NR2F1.
PN WO200209573-A2.
PD 07-FEB-2002.
PA (BGHM) BRIGHAM & WOMENS HOSPITAL INC.
Query Match 10.3%; Score 66.5; DB 5; Length 423;
Best Local Similarity 26.5%; Pred. No. 98;
RESULT 940
ID ADE62163 standard; protein; 423 AA.
DE Human Protein NP_005645, SEQ ID NO 8092.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 10.3%; Score 66.5; DB 7; Length 423;
Best Local Similarity 26.5%; Pred. No. 98;
RESULT 941
ID ADE62159 standard; protein; 423 AA.
DE Human Protein NP_005645, SEQ ID NO 8088.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 10.3%; Score 66.5; DB 7; Length 423;
Best Local Similarity 26.5%; Pred. No. 98;
RESULT 942
ID ADN95495 standard; protein; 423 AA.
DE Human BEC/LEC-related protein sequence SeqID418.
PN WO2003080640-A1.
PD 02-OCT-2003.
PA (LUDW-) LUDWIG INST CANCER RES.
PA (LICN) LICENTIA LTD.
Query Match 10.3%; Score 66.5; DB 7; Length 423;
Best Local Similarity 26.5%; Pred. No. 98;
RESULT 943
ID ADP05631 standard; protein; 423 AA.
DE Human nuclear receptor protein seqIDS.
PN WO2004045369-A2.
PD 03-JUN-2004.
PA (NURA-) NURA INC.
Query Match 10.3%; Score 66.5; DB 8; Length 423;
Best Local Similarity 26.5%; Pred. No. 98;
RESULT 944
ID ADY34352 standard; protein; 423 AA.
DE Human nuclear hormone receptor NR2F1.
PN WO2005017112-A2.
PD 24-FEB-2005.
PA (IMMU-) IMMUSOL INC.
Query Match 10.3%; Score 66.5; DB 9; Length 423;
Best Local Similarity 26.5%; Pred. No. 98;
RESULT 945
ID AD209795 standard; protein; 423 AA.
DE Human breast cancer marker NR2F1 protein.
PN EP1522594-A2.
PD 13-APR-2005.
PA (FARB) BAYER HEALTHCARE AG.
Query Match 10.3%; Score 66.5; DB 9; Length 423;
Best Local Similarity 26.5%; Pred. No. 98;
RESULT 946
ID AEC01577 standard; protein; 423 AA.
DE Human nuclear receptor subfamily 2 group F member 1 protein, SEQ ID: 10.
PN US2005176030-A1.
PD 11-AUG-2005.
PA (GANL/) GAN L.
PA (GONZ/) GONZALEZ-ZULUETA M.
PA (YESS/) YE S.
PA (URFE/) URFER R.
PA (NIKO/) NIKOLICH K.
Query Match 10.3%; Score 66.5; DB 9; Length 423;
Best Local Similarity 26.5%; Pred. No. 98;
RESULT 947
ID AAU45310 standard; protein; 913 AA.

DE Propionibacterium acnes immunogenic protein #6206.
PN WO200181581-A2.
PD 01-NOV-2001.
PA (CORI-) CORIXA CORP.
Query Match 10.3%; Score 66.5; DB 4; Length 913;
Best Local Similarity 28.4%; Pred. No. 2.5e+02;
RESULT 948
ID ABM41829 standard; protein; 913 AA.
DE Propionibacterium acnes predicted ORF-encoded polypeptide #6505.
PN WO2003033515-A1.
PD 24-APR-2003.
PA (CORI-) CORIXA CORP.
Query Match 10.3%; Score 66.5; DB 6; Length 913;
Best Local Similarity 28.4%; Pred. No. 2.5e+02;
RESULT 949
ID AAP81770 standard; protein; 3210 AA.
DE Deduced sequence encoded by middle reading frame of cDNA clone HIV-2
SBL/ISV of HIV related retrovirus strain.
PN WO8808449-A.
PD 03-NOV-1988.
PA (SBL-) SBL STATENS BAKTERI.
PA (STAT-) STATENS BAKTERIOLOGISKA LAB.
PA (STAT-) STATENS BAKTERIOLOGISKA LAB.
Query Match 10.3%; Score 66.5; DB 1; Length 3210;
Best Local Similarity 26.4%; Pred. No. 1.1e+03;
RESULT 950
ID ADO29248 standard; protein; 3301 AA.
DE Mouse GPCR CELSR3, SEQ ID NO:349.
PN WO2004040000-A2.
PD 13-MAY-2004.
PA (PRIM-) PRIMAL INC.
Query Match 10.3%; Score 66.5; DB 8; Length 3301;
Best Local Similarity 26.8%; Pred. No. 1.1e+03;
RESULT 951
ID AAU48730 standard; protein; 162 AA.
DE Propionibacterium acnes immunogenic protein #9626.
PN WO200181581-A2.
PD 01-NOV-2001.
PA (CORI-) CORIXA CORP.
Query Match 10.2%; Score 66; DB 4; Length 162;
Best Local Similarity 35.1%; Pred. No. 36;
RESULT 952
ID ABM45249 standard; protein; 162 AA.
DE Propionibacterium acnes predicted ORF-encoded polypeptide #9925.
PN WO2003033515-A1.
PD 24-APR-2003.
PA (CORI-) CORIXA CORP.
Query Match 10.2%; Score 66; DB 6; Length 162;
Best Local Similarity 35.1%; Pred. No. 36;
RESULT 953
ID AB083736 standard; protein; 178 AA.
DE Pseudomonas aeruginosa polypeptide #15911.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 10.2%; Score 66; DB 7; Length 178;
Best Local Similarity 29.1%; Pred. No. 40;
RESULT 954
ID AB076457 standard; protein; 518 AA.
DE Pseudomonas aeruginosa polypeptide #8632.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 10.2%; Score 66; DB 7; Length 518;
Best Local Similarity 24.8%; Pred. No. 1.4e+02;
RESULT 955
ID AAM13905 standard; protein; 1539 AA.
DE Human SMCY protein.
PN WO9710267-A1.
PD 20-MAR-1997.
PA (PROM-) PROMEGA CORP.
Query Match 10.2%; Score 66; DB 2; Length 1539;
Best Local Similarity 26.7%; Pred. No. 5.2e+02;

RESULT 956
ID ADM33397 standard; protein; 1539 AA.
DE Human PRO71282 protein SEQ ID NO:14.
PN WO2004028447-A2.
PD 08-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 66; DB 8; Length 1539;
Best Local Similarity 26.7%; Pred. No. 5.2e+02;
RESULT 957
ID ADP12536 standard; protein; 1539 AA.
DE Protein encoded by mRNA of the invention #146.
PN WO2004042346-A2.
PD 21-MAY-2004.
PA (EXPR-) EXPRESSION DIAGNOSTICS INC.
Query Match 10.2%; Score 66; DB 8; Length 1539;
Best Local Similarity 26.7%; Pred. No. 5.2e+02;
RESULT 958
ID AEA24048 standard; protein; 1539 AA.
DE Human PRO polypeptide SEQ ID NO 590.
PN WO2005051988-A2.
PD 09-JUN-2005.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 66; DB 9; Length 1539;
Best Local Similarity 26.7%; Pred. No. 5.2e+02;
RESULT 959
ID AAO21341 standard; protein; 106 AA.
DE Arabidopsis thaliana KCP-like protein, SEQ ID NO 96.
PN WO200222821-A2.
PD 21-MAR-2002.
PA (PION-) PIONEER HI-BRED INT INC.
Query Match 10.2%; Score 65.5; DB 5; Length 106;
Best Local Similarity 21.2%; Pred. No. 25;
RESULT 960
ID ABO76562 standard; protein; 201 AA.
DE Pseudomonas aeruginosa polypeptide #8737.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 10.2%; Score 65.5; DB 7; Length 201;
Best Local Similarity 25.0%; Pred. No. 53;
RESULT 961
ID ABG29970 standard; protein; 222 AA.
DE Novel human diagnostic protein #29961.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 10.2%; Score 65.5; DB 4; Length 222;
Best Local Similarity 23.0%; Pred. No. 59;
RESULT 962
ID ABO76208 standard; protein; 279 AA.
DE Pseudomonas aeruginosa polypeptide #8383.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 10.2%; Score 65.5; DB 7; Length 279;
Best Local Similarity 28.0%; Pred. No. 78;
RESULT 963
ID ADX80612 standard; protein; 326 AA.
DE Plant full length insert polypeptide seqid 49978.
PN US2004034888-A1.
PD 19-FEB-2004.
PA (LIUJ/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABA/) TABASKA J E.
PA (CAOV/) CAO Y.
Query Match 10.2%; Score 65.5; DB 8; Length 326;
Best Local Similarity 28.7%; Pred. No. 94;
RESULT 964
ID ABO74508 standard; protein; 342 AA.
DE Pseudomonas aeruginosa polypeptide #6683.
PN US6551795-B1.

PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 10.2%; Score 65.5; DB 7; Length 342;
Best Local Similarity 26.9%; Pred. No. 1e+02;
RESULT 965
ID ADQ96186 standard; protein; 420 AA.
DE T cell activation associated protein #182.
PN WO2004058805-A2.
PD 15-JUL-2004.
PA (ASAH-) ASAH KASEI PHARMA CORP.
Query Match 10.2%; Score 65.5; DB 8; Length 420;
Best Local Similarity 25.0%; Pred. No. 1.3e+02;
RESULT 966
ID ADQ96188 standard; protein; 420 AA.
DE T cell activation associated protein #183.
PN WO2004058805-A2.
PD 15-JUL-2004.
PA (ASAH-) ASAH KASEI PHARMA CORP.
Query Match 10.2%; Score 65.5; DB 8; Length 420;
Best Local Similarity 25.0%; Pred. No. 1.3e+02;
RESULT 967
ID RAY02383 standard; protein; 704 AA.
DE Polypeptide identified by the signal sequence trap method.
PN WO9918126-A1.
PD 15-APR-1999.
PA (ONOV) ONO PHARM CO LTD.
Query Match 10.2%; Score 65.5; DB 2; Length 704;
Best Local Similarity 25.0%; Pred. No. 2.4e+02;
RESULT 968
ID AAY15223 standard; protein; 706 AA.
DE Human receptor protein (HURP) 2 amino acid sequence.
PN WO9941375-A2.
PD 19-AUG-1999.
PA (INCY-) INCYTE PHARM INC.
Query Match 10.2%; Score 65.5; DB 2; Length 706;
Best Local Similarity 25.0%; Pred. No. 2.4e+02;
RESULT 969
ID ABUS6726 standard; protein; 706 AA.
DE Lung cancer-associated polypeptide #319.
PN WO200286443-A2.
PD 31-OCT-2002.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 10.2%; Score 65.5; DB 6; Length 706;
Best Local Similarity 25.0%; Pred. No. 2.4e+02;
RESULT 970
ID ABUS5901 standard; protein; 706 AA.
DE Human protein Frizzled-6.
PN WO200277204-A2.
PD 03-OCT-2002.
PA (AXOR-) AXORDIA LTD.
Query Match 10.2%; Score 65.5; DB 6; Length 706;
Best Local Similarity 25.0%; Pred. No. 2.4e+02;
RESULT 971
ID AAE34055 standard; protein; 706 AA.
DE FZD6 protein.
PN WO200290992-A2.
PD 14-NOV-2002.
PA (AXOR-) AXORDIA LTD.
Query Match 10.2%; Score 65.5; DB 6; Length 706;
Best Local Similarity 25.0%; Pred. No. 2.4e+02;
RESULT 972
ID ADC86003 standard; protein; 706 AA.
DE Human GPCR protein SEQ ID NO:456.
PN EP1270724-A2.
PD 02-JAN-2003.
PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
PA (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.
Query Match 10.2%; Score 65.5; DB 7; Length 706;
Best Local Similarity 25.0%; Pred. No. 2.4e+02;
RESULT 973
ID ADG74267 standard; protein; 706 AA.
DE Human frizzled protein, SEQ ID NO 52.
PN WO200292635-A2.

PD 21-NOV-2002.
PA (RECG) UNIV CALIFORNIA.
Query Match 10.2%; Score 65.5; DB 7; Length 706;
Best Local Similarity 25.0%; Pred. No. 2.4e+02;
RESULT 974
ID ADN39178 standard; protein; 706 AA.
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:496.
PN WO2003042661-A2.
PD 22-MAY-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 10.2%; Score 65.5; DB 7; Length 706;
Best Local Similarity 25.0%; Pred. No. 2.4e+02;
RESULT 975
ID ADN40014 standard; protein; 706 AA.
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:C384.
PN WO2003042661-A2.
PD 22-MAY-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 10.2%; Score 65.5; DB 7; Length 706;
Best Local Similarity 25.0%; Pred. No. 2.4e+02;
RESULT 976
ID ADO29335 standard; protein; 706 AA.
DE Human GPCR FZD6, SEQ ID NO:436.
PN WO2004040000-A2.
PD 13-MAY-2004.
PA (PRIM-) PRIMAL INC.
Query Match 10.2%; Score 65.5; DB 8; Length 706;
Best Local Similarity 25.0%; Pred. No. 2.4e+02;
RESULT 977
ID ADO22262 standard; protein; 706 AA.
DE Human FZD6 protein (homologue of Drosophila frizzled).
PN WO2004042028-A2.
PD 21-MAY-2004.
PA (RECG) UNIV CALIFORNIA.
Query Match 10.2%; Score 65.5; DB 8; Length 706;
Best Local Similarity 25.0%; Pred. No. 2.4e+02;
RESULT 978
ID ADO96190 standard; protein; 706 AA.
DE T cell activation associated protein #184.
PN WO2004058805-A2.
PD 15-JUL-2004.
PA (ASAH-) ASAH KASEI PHARMA CORP.
Query Match 10.2%; Score 65.5; DB 8; Length 706;
Best Local Similarity 25.0%; Pred. No. 2.4e+02;
RESULT 979
ID ADO96192 standard; protein; 706 AA.
DE T cell activation associated protein #185.
PN WO2004058805-A2.
PD 15-JUL-2004.
PA (ASAH-) ASAH KASEI PHARMA CORP.
Query Match 10.2%; Score 65.5; DB 8; Length 706;
Best Local Similarity 25.0%; Pred. No. 2.4e+02;
RESULT 980
ID ADY15220 standard; protein; 706 AA.
DE PRO polypeptide SEQ ID NO 1026.
PN WO2005016962-A2.
PD 24-FEB-2005.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 65.5; DB 9; Length 706;
Best Local Similarity 25.0%; Pred. No. 2.4e+02;
RESULT 981
ID ADY19746 standard; protein; 706 AA.
DE PRO polypeptide SEQ ID NO 5552.
PN WO2005016962-A2.
PD 24-FEB-2005.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 65.5; DB 9; Length 706;
Best Local Similarity 25.0%; Pred. No. 2.4e+02;
RESULT 982
ID AEA51354 standard; protein; 706 AA.
DE Human protein expressed during angiogenesis, NOC8003L17.
PN WO2005054426-A2.
PD 16-JUN-2005.

PA (ANGI-) ANGIOGENETICS SWEDEN AB.
Query Match 10.2%; Score 65.5; DB 9; Length 706;
Best Local Similarity 25.0%; Pred. No. 2.4e+02;
RESULT 983
ID AEB28130 standard; protein; 706 AA.
DE Human Frizzled receptor FZD6 protein.
PN WO2005063966-A2.
PD 14-JUL-2005.
PA (AXAR-) AXARON BIOSCIENCE AG.
Query Match 10.2%; Score 65.5; DB 9; Length 706;
Best Local Similarity 25.0%; Pred. No. 2.4e+02;
RESULT 984
ID ABM69665 standard; protein; 137 AA.
DE Photorehabitus luminescens protein sequence #2762.
PN WO200294867-A2.
PD 28-NOV-2002.
PA (INSP) INST PASTEUR.
PA (CNRS) CNRS CENT NAT RECH SCI.
Query Match 10.1%; Score 65; DB 6; Length 137;
Best Local Similarity 24.3%; Pred. No. 38;
RESULT 985
ID AAB94570 standard; protein; 152 AA.
DE Human protein sequence SEQ ID NO:15353.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 10.1%; Score 65; DB 4; Length 152;
Best Local Similarity 29.2%; Pred. No. 43;
RESULT 986
ID ABO70303 standard; protein; 190 AA.
DE Pseudomonas aeruginosa polypeptide #2478.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 10.1%; Score 65; DB 7; Length 190;
Best Local Similarity 21.1%; Pred. No. 56;
RESULT 987
ID ABO70829 standard; protein; 274 AA.
DE Pseudomonas aeruginosa polypeptide #3004.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 10.1%; Score 65; DB 7; Length 274;
Best Local Similarity 28.9%; Pred. No. 87;
RESULT 988
ID AAB66685 standard; protein; 305 AA.
DE ASH2 clone protein.
PN WO200102828-A2.
PD 11-JAN-2001.
PA (TULA-) TULARIK INC.
Query Match 10.1%; Score 65; DB 4; Length 305;
Best Local Similarity 28.8%; Pred. No. 99;
RESULT 989
ID ABG28722 standard; protein; 321 AA.
DE Novel human diagnostic protein #28713.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 10.1%; Score 65; DB 4; Length 321;
Best Local Similarity 25.7%; Pred. No. 1.1e+02;
RESULT 990
ID AAY04998 standard; protein; 388 AA.
DE Mycobacterium species protein sequence 50B.
PN WO9909186-A2.
PD 25-FEB-1999.
PA (INSP) INST PASTEUR.
Query Match 10.1%; Score 65; DB 2; Length 388;
Best Local Similarity 29.3%; Pred. No. 1.3e+02;
RESULT 991
ID ABO76986 standard; protein; 407 AA.
DE Pseudomonas aeruginosa polypeptide #9161.
PN US6551795-B1.
PD 22-APR-2003.

PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 10.1%; Score 65; DB 7; Length 407;
Best Local Similarity 28.6%; Pred. No. 1.4e+02;
RESULT 992
ID AAR11515 standard; protein; 440 AA.
DE Soybean chlorotic mottle virus coat protein.
PN AU9060867-A.
PD 07-MAR-1991.
PA (NAAG-) NAT INST AGROBIOL R.
PA (TOFU) TONEN CORP.
PA (NORQ) NORINSHO KK.
PA (TOFU) TONEN CORP.
Query Match 10.1%; Score 65; DB 2; Length 440;
Best Local Similarity 20.0%; Pred. No. 1.5e+02;
RESULT 993
ID RAB03084 standard; protein; 501 AA.
DE Human ASH2L2 protein.
PN CN1247228-A.
PD 15-MAR-2000.
PA (BASI-) INST BASIC MEDICAL SCI CHINESE ACAD MEDI.
Query Match 10.1%; Score 65; DB 3; Length 501;
Best Local Similarity 28.8%; Pred. No. 1.8e+02;
RESULT 994
ID ABU03696 standard; protein; 501 AA.
DE Human expressed protein tag (EPT) #362.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 10.1%; Score 65; DB 6; Length 501;
Best Local Similarity 28.8%; Pred. No. 1.8e+02;
RESULT 995
ID ABU03701 standard; protein; 501 AA.
DE Human expressed protein tag (EPT) #367.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 10.1%; Score 65; DB 6; Length 501;
Best Local Similarity 28.8%; Pred. No. 1.8e+02;
RESULT 996
ID ABU03704 standard; protein; 501 AA.
DE Human expressed protein tag (EPT) #370.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 10.1%; Score 65; DB 6; Length 501;
Best Local Similarity 28.8%; Pred. No. 1.8e+02;
RESULT 997
ID ABU03706 standard; protein; 534 AA.
DE Human expressed protein tag (EPT) #372.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 10.1%; Score 65; DB 6; Length 534;
Best Local Similarity 28.8%; Pred. No. 1.9e+02;
RESULT 998
ID ABU03695 standard; protein; 534 AA.
DE Human expressed protein tag (EPT) #361.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 10.1%; Score 65; DB 6; Length 534;
Best Local Similarity 28.8%; Pred. No. 1.9e+02;
RESULT 999
ID ABG07273 standard; protein; 576 AA.
DE Novel human diagnostic protein #7264.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 10.1%; Score 65; DB 4; Length 576;
Best Local Similarity 28.8%; Pred. No. 2.1e+02;
RESULT 1000
ID ABG07275 standard; protein; 626 AA.
DE Novel human diagnostic protein #7266.

PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 10.1%; Score 65; DB 4; Length 626;
Best Local Similarity 28.8%; Pred. No. 2.3e+02;
RESULT 1001
ID AAB03083 standard; protein; 628 AA.
DE Human ASH2L1 protein.
PN CN1247228-A.
PD 15-MAR-2000.
PA (BASI-) INST BASIC MEDICAL SCI CHINESE ACAD MEDI.
Query Match 10.1%; Score 65; DB 3; Length 628;
Best Local Similarity 28.8%; Pred. No. 2.3e+02;
RESULT 1002
ID ABA47150 standard; protein; 628 AA.
DE CDIFF-11, Incyte ID No. 2848676CD1.
PN WO200119860-A2.
PD 22-MAR-2001.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 10.1%; Score 65; DB 4; Length 628;
Best Local Similarity 28.8%; Pred. No. 2.3e+02;
RESULT 1003
ID ABU03702 standard; protein; 628 AA.
DE Human expressed protein tag (EPT) #368.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 10.1%; Score 65; DB 6; Length 628;
Best Local Similarity 28.8%; Pred. No. 2.3e+02;
RESULT 1004
ID ABU03703 standard; protein; 628 AA.
DE Human expressed protein tag (EPT) #369.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 10.1%; Score 65; DB 6; Length 628;
Best Local Similarity 28.8%; Pred. No. 2.3e+02;
RESULT 1005
ID ABU03700 standard; protein; 628 AA.
DE Human expressed protein tag (EPT) #366.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 10.1%; Score 65; DB 6; Length 628;
Best Local Similarity 28.8%; Pred. No. 2.3e+02;
RESULT 1006
ID ABU03707 standard; protein; 628 AA.
DE Human expressed protein tag (EPT) #373.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 10.1%; Score 65; DB 6; Length 628;
Best Local Similarity 28.8%; Pred. No. 2.3e+02;
RESULT 1007
ID ABU03699 standard; protein; 628 AA.
DE Human expressed protein tag (EPT) #365.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 10.1%; Score 65; DB 6; Length 628;
Best Local Similarity 28.8%; Pred. No. 2.3e+02;
RESULT 1008
ID ABU03705 standard; protein; 628 AA.
DE Human expressed protein tag (EPT) #371.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 10.1%; Score 65; DB 6; Length 628;
Best Local Similarity 28.8%; Pred. No. 2.3e+02;
RESULT 1009
ID ABU03698 standard; protein; 628 AA.
DE Human expressed protein tag (EPT) #364.
PN WO200278524-A2.

PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 10.1%; Score 65; DB 6; Length 628;
Best Local Similarity 28.8%; Pred. No. 2.3e+02;
RESULT 1010
ID ABU03697 standard; protein; 628 AA.
DE Human expressed protein tag (EPT) #363.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 10.1%; Score 65; DB 6; Length 628;
Best Local Similarity 28.8%; Pred. No. 2.3e+02;
RESULT 1011
ID AAB6688 standard; protein; 650 AA.
DE ASH2 isoform 707 protein.
PN WO200102828-A2.
PD 11-JAN-2001.
PA (TULA-) TULARIK INC.
Query Match 10.1%; Score 65; DB 4; Length 650;
Best Local Similarity 28.8%; Pred. No. 2.4e+02;
RESULT 1012
ID ABB6491 standard; protein; 678 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 20265.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 10.1%; Score 65; DB 4; Length 678;
Best Local Similarity 33.3%; Pred. No. 2.6e+02;
RESULT 1013
ID ABR57269 standard; protein; 1099 AA.
DE Human PHD finger protein 2 PHD_finger_2.
PN WO2003040296-A2.
PD 15-MAY-2003.
PA (DEVE-) DEVELOGEN ENTWICKLUNGSBIOLOGISCHE FORSCH.
PA (HAED-) HAEDER T.
Query Match 10.1%; Score 65; DB 6; Length 1099;
Best Local Similarity 26.7%; Pred. No. 4.6e+02;
RESULT 1014
ID ADX07391 standard; protein; 1099 AA.
DE Cyclin-dependent kinase modulation biomarker SEQ ID NO 1956.
PN WO2005012875-A2.
PD 10-FEB-2005.
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
Query Match 10.1%; Score 65; DB 9; Length 1099;
Best Local Similarity 26.7%; Pred. No. 4.6e+02;
RESULT 1015
ID AAU84346 standard; protein; 1798 AA.
DE Protein LAMB2 differentially expressed in breast cancer tissue.
PN WO200210436-A2.
PD 07-FEB-2002.
PA (BGHM) BRIGHAM & WOMENS HOSPITAL INC.
PA (BAAK/) BAAK J.
Query Match 10.1%; Score 65; DB 5; Length 1798;
Best Local Similarity 27.4%; Pred. No. 8.2e+02;
RESULT 1016
ID AAM50360 standard; protein; 1798 AA.
DE Human laminin-15 beta 2 chain.
PN WO200183516-A1.
PD 08-NOV-2001.
PA (MASS-) MASSACHUSETTS GEN HOSPITAL.
Query Match 10.1%; Score 65; DB 5; Length 1798;
Best Local Similarity 27.4%; Pred. No. 8.2e+02;
RESULT 1017
ID AAU42676 standard; protein; 113 AA.
DE Propionibacterium acnes immunogenic protein #3572.
PN WO200181581-A2.
PD 01-NOV-2001.
PA (CORI-) CORIXA CORP.
Query Match 10.0%; Score 64.5; DB 4; Length 113;
Best Local Similarity 25.0%; Pred. No. 35;
RESULT 1018
ID ABM39195 standard; protein; 113 AA.
DE Propionibacterium acnes predicted ORF-encoded polypeptide #3871.
PN WO2003033515-A1.
PD 24-APR-2003.
PA (CORI-) CORIXA CORP.
Query Match 10.0%; Score 64.5; DB 6; Length 113;
Best Local Similarity 25.0%; Pred. No. 35;
RESULT 1019
ID AD160152 standard; protein; 126 AA.
DE Secreted polypeptide #36.
PN WO2003025142-A2.
PD 27-MAR-2003.
PA (HYSE-) HYSEQ INC.
Query Match 10.0%; Score 64.5; DB 7; Length 126;
Best Local Similarity 27.7%; Pred. No. 39;
RESULT 1020
ID ADJ71800 standard; protein; 126 AA.
DE Human prokineticin-like protein.
PN WO2003040326-A2.
PD 15-MAY-2003.
PA (HYSE-) HYSEQ INC.
Query Match 10.0%; Score 64.5; DB 7; Length 126;
Best Local Similarity 27.7%; Pred. No. 39;
RESULT 1021
ID AAU42971 standard; protein; 154 AA.
DE Propionibacterium acnes immunogenic protein #3867.
PN WO200181581-A2.
PD 01-NOV-2001.
PA (CORI-) CORIXA CORP.
Query Match 10.0%; Score 64.5; DB 4; Length 154;
Best Local Similarity 28.3%; Pred. No. 50;
RESULT 1022
ID ABM39490 standard; protein; 154 AA.
DE Propionibacterium acnes predicted ORF-encoded polypeptide #4166.
PN WO2003033515-A1.
PD 24-APR-2003.
PA (CORI-) CORIXA CORP.
Query Match 10.0%; Score 64.5; DB 6; Length 154;
Best Local Similarity 28.3%; Pred. No. 50;
RESULT 1023
ID ADE31234 standard; protein; 189 AA.
DE Human diagnostic and therapeutic polypeptide (DITHP), SEQ ID NO 366.
PN WO2003062376-A2.
PD 31-JUL-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 10.0%; Score 64.5; DB 7; Length 189;
Best Local Similarity 34.1%; Pred. No. 64;
RESULT 1024
ID AAM78612 standard; protein; 227 AA.
DE Human protein SEQ ID NO 1274.
PN WO200457150-A2.
PD 09-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match 10.0%; Score 64.5; DB 4; Length 227;
Best Local Similarity 23.9%; Pred. No. 80;
RESULT 1025
ID AB053041 standard; protein; 227 AA.
DE Human putative spliceosome associated protein (SAP) #17.
PN US2003068803-A1.
PD 10-APR-2003.
PA (REED/) REED R.
PA (ZHOU/) ZHOU Z.
Query Match 10.0%; Score 64.5; DB 6; Length 227;
Best Local Similarity 23.9%; Pred. No. 80;
RESULT 1026
ID ADJ68918 standard; protein; 227 AA.
DE Human heat mitochondrial protein as a therapeutic target SeqID724.
PN WO2003087768-A2.
PD 23-OCT-2003.
PA (MITO-) MITOKOR.
PA (BUCK-) BUCK INST AGE RES.
Query Match 10.0%; Score 64.5; DB 7; Length 227;
Best Local Similarity 23.9%; Pred. No. 80;
RESULT 1027
ID AD225523 standard; protein; 227 AA.

DE Cytokine receptor activity increasing protein MP6 SEQ ID NO 51.
PN WO2005030241-A2.
PD 07-APR-2005.
PA (MEYE-) MEYER PHARM LLC.
Query Match 10.0%; Score 64.5; DB 9; Length 227;
Best Local Similarity 23.9%; Pred. No. 80;
RESULT 1028
ID AD225511 standard; protein; 255 AA.
DE Cytokine receptor activity increasing protein MP7 SEQ ID NO 39.
PN WO2005030241-A2.
PD 07-APR-2005.
PA (MEYE-) MEYER PHARM LLC.
Query Match 10.0%; Score 64.5; DB 9; Length 255;
Best Local Similarity 23.9%; Pred. No. 92;
RESULT 1029
ID ADT87996 standard; protein; 264 AA.
DE Human regulatory protein, NHRP-33.
PN US2004203109-A1.
PD 14-OCT-2004.
PA (INCY-) INCYTE CORP.
Query Match 10.0%; Score 64.5; DB 8; Length 264;
Best Local Similarity 23.9%; Pred. No. 95;
RESULT 1030
ID ABO80087 standard; protein; 382 AA.
DE Pseudomonas aeruginosa polypeptide #12262.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 10.0%; Score 64.5; DB 7; Length 382;
Best Local Similarity 26.8%; Pred. No. 1.5e+02;
RESULT 1031
ID ABB11193 standard; peptide; 431 AA.
DE Human Zn finger protein homologue, SEQ ID NO:1563.
PN WO200157188-A2.
PD 09-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match 10.0%; Score 64.5; DB 4; Length 431;
Best Local Similarity 30.8%; Pred. No. 1.7e+02;
RESULT 1032
ID ABO68760 standard; protein; 525 AA.
DE Pseudomonas aeruginosa polypeptide #935.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 10.0%; Score 64.5; DB 7; Length 525;
Best Local Similarity 31.1%; Pred. No. 2.2e+02;
RESULT 1033
ID AAB21042 standard; protein; 534 AA.
DE Human nucleic acid-binding protein, NUABP-46.
PN WO200044900-A2.
PD 03-AUG-2000.
PA (INCY-) INCYTE PHARM INC.
Query Match 10.0%; Score 64.5; DB 3; Length 534;
Best Local Similarity 30.8%; Pred. No. 2.2e+02;
RESULT 1034
ID ABO82315 standard; protein; 593 AA.
DE Pseudomonas aeruginosa polypeptide #14490.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 10.0%; Score 64.5; DB 7; Length 593;
Best Local Similarity 30.2%; Pred. No. 2.5e+02;
RESULT 1035
ID ABO68758 standard; protein; 921 AA.
DE Pseudomonas aeruginosa polypeptide #933.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 10.0%; Score 64.5; DB 7; Length 921;
Best Local Similarity 26.1%; Pred. No. 4.2e+02;
RESULT 1036
ID ADG84161 standard; protein; 1161 AA.
DE Human TWD0841 protein SeqID99.

PN WO2003089583-A2.
PD 30-OCT-2003.
PA (ORIG-) ORIGENE TECHNOLOGIES INC.
Query Match 10.0%; Score 64.5; DB 7; Length 1161;
Best Local Similarity 26.5%; Pred. No. 5.6e+02;
RESULT 1037
ID AAR80843 standard; protein; 145 AA.
DE Cross-reactive allergen CRAL51 partial sequence.
PN WO9519437-A1.
PD 20-JUL-1995.
PA (UYMA-) UNIV MANITOBA.
Query Match 9.9%; Score 64; DB 2; Length 145;
Best Local Similarity 31.4%; Pred. No. 53;
RESULT 1038
ID ADT55674 standard; protein; 182 AA.
DE Plant polypeptide, SEQ ID 5751.
PN US2004216190-A1.
PD 28-OCT-2004.
PA (KOVA/) KOVALIC D K.
Query Match 9.9%; Score 64; DB 8; Length 182;
Best Local Similarity 22.8%; Pred. No. 70;
RESULT 1039
ID ABB09175 standard; protein; 214 AA.
DE Leptin-VEGF-165-C-terminal-His tag fusion protein SEQ ID NO:1.
PN WO200226779-A2.
PD 04-APR-2002.
PA (BAXT) BAXTER AG.
PA (BAXT) BAXTER INT INC.
Query Match 9.9%; Score 64; DB 5; Length 214;
Best Local Similarity 29.1%; Pred. No. 85;
RESULT 1040
ID ABU10041 standard; protein; 214 AA.
DE Leptin-VEGF165-His tag fusion protein.
PN US2003044405-A1.
PD 06-MAR-2003.
PA (REDL/) REDL H.
PA (FUER/) FUERST W.
PA (KNEI/) KNEIDINGER R.
PA (HELG/) HELGERSON S L.
PA (LOOK/) LOOKER D.
PA (INMA/) INMAN E M.
PA (RICH/) RICHARDS J P.
PA (WONG/) WONG C.
Query Match 9.9%; Score 64; DB 6; Length 214;
Best Local Similarity 29.1%; Pred. No. 85;
RESULT 1041
ID ADS00679 standard; protein; 214 AA.
DE Leptin-VEGF165 C-terminal-His tag fusion protein.
PN US2004191261-A1.
PD 30-SEP-2004.
PA (BAXT) BAXTER AG.
PA (BAXT) BAXTER INT INC.
Query Match 9.9%; Score 64; DB 8; Length 214;
Best Local Similarity 29.1%; Pred. No. 85;
RESULT 1042
ID AAB73602 standard; protein; 220 AA.
DE Human zinc finger protein ZNFPT1 fragment (residues 67-286).
PN WO200130840-A1.
PD 03-MAY-2001.
PA (SHAN-) SHANGHAI BIO ROAD GENE DEV LTD.
Query Match 9.9%; Score 64; DB 4; Length 220;
Best Local Similarity 28.8%; Pred. No. 88;
RESULT 1043
ID ADQ20492 standard; protein; 227 AA.
DE Human soft tissue sarcoma-upregulated protein - SEQ ID 3312.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 9.9%; Score 64; DB 8; Length 227;
Best Local Similarity 28.8%; Pred. No. 91;
RESULT 1044
ID ABO74758 standard; protein; 366 AA.
DE Pseudomonas aeruginosa polypeptide #6933.

PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 9.9%; Score 64; DB 7; Length 366;
Best Local Similarity 30.2%; Pred. No. 1.6e+02;
RESULT 1045
ID AAY21803 standard; protein; 1855 AA.
DE B. subtilis rib operon protein translated from reading frame 3.
PN US925538-A.
PD 20-JUL-1999.
PA (HOFF) ROCHE VITAMINS INC.
Query Match 9.9%; Score 64; DB 2; Length 1855;
Best Local Similarity 28.3%; Pred. No. 1.1e+03;
RESULT 1046
ID AAY83271 standard; protein; 1855 AA.
DE Polypeptide encoded by rib operon of Bacillus subtilis.
PN EP101026-A2.
PD 17-MAY-2000.
PA (HOFF) HOFFMANN LA ROCHE & CO AG F.
Query Match 9.9%; Score 64; DB 3; Length 1855;
Best Local Similarity 28.3%; Pred. No. 1.1e+03;
RESULT 1047
ID AAO21324 standard; protein; 106 AA.
DE Arabidopsis thaliana KCP-like protein, SEQ ID NO 79.
PN WO200222821-A2.
PD 21-MAR-2002.
PA (PION-) PIONEER HI-BRED INT INC.
Query Match 9.9%; Score 63.5; DB 5; Length 106;
Best Local Similarity 21.2%; Pred. No. 42;
RESULT 1048
ID AAU51371 standard; protein; 129 AA.
DE Propionibacterium acnes immunogenic protein #12267.
PN WO200181581-A2.
PD 01-NOV-2001.
PA (CORI-) CORIXA CORP.
Query Match 9.9%; Score 63.5; DB 4; Length 129;
Best Local Similarity 28.4%; Pred. No. 53;
RESULT 1049
ID ABM47890 standard; protein; 129 AA.
DE Propionibacterium acnes predicted ORF-encoded polypeptide #12566.
PN WO2003033515-A1.
PD 24-APR-2003.
PA (CORI-) CORIXA CORP.
Query Match 9.9%; Score 63.5; DB 6; Length 129;
Best Local Similarity 28.4%; Pred. No. 53;
RESULT 1050
ID ABO69906 standard; protein; 148 AA.
DE Pseudomonas aeruginosa polypeptide #2081.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 9.9%; Score 63.5; DB 7; Length 148;
Best Local Similarity 32.9%; Pred. No. 62;
RESULT 1051
ID ADY25230 standard; protein; 199 AA.
DE Plant full length insert polypeptide seqid 73014.
PN US2004034888-A1.
PD 19-FEB-2004.
PA (LIUJ/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABA/) TABASKA J E.
PA (CAOY/) CAO Y.
Query Match 9.9%; Score 63.5; DB 8; Length 199;
Best Local Similarity 27.3%; Pred. No. 89;
RESULT 1052
ID ADM04665 standard; protein; 215 AA.
DE Human protein of the invention SEQ ID NO:3350.
PN EP1347046-A1.
PD 24-SEP-2003.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 9.9%; Score 63.5; DB 7; Length 215;

Best Local Similarity 32.8%; Pred. No. 98;
RESULT 1053
ID AEC87595 standard; protein; 215 AA.
DE Human cDNA clone protein FEBRA20211710, SEQ ID 3350.
PN EP1580263-A1.
PD 28-SEP-2005.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 9.9%; Score 63.5; DB 9; Length 215;
Best Local Similarity 32.8%; Pred. No. 98;
RESULT 1054
ID ABO00623 standard; protein; 260 AA.
DE Novel human polypeptide #210.
PN WO2003023013-A2.
PD 20-MAR-2003.
PA (HYSE-) HYSEQ INC.
Query Match 9.9%; Score 63.5; DB 6; Length 260;
Best Local Similarity 43.9%; Pred. No. 1.2e+02;
RESULT 1055
ID ADV07390 standard; protein; 261 AA.
DE Plant full length insert polypeptide seqid 63205.
PN US2004034888-A1.
PD 19-FEB-2004.
PA (LIUJ/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABA/) TABASKA J E.
PA (CAOY/) CAO Y.
Query Match 9.9%; Score 63.5; DB 8; Length 261;
Best Local Similarity 31.7%; Pred. No. 1.2e+02;
RESULT 1056
ID ADU02419 standard; protein; 338 AA.
DE Novel human polypeptide seqid 886.
PN WO2004093804-A2.
PD 04-NOV-2004.
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
Query Match 9.9%; Score 63.5; DB 8; Length 338;
Best Local Similarity 43.9%; Pred. No. 1.7e+02;
RESULT 1057
ID ADX91872 standard; protein; 367 AA.
DE Plant full length insert polypeptide seqid 54536.
PN US2004034888-A1.
PD 19-FEB-2004.
PA (LIUJ/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABA/) TABASKA J E.
PA (CAOY/) CAO Y.
Query Match 9.9%; Score 63.5; DB 8; Length 367;
Best Local Similarity 21.6%; Pred. No. 1.8e+02;
RESULT 1058
ID ABG60058 standard; protein; 375 AA.
DE Human D1THP polypeptide #116.
PN WO200220754-A2.
PD 14-MAR-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 9.9%; Score 63.5; DB 5; Length 375;
Best Local Similarity 35.2%; Pred. No. 1.9e+02;
RESULT 1059
ID ABG26874 standard; protein; 392 AA.
DE Novel human diagnostic protein #26865.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 9.9%; Score 63.5; DB 4; Length 392;
Best Local Similarity 24.0%; Pred. No. 2e+02;
RESULT 1060
ID ABG27718 standard; protein; 435 AA.
DE Novel human diagnostic protein #27709.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.

Query Match
Best Local Similarity 9.9%; Score 63.5; DB 4; Length 435;
RESULT 1061
ID AAB94169 standard; protein; 464 AA.
DE Human protein sequence SEQ ID NO:14472.
PN EPI074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match
Best Local Similarity 9.9%; Score 63.5; DB 4; Length 464;
RESULT 1062
ID AEA00452 standard; protein; 786 AA.
DE Human KRC zinc finger-acidic domain structures (ZAS) domain.
PN WO2005042726-A2.
PD 12-MAY-2005.
PA (HARD) HARVARD COLLEGE.
Query Match
Best Local Similarity 9.9%; Score 63.5; DB 9; Length 786;
RESULT 1063
ID ABP69375 standard; protein; 1708 AA.
DE Human polypeptide SEQ ID NO 1422.
PN WO200270539-A2.
PD 12-SEP-2002.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 9.9%; Score 63.5; DB 5; Length 1708;
RESULT 1064
ID ABB82733 standard; protein; 2406 AA.
DE Human KRC protein.
PN WO200290595-A1.
PD 14-NOV-2002.
PA (HARD) HARVARD COLLEGE.
Query Match
Best Local Similarity 9.9%; Score 63.5; DB 6; Length 2406;
RESULT 1065
ID ADJ69698 standard; protein; 2406 AA.
DE Human heat mitochondrial protein as a therapeutic target SeqID1504.
PN WO2003087768-A2.
PD 23-OCT-2003.
PA (MITO-) MITOKOR.
PA (BUCK-) BUCK INST AGE RES.
Query Match
Best Local Similarity 9.9%; Score 63.5; DB 7; Length 2406;
RESULT 1066
ID ADQ97930 standard; protein; 2406 AA.
DE Human cancer associated sequence HP11-024, SEQ ID 907.
PN WO2004060304-A2.
PD 22-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match
Best Local Similarity 9.9%; Score 63.5; DB 8; Length 2406;
RESULT 1067
ID AEA00446 standard; protein; 2406 AA.
DE Human kappa recognition component (KRC) polypeptide.
PN WO2005042726-A2.
PD 12-MAY-2005.
PA (HARD) HARVARD COLLEGE.
Query Match
Best Local Similarity 9.9%; Score 63.5; DB 9; Length 2406;
RESULT 1068
ID AAU47558 standard; protein; 123 AA.
DE Propionibacterium acnes immunogenic protein #8454.
PN WO200181581-A2.
PD 01-NOV-2001.
PA (CORI-) CORIXA CORP.
Query Match
Best Local Similarity 9.8%; Score 63; DB 4; Length 123;
RESULT 1069
ID ABM44077 standard; protein; 123 AA.
DE Propionibacterium acnes predicted ORF-encoded polypeptide #8753.
PN WO2003033515-A1.
PD 24-APR-2003.
PA (CORI-) CORIXA CORP.

Query Match
Best Local Similarity 9.8%; Score 63; DB 6; Length 123;
RESULT 1070
ID ADX79085 standard; protein; 127 AA.
DE Plant full length insert polypeptide seqid 48451.
PN US2004034888-A1.
PD 19-FEB-2004.
PA (LIUJ-) LIU J.
PA (ZHOU-) ZHOU Y.
PA (KOVA-) KOVALIC D K.
PA (SCRE-) SCREEN S E.
PA (TABA-) TABASKA J E.
PA (CAOY-) CAO Y.
Query Match
Best Local Similarity 9.8%; Score 63; DB 8; Length 127;
RESULT 1071
ID ABG00364 standard; protein; 160 AA.
DE Novel human diagnostic protein #355.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 9.8%; Score 63; DB 4; Length 160;
RESULT 1072
ID AAU55928 standard; protein; 172 AA.
DE Propionibacterium acnes immunogenic protein #16824.
PN WO200181581-A2.
PD 01-NOV-2001.
PA (CORI-) CORIXA CORP.
Query Match
Best Local Similarity 9.8%; Score 63; DB 4; Length 172;
RESULT 1073
ID ABM52447 standard; protein; 172 AA.
DE Propionibacterium acnes predicted ORF-encoded polypeptide #17123.
PN WO2003033515-A1.
PD 24-APR-2003.
PA (CORI-) CORIXA CORP.
Query Match
Best Local Similarity 9.8%; Score 63; DB 6; Length 172;
RESULT 1074
ID AAU55408 standard; protein; 190 AA.
DE Propionibacterium acnes immunogenic protein #16304.
PN WO200181581-A2.
PD 01-NOV-2001.
PA (CORI-) CORIXA CORP.
Query Match
Best Local Similarity 9.8%; Score 63; DB 4; Length 190;
RESULT 1075
ID ABM51927 standard; protein; 190 AA.
DE Propionibacterium acnes predicted ORF-encoded polypeptide #16603.
PN WO2003033515-A1.
PD 24-APR-2003.
PA (CORI-) CORIXA CORP.
Query Match
Best Local Similarity 9.8%; Score 63; DB 6; Length 190;
RESULT 1076
ID ABG14052 standard; protein; 198 AA.
DE Novel human diagnostic protein #14043.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 9.8%; Score 63; DB 4; Length 198;
RESULT 1077
ID ABO74665 standard; protein; 267 AA.
DE Pseudomonas aeruginosa polypeptide #6840.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match
Best Local Similarity 9.8%; Score 63; DB 7; Length 267;
RESULT 1078
ID ADY05166 standard; protein; 295 AA.

DE Plant full length insert polypeptide seqid 60981.
PN US200403488-A1.
PA (LIUJ/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABA/) TABASKA J E.
PA (CAOY/) CAO Y.
Query Match
Best Local Similarity 9.8%; Score 63; DB 8; Length 295;
Best Local Similarity 25.0%; Pred. No. 1.6e+02;
RESULT 1079
ID ABO76978 standard; protein; 302 AA.
DE Pseudomonas aeruginosa polypeptide #9153.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match
Best Local Similarity 9.8%; Score 63; DB 7; Length 302;
Best Local Similarity 25.5%; Pred. No. 1.7e+02;
RESULT 1080
ID ADQ19814 standard; protein; 332 AA.
DE Human soft tissue sarcoma-upregulated protein - SEQ ID 2633.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match
Best Local Similarity 9.8%; Score 63; DB 8; Length 332;
Best Local Similarity 25.8%; Pred. No. 1.9e+02;
RESULT 1081
ID ABG23967 standard; protein; 343 AA.
DE Novel human diagnostic protein #23958.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEE INC.
Query Match
Best Local Similarity 9.8%; Score 63; DB 4; Length 343;
Best Local Similarity 27.4%; Pred. No. 1.9e+02;
RESULT 1082
ID AM93267 standard; protein; 447 AA.
DE Human polypeptide, SEQ ID NO: 2729.
PN EP130094-A2.
PD 05-SEP-2001.
PA (HELI-) HELIX RES INST.
Query Match
Best Local Similarity 9.8%; Score 63; DB 4; Length 447;
Best Local Similarity 24.5%; Pred. No. 2.7e+02;
RESULT 1083
ID ADL30696 standard; protein; 447 AA.
DE Human protein encoded by a full length cDNA clone seqid 2729.
PN EP1396543-A2.
PD 10-MAR-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match
Best Local Similarity 9.8%; Score 63; DB 8; Length 447;
Best Local Similarity 24.5%; Pred. No. 2.7e+02;
RESULT 1084
ID ADU02730 standard; protein; 492 AA.
DE Novel human polypeptide seqid 1197.
PN WO2004093804-A2.
PD 04-NOV-2004.
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
Query Match
Best Local Similarity 9.8%; Score 63; DB 8; Length 492;
Best Local Similarity 27.3%; Pred. No. 3e+02;
RESULT 1085
ID ADM29286 standard; protein; 1787 AA.
DE Human novel protein NOV4b.
PN WO2003064628-A2.
PD 07-AUG-2003.
PA (CURA-) CURAGEN CORP.
Query Match
Best Local Similarity 9.8%; Score 63; DB 7; Length 1787;
Best Local Similarity 20.8%; Pred. No. 1.4e+03;
RESULT 1086
ID ADQ97927 standard; protein; 2353 AA.
DE Mouse cancer associated sequence MP11-024, SEQ ID 904.
PN WO2004060304-A2.
PD 22-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match
Best Local Similarity 9.8%; Score 63; DB 8; Length 2353;
Best Local Similarity 25.2%; Pred. No. 1.9e+03;
RESULT 1087
ID AAU40478 standard; protein; 69 AA.
DE Propionibacterium acnes immunogenic protein #1374.
PN WO200181581-A2.
PD 01-NOV-2001.
PA (CORI-) CORIXA CORP.
Query Match
Best Local Similarity 9.7%; Score 62.5; DB 4; Length 69;
Best Local Similarity 29.0%; Pred. No. 33;
RESULT 1088
ID ABM36997 standard; protein; 69 AA.
DE Propionibacterium acnes predicted ORF-encoded polypeptide #1673.
PN WO2003033515-A1.
PD 24-APR-2003.
PA (CORI-) CORIXA CORP.
Query Match
Best Local Similarity 9.7%; Score 62.5; DB 6; Length 69;
Best Local Similarity 29.0%; Pred. No. 33;
RESULT 1089
ID ABE69709 standard; protein; 77 AA.
DE Human papillomavirus protein #279.
PN WO2005115458-A2.
PD 08-DEC-2005.
PA (UABR-) UAB RES FOUND.
Query Match
Best Local Similarity 9.7%; Score 62.5; DB 10; Length 77;
Best Local Similarity 24.6%; Pred. No. 37;
RESULT 1090
ID AAY44192 standard; protein; 156 AA.
DE Human keratinocyte-derived RNase-like protein.
PN EP943679-A1.
PD 22-SEP-1999.
PA (INNO-) INNOGENETICS NV.
Query Match
Best Local Similarity 9.7%; Score 62.5; DB 2; Length 156;
Best Local Similarity 23.2%; Pred. No. 87;
RESULT 1091
ID AAB10601 standard; protein; 156 AA.
DE Human SAP-2 pre-protein.
PN WO200046245-A2.
PD 10-AUG-2000.
PA (SCHD) SCHERING AG.
Query Match
Best Local Similarity 9.7%; Score 62.5; DB 3; Length 156;
Best Local Similarity 23.2%; Pred. No. 87;
RESULT 1092
ID AAB66270 standard; protein; 156 AA.
DE Human TANGO 295 SEQ ID NO: 23.
PN WO200100673-A1.
PD 04-JAN-2001.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match
Best Local Similarity 9.7%; Score 62.5; DB 4; Length 156;
Best Local Similarity 23.2%; Pred. No. 87;
RESULT 1093
ID AAB50934 standard; protein; 156 AA.
DE Human PRO6006 protein.
PN WO200073452-A2.
PD 07-DEC-2000.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 9.7%; Score 62.5; DB 4; Length 156;
Best Local Similarity 23.2%; Pred. No. 87;
RESULT 1094
ID ABB84987 standard; protein; 156 AA.
DE Human PRO6006 protein sequence SEQ ID NO:342.
PN WO2002006590-A2.
PD 03-JAN-2002.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 9.7%; Score 62.5; DB 5; Length 156;
Best Local Similarity 23.2%; Pred. No. 87;
RESULT 1095
ID ABG34059 standard; protein; 156 AA.
DE Human Pro peptide #30.
PN WO200224888-A2.
PD 28-MAR-2002.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 9.7%; Score 62.5; DB 5; Length 156;


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Best Local Similarity 23.2%; Pred. No. 87;
RESULT 1096
ID ABB95593 standard; protein; 156 AA.
DE Human angiogenesis related protein PRO6006 SEQ ID NO: 342.
PN W0200208284-A2.
PA (GETH ) GENENTECH INC.
Query Match 9.7%; Score 62.5; DB 5; Length 156;
Best Local Similarity 23.2%; Pred. No. 87;
RESULT 1097
ID ADA01328 standard; protein; 156 AA.
DE Human PRO polypeptide #30.
PN US2003068779-A1.
PA (GETH ) GENENTECH INC.
Query Match 9.7%; Score 62.5; DB 6; Length 156;
Best Local Similarity 23.2%; Pred. No. 87;
RESULT 1098
ID ADA43757 standard; protein; 156 AA.
DE Human secreted/transmembrane polypeptide PRO6006.
PN US2003064474-A1.
PA (GETH ) GENENTECH INC.
Query Match 9.7%; Score 62.5; DB 6; Length 156;
Best Local Similarity 23.2%; Pred. No. 87;
RESULT 1099
ID ADA43525 standard; protein; 156 AA.
DE Human secreted/transmembrane polypeptide PRO6006.
PN US2003073196-A1.
PA (GETH ) GENENTECH INC.
Query Match 9.7%; Score 62.5; DB 6; Length 156;
Best Local Similarity 23.2%; Pred. No. 87;
RESULT 1100
ID ADA01200 standard; protein; 156 AA.
DE Human PRO polypeptide #30.
PN US2003068782-A1.
PA (GETH ) GENENTECH INC.
Query Match 9.7%; Score 62.5; DB 6; Length 156;
Best Local Similarity 23.2%; Pred. No. 87;
RESULT 1101
ID ADA01084 standard; protein; 156 AA.
DE Human secreted/transmembrane polypeptide PRO6006.
PN US2003068780-A1.
PA (GETH ) GENENTECH INC.
Query Match 9.7%; Score 62.5; DB 7; Length 156;
Best Local Similarity 23.2%; Pred. No. 87;
RESULT 1102
ID ADA43641 standard; protein; 156 AA.
DE Human secreted/transmembrane polypeptide PRO6006.
PN US2003073190-A1.
PA (GETH ) GENENTECH INC.
Query Match 9.7%; Score 62.5; DB 7; Length 156;
Best Local Similarity 23.2%; Pred. No. 87;
RESULT 1103
ID ADA06903 standard; protein; 156 AA.
DE Human PRO polypeptide #30.
PN US2003068781-A1.
PA (GETH ) GENENTECH INC.
Query Match 9.7%; Score 62.5; DB 7; Length 156;
Best Local Similarity 23.2%; Pred. No. 87;
RESULT 1104
ID ADA08391 standard; protein; 156 AA.
DE Novel human secreted and transmembrane protein PRO6006.
PN US2003068783-A1.
PA (GETH ) GENENTECH INC.
Query Match 9.7%; Score 62.5; DB 7; Length 156;
Best Local Similarity 23.2%; Pred. No. 87;
RESULT 1105
ID ADB99684 standard; protein; 156 AA.
DE Human PRO polypeptide SEQ ID 60.
PN US2003082728-A1.
PA (GETH ) GENENTECH INC.
Query Match 9.7%; Score 62.5; DB 7; Length 156;
Best Local Similarity 23.2%; Pred. No. 87;
RESULT 1106
ID ADB86967 standard; protein; 156 AA.
DE Human PRO polypeptide #30.
PN US2003082726-A1.
PA (GETH ) GENENTECH INC.
Query Match 9.7%; Score 62.5; DB 7; Length 156;
Best Local Similarity 23.2%; Pred. No. 87;
RESULT 1107
ID ADB66122 standard; protein; 156 AA.
DE Human secreted/transmembrane polypeptide PRO6006.
PN US2003082729-A1.
PA (GETH ) GENENTECH INC.
Query Match 9.7%; Score 62.5; DB 7; Length 156;
Best Local Similarity 23.2%; Pred. No. 87;
RESULT 1108
ID ADB99800 standard; protein; 156 AA.
DE Human PRO polypeptide SEQ ID 60.
PN US2003073192-A1.
PA (GETH ) GENENTECH INC.
Query Match 9.7%; Score 62.5; DB 7; Length 156;
Best Local Similarity 23.2%; Pred. No. 87;
RESULT 1109
ID ADB99455 standard; protein; 156 AA.
DE Novel human secreted and transmembrane protein PRO6006.
PN US2003082731-A1.
PA (GETH ) GENENTECH INC.
Query Match 9.7%; Score 62.5; DB 7; Length 156;
Best Local Similarity 23.2%; Pred. No. 87;
RESULT 1110
ID ADB66006 standard; protein; 156 AA.
DE Human secreted/transmembrane polypeptide PRO6006.
PN US2003082732-A1.
PA (GETH ) GENENTECH INC.
Query Match 9.7%; Score 62.5; DB 7; Length 156;
Best Local Similarity 23.2%; Pred. No. 87;
RESULT 1111
ID ADC23404 standard; protein; 156 AA.
DE Human transmembrane PRO polypeptide (SeqID 60).
PN US2003073193-A1.
PA (GETH ) GENENTECH INC.
Query Match 9.7%; Score 62.5; DB 7; Length 156;
Best Local Similarity 23.2%; Pred. No. 87;
RESULT 1112
ID ADC26097 standard; protein; 156 AA.
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DE Human PRO6006 protein.
PN US2003073194-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 9.7%; Score 62.5; DB 7; Length 156;
RESULT 1113
ID ADD10631 standard; protein; 156 AA.
DE Human secreted/transmembrane PRO polypeptide #171.
PN US2003105011-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 9.7%; Score 62.5; DB 7; Length 156;
RESULT 1114
ID ADD11591 standard; protein; 156 AA.
DE Human secreted/transmembrane PRO polypeptide #171.
PN US2003105013-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 9.7%; Score 62.5; DB 7; Length 156;
RESULT 1115
ID ADD37384 standard; protein; 156 AA.
DE Human secreted/transmembrane PRO polypeptide #171.
PN US2003105012-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 9.7%; Score 62.5; DB 7; Length 156;
RESULT 1116
ID ADE04924 standard; protein; 156 AA.
DE Human PRO polypeptide #30.
PN US2003068778-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 9.7%; Score 62.5; DB 7; Length 156;
RESULT 1117
ID ADE11230 standard; protein; 156 AA.
DE Human PRO polypeptide #30.
PN US2003073191-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 9.7%; Score 62.5; DB 7; Length 156;
RESULT 1118
ID ADD88161 standard; protein; 156 AA.
DE Human PRO polypeptide #30.
PN US2003082733-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 9.7%; Score 62.5; DB 7; Length 156;
RESULT 1119
ID ADD95456 standard; protein; 156 AA.
DE Human secreted/transmembrane polypeptide PRO6006.
PN US2003064473-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 9.7%; Score 62.5; DB 7; Length 156;
RESULT 1120
ID ADE06386 standard; protein; 156 AA.
DE Human PRO polypeptide #30.
PN US2003073195-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 9.7%; Score 62.5; DB 7; Length 156;
RESULT 1121
ID ADE38161 standard; protein; 156 AA.
DE Human PRO polypeptide #30.
PN US2003104564-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 9.7%; Score 62.5; DB 8; Length 156;
RESULT 1122
ID ADD88277 standard; protein; 156 AA.
DE Human PRO polypeptide #30.
PN US2003073189-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 9.7%; Score 62.5; DB 7; Length 156;
RESULT 1123
ID ADD90858 standard; protein; 156 AA.
DE Human secreted/transmembrane polypeptide PRO6006.
PN US2003073188-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 9.7%; Score 62.5; DB 7; Length 156;
RESULT 1124
ID ADF98413 standard; protein; 156 AA.
DE Human secreted/transmembrane polypeptide PRO6006.
PN US2003078401-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 9.7%; Score 62.5; DB 7; Length 156;
RESULT 1125
ID ADG06506 standard; protein; 156 AA.
DE Human PRO polypeptide #30.
PN US2003077742-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 9.7%; Score 62.5; DB 7; Length 156;
RESULT 1126
ID ADG05457 standard; protein; 156 AA.
DE Human PRO polypeptide #30.
PN US2003077741-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 9.7%; Score 62.5; DB 7; Length 156;
RESULT 1127
ID ADG82458 standard; protein; 156 AA.
DE Human PRO polypeptide #30.
PN US2003077744-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 9.7%; Score 62.5; DB 7; Length 156;
RESULT 1128
ID ADE51711 standard; protein; 156 AA.
DE Human secreted/transmembrane polypeptide PRO6006.
PN US2003104560-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 9.7%; Score 62.5; DB 8; Length 156;
RESULT 1129
ID ADE51827 standard; protein; 156 AA.
DE Human secreted/transmembrane polypeptide PRO6006.
PN US2003104561-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 9.7%; Score 62.5; DB 8; Length 156;
RESULT 1130
ID ADE37685 standard; protein; 156 AA.
DE Human secreted/transmembrane polypeptide PRO6006.
PN US2003104564-A1.
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PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 9.7%; Score 62.5; DB 8; Length 156;
Best Local Similarity 23.2%; Pred. No. 87;
RESULT 1131
ID ADE37569 standard; protein; 156 AA.
DE Human secreted/transmembrane polypeptide PRO6006.
PN US2003104565-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 9.7%; Score 62.5; DB 8; Length 156;
Best Local Similarity 23.2%; Pred. No. 87;
RESULT 1132
ID ADD95340 standard; protein; 156 AA.
DE Human secreted/transmembrane polypeptide PRO6006.
PN US2003138901-A1.
PD 24-JUL-2003.
PA (GETH ) GENENTECH INC.
Query Match 9.7%; Score 62.5; DB 8; Length 156;
Best Local Similarity 23.2%; Pred. No. 87;
RESULT 1133
ID ADE38040 standard; protein; 156 AA.
DE Human PRO polypeptide #30.
PN US2003104566-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 9.7%; Score 62.5; DB 8; Length 156;
Best Local Similarity 23.2%; Pred. No. 87;
RESULT 1134
ID ADE76129 standard; protein; 156 AA.
DE Human PRO polypeptide #30.
PN US2003124665-A1.
PD 03-JUL-2003.
PA (GETH ) GENENTECH INC.
Query Match 9.7%; Score 62.5; DB 8; Length 156;
Best Local Similarity 23.2%; Pred. No. 87;
RESULT 1135
ID ADE39452 standard; protein; 156 AA.
DE Human PRO polypeptide #30.
PN US2003119117-A1.
PD 26-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 9.7%; Score 62.5; DB 8; Length 156;
Best Local Similarity 23.2%; Pred. No. 87;
RESULT 1136
ID ADE04256 standard; protein; 156 AA.
DE Human PRO polypeptide #30.
PN US2003096364-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 9.7%; Score 62.5; DB 8; Length 156;
Best Local Similarity 23.2%; Pred. No. 87;
RESULT 1137
ID ADE39853 standard; protein; 156 AA.
DE Human PRO polypeptide #30.
PN US2003138896-A1.
PD 24-JUL-2003.
PA (GETH ) GENENTECH INC.
Query Match 9.7%; Score 62.5; DB 8; Length 156;
Best Local Similarity 23.2%; Pred. No. 87;
RESULT 1138
ID ADE19718 standard; protein; 156 AA.
DE Human PRO polypeptide #30.
PN US2003138903-A1.
PD 24-JUL-2003.
PA (GETH ) GENENTECH INC.
Query Match 9.7%; Score 62.5; DB 8; Length 156;
Best Local Similarity 23.2%; Pred. No. 87;
RESULT 1139
ID ADE77296 standard; protein; 156 AA.
DE Human secreted/transmembrane polypeptide PRO6006.
PN US2003124666-A1.
PD 03-JUL-2003.

PA (GETH ) GENENTECH INC.
Query Match 9.7%; Score 62.5; DB 8; Length 156;
Best Local Similarity 23.2%; Pred. No. 87;
RESULT 1140
ID ADE65404 standard; protein; 156 AA.
DE Human PRO polypeptide #30.
PN US2003119116-A1.
PD 26-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 9.7%; Score 62.5; DB 8; Length 156;
Best Local Similarity 23.2%; Pred. No. 87;
RESULT 1141
ID ADE76013 standard; protein; 156 AA.
DE Human PRO polypeptide #30.
PN US2003124663-A1.
PD 03-JUL-2003.
PA (GETH ) GENENTECH INC.
Query Match 9.7%; Score 62.5; DB 8; Length 156;
Best Local Similarity 23.2%; Pred. No. 87;
RESULT 1142
ID ADE37924 standard; protein; 156 AA.
DE Human PRO polypeptide #30.
PN US2003119119-A1.
PD 26-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 9.7%; Score 62.5; DB 8; Length 156;
Best Local Similarity 23.2%; Pred. No. 87;
RESULT 1143
ID ADE64534 standard; protein; 156 AA.
DE Human PRO polypeptide #30.
PN US2003119114-A1.
PD 26-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 9.7%; Score 62.5; DB 8; Length 156;
Best Local Similarity 23.2%; Pred. No. 87;
RESULT 1144
ID ADE41592 standard; protein; 156 AA.
DE Human secreted/transmembrane PRO polypeptide #171.
PN US2003100497-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 9.7%; Score 62.5; DB 8; Length 156;
Best Local Similarity 23.2%; Pred. No. 87;
RESULT 1145
ID ADE38869 standard; protein; 156 AA.
DE Human PRO polypeptide #30.
PN US2003096363-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 9.7%; Score 62.5; DB 8; Length 156;
Best Local Similarity 23.2%; Pred. No. 87;
RESULT 1146
ID ADE51943 standard; protein; 156 AA.
DE Human secreted/transmembrane polypeptide PRO6006.
PN US2003104562-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 9.7%; Score 62.5; DB 8; Length 156;
Best Local Similarity 23.2%; Pred. No. 87;
RESULT 1147
ID ADD90974 standard; protein; 156 AA.
DE Human secreted/transmembrane polypeptide PRO6006.
PN US2003138902-A1.
PD 24-JUL-2003.
PA (GETH ) GENENTECH INC.
Query Match 9.7%; Score 62.5; DB 8; Length 156;
Best Local Similarity 23.2%; Pred. No. 87;
RESULT 1148
ID ADE38753 standard; protein; 156 AA.
DE Human PRO polypeptide #30.
PN US2003108996-A1.
PD 12-JUN-2003.
PA (GETH ) GENENTECH INC.
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RESULT 1167
ID ADH27002 standard; protein; 156 AA.
DE Human secreted/transmembrane polypeptide PRO6006.
PN US2003119135-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 9.7%; Score 62.5; DB 8; Length 156;
Best Local Similarity 23.2%; Pred. No. 87;
RESULT 1168
ID ADH38270 standard; protein; 156 AA.
DE Novel human secreted and transmembrane protein PRO6006.
PN US2003119124-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 9.7%; Score 62.5; DB 8; Length 156;
Best Local Similarity 23.2%; Pred. No. 87;
RESULT 1169
ID ADH26886 standard; protein; 156 AA.
DE Human secreted/transmembrane polypeptide PRO6006.
PN US2003119134-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 9.7%; Score 62.5; DB 8; Length 156;
Best Local Similarity 23.2%; Pred. No. 87;
RESULT 1170
ID ADH38154 standard; protein; 156 AA.
DE Novel human secreted and transmembrane protein PRO6006.
PN US2003119123-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 9.7%; Score 62.5; DB 8; Length 156;
Best Local Similarity 23.2%; Pred. No. 87;
RESULT 1171
ID ADH38850 standard; protein; 156 AA.
DE Human secreted/transmembrane polypeptide PRO6006.
PN US2003119141-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 9.7%; Score 62.5; DB 8; Length 156;
Best Local Similarity 23.2%; Pred. No. 87;
RESULT 1172
ID ADH23788 standard; protein; 156 AA.
DE Human secreted/transmembrane polypeptide PRO6006.
PN US2003119142-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 9.7%; Score 62.5; DB 8; Length 156;
Best Local Similarity 23.2%; Pred. No. 87;
RESULT 1173
ID ADH40164 standard; protein; 156 AA.
DE Human PRO6006 protein.
PN US2003119132-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 9.7%; Score 62.5; DB 8; Length 156;
Best Local Similarity 23.2%; Pred. No. 87;
RESULT 1174
ID ADH40048 standard; protein; 156 AA.
DE Human PRO6006 protein.
PN US2003119133-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 9.7%; Score 62.5; DB 8; Length 156;
Best Local Similarity 23.2%; Pred. No. 87;
RESULT 1175
ID ADH31370 standard; protein; 156 AA.
DE Human PRO polypeptide #30.
PN US2003119138-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 9.7%; Score 62.5; DB 8; Length 156;
Best Local Similarity 23.2%; Pred. No. 87;
RESULT 1176
ID ADH58372 standard; protein; 156 AA.

ID ADH29248 standard; protein; 156 AA.
DE Human secreted/transmembrane polypeptide PRO6006.
PN US2003119136-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 9.7%; Score 62.5; DB 8; Length 156;
Best Local Similarity 23.2%; Pred. No. 87;
RESULT 1177
ID ADH49463 standard; protein; 156 AA.
DE Novel human secreted and transmembrane protein PRO6006.
PN US2003119127-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 9.7%; Score 62.5; DB 8; Length 156;
Best Local Similarity 23.2%; Pred. No. 87;
RESULT 1178
ID ADH51927 standard; protein; 156 AA.
DE Novel human secreted and transmembrane protein PRO6006.
PN US2003119125-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 9.7%; Score 62.5; DB 8; Length 156;
Best Local Similarity 23.2%; Pred. No. 87;
RESULT 1179
ID ADH49782 standard; protein; 156 AA.
DE Novel human secreted and transmembrane protein PRO6006.
PN US2003119128-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 9.7%; Score 62.5; DB 8; Length 156;
Best Local Similarity 23.2%; Pred. No. 87;
RESULT 1180
ID ADH52383 standard; protein; 156 AA.
DE Novel human secreted and transmembrane protein PRO6006.
PN US2003119130-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 9.7%; Score 62.5; DB 8; Length 156;
Best Local Similarity 23.2%; Pred. No. 87;
RESULT 1181
ID ADH43775 standard; protein; 156 AA.
DE Human PRO polypeptide #171.
PN US2003224984-A1.
PD 04-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match 9.7%; Score 62.5; DB 8; Length 156;
Best Local Similarity 23.2%; Pred. No. 87;
RESULT 1182
ID ADH52499 standard; protein; 156 AA.
DE Novel human secreted and transmembrane protein PRO6006.
PN US2003119129-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 9.7%; Score 62.5; DB 8; Length 156;
Best Local Similarity 23.2%; Pred. No. 87;
RESULT 1183
ID ADH58496 standard; protein; 156 AA.
DE Novel human secreted and transmembrane protein PRO6006.
PN US2003119121-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 9.7%; Score 62.5; DB 8; Length 156;
Best Local Similarity 23.2%; Pred. No. 87;
RESULT 1184
ID ADH51811 standard; protein; 156 AA.
DE Novel human secreted and transmembrane protein PRO6006.
PN US2003119126-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 9.7%; Score 62.5; DB 8; Length 156;
Best Local Similarity 23.2%; Pred. No. 87;
RESULT 1185
ID ADH58372 standard; protein; 156 AA.

DE Novel human secreted and transmembrane protein PRO6006.
PN US2003119122-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC. 9.7%; Score 62.5; DB 8; Length 156;
Query Match 23.2%; Pred. No. 87;
Best Local Similarity 23.2%; Pred. No. 87;
RESULT 1186
ID ADI13569 standard; protein; 156 AA.
DE Novel human secreted and transmembrane protein PRO6006.
PN US2003119131-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC. 9.7%; Score 62.5; DB 8; Length 156;
Query Match 23.2%; Pred. No. 87;
Best Local Similarity 23.2%; Pred. No. 87;
RESULT 1187
ID ADK00825 standard; protein; 156 AA.
DE Human PRO polypeptide #30.
PN US2003186373-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC. 9.7%; Score 62.5; DB 8; Length 156;
Query Match 23.2%; Pred. No. 87;
Best Local Similarity 23.2%; Pred. No. 87;
RESULT 1188
ID ADL08566 standard; protein; 156 AA.
DE Human secreted/transmembrane polypeptide PRO6006.
PN US2003186372-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC. 9.7%; Score 62.5; DB 8; Length 156;
Query Match 23.2%; Pred. No. 87;
Best Local Similarity 23.2%; Pred. No. 87;
RESULT 1189
ID ADR83120 standard; protein; 156 AA.
DE Human PRO polypeptide #171.
PN US2004043927-A1.
PD 04-MAR-2004.
PA (GETH) GENENTECH INC. 9.7%; Score 62.5; DB 8; Length 156;
Query Match 23.2%; Pred. No. 87;
Best Local Similarity 23.2%; Pred. No. 87;
RESULT 1190
ID ADN05526 standard; protein; 156 AA.
DE Antiposoriatic protein sequence #929.
PN WO2004028479-A2.
PD 08-APR-2004.
PA (GETH) GENENTECH INC. 9.7%; Score 62.5; DB 8; Length 156;
Query Match 23.2%; Pred. No. 87;
Best Local Similarity 23.2%; Pred. No. 87;
RESULT 1191
ID AAY44194 standard; peptide; 164 AA.
DE Hexa-His tagged human keratinocyte-derived RNase-like protein.
PN EP943679-A1.
PD 22-SEP-1999.
PA (INNO-) INNOGENETICS NV. 9.7%; Score 62.5; DB 2; Length 164;
Query Match 23.2%; Pred. No. 92;
Best Local Similarity 23.2%; Pred. No. 92;
RESULT 1192
ID ADM17825 standard; protein; 323 AA.
DE Pirus radiata transcription factor protein SBP family Seq 1601.
PN WO200501050-A2.
PD 06-JAN-2005.
PA (ARBO-) ARBORGEN LLC. 9.7%; Score 62.5; DB 9; Length 323;
Query Match 30.7%; Pred. No. 2.1e+02;
Best Local Similarity 30.7%; Pred. No. 2.1e+02;
RESULT 1193
ID ABP73597 standard; protein; 328 AA.
DE Candida albicans essential protein SEQ ID NO 7434.
PN WO200253728-A2.
PD 11-JUL-2002.
PA (ELIT-) ELITRA PHARM INC. 9.7%; Score 62.5; DB 5; Length 328;
Query Match 24.4%; Pred. No. 2.1e+02;
Best Local Similarity 24.4%; Pred. No. 2.1e+02;
RESULT 1194
ID AAY47239 standard; protein; 414 AA.
DE Human apolipoprotein AI regulatory protein-1.

PN US5721096-A.
PD 24-FEB-1998.
PA (CHIL-) CHILDRENS MEDICAL CENT. 9.7%; Score 62.5; DB 2; Length 414;
Query Match 25.3%; Pred. No. 2.8e+02;
Best Local Similarity 25.3%; Pred. No. 2.8e+02;
RESULT 1195
ID ABB57372 standard; protein; 414 AA.
DE Mouse ischaemic condition related protein sequence SEQ ID NO:1055.
PN WO200188188-A2.
PD 22-NOV-2001.
PA (UTNI-) UNIV NIHON SCHOOL JURIDICAL PERSON. 9.7%; Score 62.5; DB 5; Length 414;
Query Match 25.3%; Pred. No. 2.8e+02;
Best Local Similarity 25.3%; Pred. No. 2.8e+02;
RESULT 1196
ID ADS60663 standard; protein; 414 AA.
DE Rat Protein O09018, SEQ ID NO 6575.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP. 9.7%; Score 62.5; DB 7; Length 414;
PA (FARB) BAYER AG. 9.7%; Score 62.5; DB 7; Length 414;
Query Match 25.3%; Pred. No. 2.8e+02;
Best Local Similarity 25.3%; Pred. No. 2.8e+02;
RESULT 1197
ID ADS60665 standard; protein; 414 AA.
DE Human Protein P24468, SEQ ID NO 6577.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP. 9.7%; Score 62.5; DB 7; Length 414;
PA (FARB) BAYER AG. 9.7%; Score 62.5; DB 7; Length 414;
Query Match 25.3%; Pred. No. 2.8e+02;
Best Local Similarity 25.3%; Pred. No. 2.8e+02;
RESULT 1198
ID ADP05637 standard; protein; 414 AA.
DE Mouse nuclear receptor protein SeqID11.
PN WO2004045369-A2.
PD 03-JUN-2004.
PA (NURA-) NURA INC. 9.7%; Score 62.5; DB 8; Length 414;
Query Match 25.3%; Pred. No. 2.8e+02;
Best Local Similarity 25.3%; Pred. No. 2.8e+02;
RESULT 1199
ID ADP05635 standard; protein; 414 AA.
DE Human nuclear receptor protein SeqID9.
PN WO2004045369-A2.
PD 03-JUN-2004.
PA (NURA-) NURA INC. 9.7%; Score 62.5; DB 8; Length 414;
Query Match 25.3%; Pred. No. 2.8e+02;
Best Local Similarity 25.3%; Pred. No. 2.8e+02;
RESULT 1200
ID ADX07466 standard; protein; 414 AA.
DE Cyclin-dependent kinase modulation biomarker SEQ ID NO 2031.
PN WO2005012875-A2.
PD 10-FEB-2005.
PA (BRIM) BRISTOL-MYERS SQUIBB CO. 9.7%; Score 62.5; DB 9; Length 414;
Query Match 25.3%; Pred. No. 2.8e+02;
Best Local Similarity 25.3%; Pred. No. 2.8e+02;
RESULT 1201
ID ADC31143 standard; protein; 516 AA.
DE Human novel polypeptide sequence, SEQ ID NO:1225.
PN WO2003029271-A2.
PD 10-APR-2003.
PA (HYSE-) HYSEQ INC. 9.7%; Score 62.5; DB 7; Length 516;
Query Match 30.8%; Pred. No. 3.6e+02;
Best Local Similarity 30.8%; Pred. No. 3.6e+02;
RESULT 1202
ID ABU96691 standard; protein; 569 AA.
DE Human nucleic acid-associated protein (NAAP) #20.
PN WO2003023003-A2.
PD 20-MAR-2003.
PA (INCY-) INCYTE GENOMICS INC. 9.7%; Score 62.5; DB 6; Length 569;
Query Match 29.0%; Pred. No. 4.1e+02;
Best Local Similarity 29.0%; Pred. No. 4.1e+02;
RESULT 1203
ID ABM65727 standard; protein; 751 AA.

DE Propionibacterium acnes immunogenic polypeptide #30403.
PN WO2003033515-A1.
PD 24-APR-2003.
PA (CORI-) CORIXA CORP.
Query Match 9.7%; Score 62.5; DB 6; Length 751;
Best Local Similarity 29.0%; Pred. No. 5.7e+02;
RESULT 1204
ID ADA55031 standard; protein; 752 AA.
DE Human protein, SEQ ID 2599.
PN EP1293569-A2.
PD 19-MAR-2003.
PA (HELI-) HELIX RES INST.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 9.7%; Score 62.5; DB 6; Length 752;
Best Local Similarity 29.0%; Pred. No. 5.7e+02;
RESULT 1205
ID AAU72900 standard; protein; 1094 AA.
DE Human metalloprotease partial protein sequence #12.
PN WO200183782-A2.
PD 08-NOV-2001.
PA (SUGS-) SUGEN INC.
Query Match 9.7%; Score 62.5; DB 5; Length 1094;
Best Local Similarity 24.1%; Pred. No. 8.9e+02;
RESULT 1206
ID ABP01721 standard; protein; 70 AA.
DE Human ORFX protein sequence SEQ ID NO:3424.
PN WO200192523-A2.
PD 06-DEC-2001.
PA (CURA-) CURAGEN CORP.
Query Match 9.6%; Score 62; DB 5; Length 70;
Best Local Similarity 31.1%; Pred. No. 38;
RESULT 1207
ID AAY44195 standard; peptide; 136 AA.
DE Hexa-His tagged human keratinocyte-derived RNase-like mature protein.
PN EP943679-A1.
PD 22-SEP-1999.
PA (INNO-) INNOGENETICS NV.
Query Match 9.6%; Score 62; DB 2; Length 136;
Best Local Similarity 22.8%; Pred. No. 84;
RESULT 1208
ID ABO68420 standard; protein; 151 AA.
DE Pseudomonas aeruginosa polypeptide #595.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 9.8%; Score 62; DB 7; Length 151;
Best Local Similarity 22.2%; Pred. No. 95;
RESULT 1209
ID ADE08357 standard; protein; 166 AA.
DE Novel protein (useful for identifying genetic disorders) #512.
PN WO2003054152-A2.
PD 03-JUL-2003.
PA (HYSE-) HYSEQ INC.
Query Match 9.6%; Score 62; DB 7; Length 166;
Best Local Similarity 24.6%; Pred. No. 1.1e+02;
RESULT 1210
ID ADY04755 standard; protein; 182 AA.
DE Plant full length insert polypeptide seqid 60570.
PN US2004034888-A1.
PD 19-FEB-2004.
PA (LIUJ/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABA/) TABASKA J E.
PA (CAOY/) CAO Y.
Query Match 9.6%; Score 62; DB 8; Length 182;
Best Local Similarity 25.9%; Pred. No. 1.2e+02;
RESULT 1211
ID ABB78817 standard; protein; 218 AA.
DE Human NOV8 protein sequence SEQ ID NO:24.
PN WO200230974-A2.
PD 18-APR-2002.

PA (CURA-) CURAGEN CORP.
PA (MILL/) MILLET I.
Query Match 9.6%; Score 62; DB 5; Length 218;
Best Local Similarity 26.6%; Pred. No. 1.5e+02;
RESULT 1212
ID AAU18157 standard; protein; 303 AA.
DE Novel human DNA-binding protein #4.
PN WO200155162-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 9.6%; Score 62; DB 4; Length 303;
Best Local Similarity 25.0%; Pred. No. 2.2e+02;
RESULT 1213
ID ABG92578 standard; protein; 303 AA.
DE Human DNA-binding protein #4.
PN US2002102638-A1.
PD 01-AUG-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 9.6%; Score 62; DB 5; Length 303;
Best Local Similarity 25.0%; Pred. No. 2.2e+02;
RESULT 1214
ID ADC25295 standard; protein; 303 AA.
DE Human extracellular matrix protein from gene 4.
PN US2003049650-A1.
PD 13-MAR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 9.6%; Score 62; DB 7; Length 303;
Best Local Similarity 25.0%; Pred. No. 2.2e+02;
RESULT 1215
ID ABR53477 standard; protein; 371 AA.
DE Protein sequence #SEQ ID 1819.
PN EP1258494-A1.
PD 20-NOV-2002.
PA (CELL-) CELLZOME AG.
Query Match 9.6%; Score 62; DB 6; Length 371;
Best Local Similarity 23.8%; Pred. No. 2.8e+02;
RESULT 1216
ID ADK64574 standard; protein; 371 AA.
DE Disease treating protein complex-derived protein #1088.
PN EP1338608-A2.
PD 27-AUG-2003.
PA (CELL-) CELLZOME AG.
Query Match 9.6%; Score 62; DB 7; Length 371;
Best Local Similarity 23.8%; Pred. No. 2.8e+02;
RESULT 1217
ID ABO58806 standard; protein; 412 AA.
DE Human genome derived single exon protein #5040.
PN US2003194704-A1.
PD 16-OCT-2003.
PA (PENN/) PENN S G.
PA (RANK/) RANK D R.
PA (HANZ/) HANZEL D K.
Query Match 9.6%; Score 62; DB 8; Length 412;
Best Local Similarity 28.0%; Pred. No. 3.2e+02;
RESULT 1218
ID ADB84071 standard; protein; 577 AA.
DE Frog NURR1-related protein sequence, SEQ ID 84.
PN WO2003012040-A2.
PD 13-FEB-2003.
PA (BAYU) BAYLOR COLLEGE MEDICINE.
Query Match 9.6%; Score 62; DB 7; Length 577;
Best Local Similarity 31.7%; Pred. No. 4.7e+02;
RESULT 1219
ID ADL22717 standard; protein; 705 AA.
DE Human disease detection and treatment (MDDT) protein - SEQ ID 166.
PN WO2003062379-A2.
PD 31-JUL-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 9.6%; Score 62; DB 7; Length 705;
Best Local Similarity 31.9%; Pred. No. 6e+02;
RESULT 1220

ID ABB65602 standard; protein; 954 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 23598.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY. 9.6%; Score 62; DB 4; Length 954;
Best Local Similarity 24.1%; Pred. No. 8.6e+02;
Query Match 9.6%; Score 62; DB 4; Length 954;
Best Local Similarity 24.1%; Pred. No. 8.6e+02;
RESULT 1221
ID ABO73001 standard; protein; 959 AA.
DE Pseudomonas aeruginosa polypeptide #5176.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 9.6%; Score 62; DB 7; Length 959;
Best Local Similarity 27.1%; Pred. No. 8.7e+02;
RESULT 1222
ID ABB62516 standard; protein; 1162 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 14340.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY. 9.6%; Score 62; DB 4; Length 1162;
Best Local Similarity 31.2%; Pred. No. 1.1e+03;
RESULT 1223
ID ADK67911 standard; protein; 1270 AA.
DE Human extracellular messenger (EXMES) polypeptide.
PN WO2004013292-A2.
PD 12-FEB-2004.
PA (INCY-) INCYTE CORP. 9.6%; Score 62; DB 8; Length 1270;
Best Local Similarity 28.1%; Pred. No. 1.2e+03;
Query Match 9.6%; Score 62; DB 8; Length 1270;
Best Local Similarity 28.1%; Pred. No. 1.2e+03;
RESULT 1224
ID ADQ14315 standard; protein; 1424 AA.
DE Human collagen type IV alpha 3 (Goodpasture antigen).
PN WO2004060262-A2.
PD 22-JUL-2004.
PA (LORA-) LORANTIS LTD. 9.6%; Score 62; DB 8; Length 1424;
Best Local Similarity 25.7%; Pred. No. 1.4e+03;
Query Match 9.6%; Score 62; DB 8; Length 1424;
Best Local Similarity 25.7%; Pred. No. 1.4e+03;
RESULT 1225
ID ADR41697 standard; protein; 1424 AA.
DE Human collagen (aa sequence), type IV, alpha 3 (Goodpasture antigen).
PN WO2004064863-A1.
PD 05-AUG-2004.
PA (LORA-) LORANTIS LTD. 9.6%; Score 62; DB 8; Length 1424;
Best Local Similarity 25.7%; Pred. No. 1.4e+03;
Query Match 9.6%; Score 62; DB 8; Length 1424;
Best Local Similarity 25.7%; Pred. No. 1.4e+03;
RESULT 1226
ID ADU06693 standard; protein; 1424 AA.
DE Novel bronchial cancer-associated human protein SeqID919.
PN DE10316701-A1.
PD 04-NOV-2004.
PA (HINZ/) HINZMANN B. 9.6%; Score 62; DB 8; Length 1424;
PA (HERM/) HERMANN K. 9.6%; Score 62; DB 8; Length 1424;
PA (CAST/) HEIDEN CASTANOS-VELEZ E. 9.6%; Score 62; DB 8; Length 1424;
Query Match 9.6%; Score 62; DB 8; Length 1424;
Best Local Similarity 25.7%; Pred. No. 1.4e+03;
RESULT 1227
ID AEB77777 standard; protein; 1424 AA.
DE Human Goodpasture antigen, collagen, type IV, alpha 3.
PN WO2005073250-A2.
PD 11-AUG-2005.
PA (LORA-) LORANTIS LTD. 9.6%; Score 62; DB 9; Length 1424;
Best Local Similarity 25.7%; Pred. No. 1.4e+03;
Query Match 9.6%; Score 62; DB 9; Length 1424;
Best Local Similarity 25.7%; Pred. No. 1.4e+03;
RESULT 1228
ID ABM84483 standard; protein; 1611 AA.
DE Human diagnostic and therapeutic pproteins SEQ ID NO:4732.
PN WO2004023973-A2.
PD 25-NAR-2004.
PA (INCY-) INCYTE CORP. 9.6%; Score 62; DB 8; Length 1611;
Query Match 9.6%; Score 62; DB 8; Length 1611;
Best Local Similarity 25.7%; Pred. No. 1.6e+03;
RESULT 1229
ID ABA64562 standard; protein; 1642 AA.
DE Human lupus-related protein #10.
PN WO2004076639-A2.
PD 10-SEP-2004.
PA (AMHP) WYETH. 9.6%; Score 62; DB 8; Length 1642;
PA (OTOO/) O'TOOLE M M. 9.6%; Score 62; DB 8; Length 1642;
PA (WEIL/) WEI L. 9.6%; Score 62; DB 8; Length 1642;
Query Match 9.6%; Score 62; DB 8; Length 1642;
Best Local Similarity 25.7%; Pred. No. 1.6e+03;
RESULT 1230
ID ADD47063 standard; protein; 1670 AA.
DE Human Protein NP_000082, SEQ ID NO 12751.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP. 9.6%; Score 62; DB 7; Length 1670;
PA (FARB) BAYER AG. 9.6%; Score 62; DB 7; Length 1670;
Query Match 9.6%; Score 62; DB 7; Length 1670;
Best Local Similarity 25.7%; Pred. No. 1.7e+03;
RESULT 1231
ID ABA64561 standard; protein; 1670 AA.
DE Human lupus-related protein #9.
PN WO2004076639-A2.
PD 10-SEP-2004.
PA (AMHP) WYETH. 9.6%; Score 62; DB 8; Length 1670;
PA (OTOO/) O'TOOLE M M. 9.6%; Score 62; DB 8; Length 1670;
PA (WEIL/) WEI L. 9.6%; Score 62; DB 8; Length 1670;
Query Match 9.6%; Score 62; DB 8; Length 1670;
Best Local Similarity 25.7%; Pred. No. 1.7e+03;
RESULT 1232
ID AAB33149 standard; protein; 112 AA.
DE Pinus radiata transcription factor protein sequence #266.
PN WO200053724-A2.
PD 14-SEP-2000.
PA (GENE-) GENESIS RES & DEV CORP LTD. 9.5%; Score 61.5; DB 3; Length 112;
PA (FLET-) FLETCHER CHALLENGE FORESTS LTD. 9.5%; Score 61.5; DB 3; Length 112;
Query Match 9.5%; Score 61.5; DB 3; Length 112;
Best Local Similarity 27.1%; Pred. No. 76;
RESULT 1233
ID AAG00283 standard; protein; 121 AA.
DE Human secreted protein, SEQ ID NO: 4364.
PN EP1033401-A2.
PD 06-SEP-2000.
PA (GEST) GENSET. 9.5%; Score 61.5; DB 3; Length 121;
Query Match 9.5%; Score 61.5; DB 3; Length 121;
Best Local Similarity 22.3%; Pred. No. 84;
RESULT 1234
ID ABU03604 standard; protein; 121 AA.
DE Human expressed protein tag (EPT) #270.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCO INC. 9.5%; Score 61.5; DB 6; Length 121;
Query Match 9.5%; Score 61.5; DB 6; Length 121;
Best Local Similarity 22.3%; Pred. No. 84;
RESULT 1235
ID ABO78982 standard; protein; 226 AA.
DE Pseudomonas aeruginosa polypeptide #1157.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP. 9.5%; Score 61.5; DB 7; Length 226;
Query Match 9.5%; Score 61.5; DB 7; Length 226;
Best Local Similarity 29.5%; Pred. No. 1.8e+02;
RESULT 1236
ID ABO81392 standard; protein; 244 AA.
DE Pseudomonas aeruginosa polypeptide #13567.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP. 9.5%; Score 61.5; DB 7; Length 244;
Query Match 9.5%; Score 61.5; DB 7; Length 244;
Best Local Similarity 26.9%; Pred. No. 1.9e+02;
RESULT 1237
ID ABO83546 standard; protein; 249 AA.
DE Pseudomonas aeruginosa polypeptide #15721.

PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 9.5%; Score 61.5; DB 7; Length 249;
Best Local Similarity 24.7%; Pred. No. 2e+02;
RESULT 1238
ID AAR47150 standard; protein; 252 AA.
DE IL-2 receptor gamma chain.
PN EP578932-A2.
PD 19-JAN-1994.
PA (AJIN) AJINOMOTO KK.
PA (SUGA/) SUGAMURA K.
Query Match 9.5%; Score 61.5; DB 2; Length 252;
Best Local Similarity 22.3%; Pred. No. 2e+02;
RESULT 1239
ID ABU03606 standard; protein; 252 AA.
DE Human expressed protein tag (EPT) #272.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 9.5%; Score 61.5; DB 6; Length 252;
Best Local Similarity 22.3%; Pred. No. 2e+02;
RESULT 1240
ID ABO77598 standard; protein; 269 AA.
DE Pseudomonas aeruginosa polypeptide #9773.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 9.5%; Score 61.5; DB 7; Length 269;
Best Local Similarity 31.5%; Pred. No. 2.2e+02;
RESULT 1241
ID ABB97515 standard; protein; 277 AA.
DE Novel human protein SEQ ID NO: 783.
PN WO200222860-A2.
PD 21-MAR-2002.
PA (HYSE-) HYSEQ INC.
Query Match 9.5%; Score 61.5; DB 5; Length 277;
Best Local Similarity 20.9%; Pred. No. 2.2e+02;
RESULT 1242
ID ADP22440 standard; protein; 301 AA.
DE Sea-squirt (Ciona intestinalis) zinc finger protein #7.
PN JP2004057126-A.
PD 26-FEB-2004.
PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
Query Match 9.5%; Score 61.5; DB 8; Length 301;
Best Local Similarity 33.3%; Pred. No. 2.5e+02;
RESULT 1243
ID ABR61610 standard; peptide; 341 AA.
DE IL-2 common gamma chain (cgammac) fragment (residues 1-341).
PN WO2003087374-A1.
PD 23-OCT-2003.
PA (YEDA) YEDA RES & DEV CO LTD.
Query Match 9.5%; Score 61.5; DB 7; Length 341;
Best Local Similarity 22.3%; Pred. No. 2.9e+02;
RESULT 1244
ID ABR61609 standard; peptide; 357 AA.
DE IL-2 common gamma chain (cgammac) fragment (residues 1-357).
PN WO2003087374-A1.
PD 23-OCT-2003.
PA (YEDA) YEDA RES & DEV CO LTD.
Query Match 9.5%; Score 61.5; DB 7; Length 357;
Best Local Similarity 22.3%; Pred. No. 3e+02;
RESULT 1245
ID ABM87580 standard; protein; 359 AA.
DE Rice abiotic stress responsive polypeptide SEQ ID NO:5826.
PN WO2003008540-A2.
PD 30-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 9.5%; Score 61.5; DB 7; Length 359;
Best Local Similarity 23.9%; Pred. No. 3.1e+02;
RESULT 1246
ID AAE13734 standard; protein; 360 AA.
DE Human soluble IL-2Rgamma/kappa light chain chimeric DNA construct.

PN WO200177171-A2.
PD 18-OCT-2001.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 9.5%; Score 61.5; DB 5; Length 360;
Best Local Similarity 22.3%; Pred. No. 3.1e+02;
RESULT 1247
ID AAR47148 standard; protein; 369 AA.
DE IL-2 receptor gamma chain.
PN EP578932-A2.
PD 19-JAN-1994.
PA (AJIN) AJINOMOTO KK.
PA (SUGA/) SUGAMURA K.
Query Match 9.5%; Score 61.5; DB 2; Length 369;
Best Local Similarity 22.3%; Pred. No. 3.2e+02;
RESULT 1248
ID AAU96932 standard; protein; 369 AA.
DE Human cytokine receptor common gamma chain.
PN US6372898-B1.
PD 16-APR-2002.
PA (SCHE) SCHERING CORP.
Query Match 9.5%; Score 61.5; DB 5; Length 369;
Best Local Similarity 22.3%; Pred. No. 3.2e+02;
RESULT 1249
ID ABU03612 standard; protein; 369 AA.
DE Human expressed protein tag (EPT) #278.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 9.5%; Score 61.5; DB 6; Length 369;
Best Local Similarity 22.3%; Pred. No. 3.2e+02;
RESULT 1250
ID ABU03613 standard; protein; 369 AA.
DE Human expressed protein tag (EPT) #279.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 9.5%; Score 61.5; DB 6; Length 369;
Best Local Similarity 22.3%; Pred. No. 3.2e+02;
RESULT 1251
ID ABU03602 standard; protein; 369 AA.
DE Human expressed protein tag (EPT) #268.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 9.5%; Score 61.5; DB 6; Length 369;
Best Local Similarity 22.3%; Pred. No. 3.2e+02;
RESULT 1252
ID ABU03603 standard; protein; 369 AA.
DE Human expressed protein tag (EPT) #269.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 9.5%; Score 61.5; DB 6; Length 369;
Best Local Similarity 22.3%; Pred. No. 3.2e+02;
RESULT 1253
ID ABU03605 standard; protein; 369 AA.
DE Human expressed protein tag (EPT) #271.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 9.5%; Score 61.5; DB 6; Length 369;
Best Local Similarity 22.3%; Pred. No. 3.2e+02;
RESULT 1254
ID ABU03600 standard; protein; 369 AA.
DE Human expressed protein tag (EPT) #266.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 9.5%; Score 61.5; DB 6; Length 369;
Best Local Similarity 22.3%; Pred. No. 3.2e+02;
RESULT 1255
ID ABU03601 standard; protein; 369 AA.
DE Human expressed protein tag (EPT) #267.

PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 9.5%; Score 61.5; DB 6; Length 369;
Best Local Similarity 22.3%; Pred. No. 3.2e+02;
RESULT 1256
ID ADP65163 standard; protein; 369 AA.
DE Human interleukin 2 receptor, gamma chain, precursor, Interleukin-2.
PN WO2003072827-A1.
PD 04-SEP-2003.
PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.
Query Match 9.5%; Score 61.5; DB 7; Length 369;
Best Local Similarity 22.3%; Pred. No. 3.2e+02;
RESULT 1257
ID ADP12957 standard; protein; 369 AA.
DE Protein encoding reference mRNA sequence #42.
PN WO2004042346-A2.
PD 21-MAY-2004.
PA (EXPR-) EXPRESSION DIAGNOSTICS INC.
Query Match 9.5%; Score 61.5; DB 8; Length 369;
Best Local Similarity 22.3%; Pred. No. 3.2e+02;
RESULT 1258
ID ADU07285 standard; protein; 369 AA.
DE Human IL-9R gamma chain.
PN WO2004091519-A2.
PD 28-OCT-2004.
PA (MEDI-) MEDIMMUNE INC.
Query Match 9.5%; Score 61.5; DB 8; Length 369;
Best Local Similarity 22.3%; Pred. No. 3.2e+02;
RESULT 1259
ID ADT88352 standard; protein; 369 AA.
DE Human IL-19R gamma subunit isoform seqid 60.
PN WO2004091510-A2.
PD 28-OCT-2004.
PA (MEDI-) MEDIMMUNE INC.
Query Match 9.5%; Score 61.5; DB 8; Length 369;
Best Local Similarity 22.3%; Pred. No. 3.2e+02;
RESULT 1260
ID ADY19463 standard; protein; 369 AA.
DE PRO polypeptide SEQ ID NO 5269.
PN WO2005016962-A2.
PD 24-FEB-2005.
PA (GETH) GENENTECH INC.
Query Match 9.5%; Score 61.5; DB 9; Length 369;
Best Local Similarity 22.3%; Pred. No. 3.2e+02;
RESULT 1261
ID AED66944 standard; protein; 369 AA.
DE Human interleukin-9 receptor (IL-9R) gamma chain protein, SEQ ID: 60.
PN US2005260204-A1.
PD 24-NOV-2005.
PA (MEDI-) MEDIMMUNE INC.
Query Match 9.5%; Score 61.5; DB 9; Length 369;
Best Local Similarity 22.3%; Pred. No. 3.2e+02;
RESULT 1262
ID ADX95163 standard; protein; 415 AA.
DE Plant full length insert polypeptide seqid 57827.
PN US2004034888-A1.
PD 19-FEB-2004.
PA (LIUJ) LIU J.
PA (ZHOU) ZHOU Y.
PA (KOVA) KOVALIC D K.
PA (SCRE) SCREEN S E.
PA (TAB) TABASKA J E.
PA (CAOY) CAO Y.
Query Match 9.5%; Score 61.5; DB 8; Length 415;
Best Local Similarity 22.2%; Pred. No. 3.6e+02;
RESULT 1263
ID ADY09233 standard; protein; 420 AA.
DE Plant full length insert polypeptide seqid 65048.
PN US2004034888-A1.
PD 19-FEB-2004.
PA (LIUJ) LIU J.
PA (ZHOU) ZHOU Y.

PA (KOVA) KOVALIC D K.
PA (SCRE) SCREEN S E.
PA (TAB) TABASKA J E.
PA (CAOY) CAO Y.
Query Match 9.5%; Score 61.5; DB 8; Length 420;
Best Local Similarity 22.2%; Pred. No. 3.7e+02;
RESULT 1264
ID AEF32726 standard; protein; 444 AA.
DE Human coronavirus HKU1 amino acid sequence SEQ ID NO:1312.
PN US2006018923-A1.
PD 26-JAN-2006.
PA (YUEN) YUEN K Y.
PA (WOOC) WOO C Y P.
PA (LAUK) LAU K P S.
PA (CHAN) CHAN K H.
PA (POON) POON L M.
PA (PEIR) PEIRIS J S M.
PA (GUAN) GUAN Y.
Query Match 9.5%; Score 61.5; DB 10; Length 444;
Best Local Similarity 32.1%; Pred. No. 3.9e+02;
RESULT 1265
ID AAW31646 standard; protein; 482 AA.
DE Human cytokine receptor gc chain-Ig fusion protein.
PN WO9743416-A1.
PD 20-NOV-1997.
PA (BIOJ) BIOGEN INC.
Query Match 9.5%; Score 61.5; DB 2; Length 482;
Best Local Similarity 22.3%; Pred. No. 4.4e+02;
RESULT 1266
ID ABU03608 standard; protein; 482 AA.
DE Human expressed protein tag (EPT) #274.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 9.5%; Score 61.5; DB 6; Length 482;
Best Local Similarity 22.3%; Pred. No. 4.4e+02;
RESULT 1267
ID AAB73600 standard; protein; 513 AA.
DE Zinc finger protein 57.
PN WO200130840-A1.
PD 03-MAY-2001.
PA (SHAN) SHANGHAI BIO ROAD GENE DEV LTD.
Query Match 9.5%; Score 61.5; DB 4; Length 513;
Best Local Similarity 20.9%; Pred. No. 4.7e+02;
RESULT 1268
ID ADM87387 standard; protein; 545 AA.
DE Human protein SEQ ID NO:480.
PN WO2004009834-A2.
PD 29-JAN-2004.
PA (NUVE-) NUVELO INC.
Query Match 9.5%; Score 61.5; DB 8; Length 545;
Best Local Similarity 20.9%; Pred. No. 5e+02;
RESULT 1269
ID ADP04927 standard; protein; 573 AA.
DE Sea squirt protein with tissue specific expression in development Seq522.
PN JP2004057129-A.
PD 26-FEB-2004.
PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
Query Match 9.5%; Score 61.5; DB 8; Length 573;
Best Local Similarity 28.6%; Pred. No. 5.3e+02;
RESULT 1270
ID AAB85509 standard; protein; 629 AA.
DE Human protein kinase SGK214.
PN WO200155356-A2.
PD 02-AUG-2001.
PA (SUGE-) SUGEN INC.
Query Match 9.5%; Score 61.5; DB 4; Length 629;
Best Local Similarity 30.8%; Pred. No. 6e+02;
RESULT 1271
ID AAY92202 standard; protein; 691 AA.
DE Fusion polypeptide 603, IL-4 trap.
PN WO200018932-A2.
PD 06-APR-2000.

PA (REGE-) REGENERON PHARM INC.
Query Match 9.5%; Score 61.5; DB 3; Length 691;
Best Local Similarity 22.3%; Pred. No. 6.7e+02;
RESULT 1272
ID ABU03610 standard; protein; 691 AA.
DE Human expressed protein tag (EPT) #276.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 9.5%; Score 61.5; DB 6; Length 691;
Best Local Similarity 22.3%; Pred. No. 6.7e+02;
RESULT 1273
ID ABW02176 standard; protein; 691 AA.
DE Human cytokine trap-603 protein.
PN US2003143697-A1.
PD 31-JUL-2003.
PA (STAH/) STAHL N.
PA (YANC/) YANCOPOULOS G D.
Query Match 9.5%; Score 61.5; DB 7; Length 691;
Best Local Similarity 22.3%; Pred. No. 6.7e+02;
RESULT 1274
ID AAY92201 standard; protein; 694 AA.
DE Fusion polypeptide 424, IL-4 trap.
PN WO200018932-A2.
PD 06-APR-2000.
PA (REGE-) REGENERON PHARM INC.
Query Match 9.5%; Score 61.5; DB 3; Length 694;
Best Local Similarity 22.3%; Pred. No. 6.7e+02;
RESULT 1275
ID AAY92203 standard; protein; 694 AA.
DE Fusion polypeptide 622, IL-4 trap.
PN WO200018932-A2.
PD 06-APR-2000.
PA (REGE-) REGENERON PHARM INC.
Query Match 9.5%; Score 61.5; DB 3; Length 694;
Best Local Similarity 22.3%; Pred. No. 6.7e+02;
RESULT 1276
ID ABU03611 standard; protein; 694 AA.
DE Human expressed protein tag (EPT) #277.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 9.5%; Score 61.5; DB 6; Length 694;
Best Local Similarity 22.3%; Pred. No. 6.7e+02;
RESULT 1277
ID ABU03609 standard; protein; 694 AA.
DE Human expressed protein tag (EPT) #275.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 9.5%; Score 61.5; DB 6; Length 694;
Best Local Similarity 22.3%; Pred. No. 6.7e+02;
RESULT 1278
ID ABW02174 standard; protein; 694 AA.
DE Human cytokine trap-424 protein.
PN US2003143697-A1.
PD 31-JUL-2003.
PA (STAH/) STAHL N.
PA (YANC/) YANCOPOULOS G D.
Query Match 9.5%; Score 61.5; DB 7; Length 694;
Best Local Similarity 22.3%; Pred. No. 6.7e+02;
RESULT 1279
ID ABW02176 standard; protein; 694 AA.
DE Human cytokine trap-622 protein.
PN US2003143697-A1.
PD 31-JUL-2003.
PA (STAH/) STAHL N.
PA (YANC/) YANCOPOULOS G D.
Query Match 9.5%; Score 61.5; DB 7; Length 694;
Best Local Similarity 22.3%; Pred. No. 6.7e+02;
RESULT 1280
ID ABB65096 standard; protein; 707 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 22080.

PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 9.5%; Score 61.5; DB 4; Length 707;
Best Local Similarity 24.2%; Pred. No. 6.9e+02;
RESULT 1281
ID ABJ19352 standard; protein; 1247 AA.
DE NOVX related protein SEQ ID NO 70.
PN WO200299062-A2.
PD 12-DEC-2002.
PA (CURA-) CURAGEN CORP.
Query Match 9.5%; Score 61.5; DB 6; Length 1247;
Best Local Similarity 33.3%; Pred. No. 1.4e+03;
RESULT 1282
ID ADO41704 standard; protein; 1247 AA.
DE Novel human polypeptide NOV26a.
PN US2004018555-A1.
PD 29-JAN-2004.
PA (ANDE/) ANDERSON D W.
PA (ZERR/) ZERRHUSEN B D.
PA (LILL/) LI L.
PA (ZHON/) ZHONG M.
PA (CASW/) CASHMAN S J.
PA (GERL/) GERLACH V.
PA (SHIM/) SHIMKETS R A.
PA (GORM/) GORMAN L.
PA (PENA/) PENA C E A.
PA (KEKU/) KEKUDA R.
PA (PATT/) PATTURAJAN M.
PA (SPYT/) SPYTEK K A.
PA (LEIT/) LEITE M W.
PA (RAST/) RASTELLI L.
PA (MACD/) MACDOUGALL J R.
PA (TAUP/) TAUPIER R J.
PA (GUOX/) GUO X S.
PA (MILL/) MILLER C E.
PA (SHEN/) SHENOY S G.
PA (HJAL/) HJALT T.
PA (VOSS/) VOSS E Z.
PA (BOLD/) BOLDOG F L.
PA (MALY/) MADIYANGAR U M.
PA (PADI/) PADIGARU M.
PA (JIWW/) JI W.
PA (SMIT/) SMITHSON G.
PA (EDIN/) EDINGER S R.
PA (MILL/) MILLET I.
PA (ELLE/) ELLERMAN K.
Query Match 9.5%; Score 61.5; DB 8; Length 1247;
Best Local Similarity 33.3%; Pred. No. 1.4e+03;
RESULT 1283
ID ABP76680 standard; protein; 19938 AA.
DE Streptomyces viridochromogenes Avi gene cluster polypeptide frame 4.
PN WO200268436-A1.
PD 06-SEP-2002.
PA (COMB-) COMBINATURE BIOPHARM AG.
Query Match 9.5%; Score 61.5; DB 6; Length 19938;
Best Local Similarity 25.0%; Pred. No. 3.7e+04;
RESULT 1284
ID AAY48277 standard; protein; 66 AA.
DE Human prostate cancer-associated protein 63.
PN DE19811193-A1.
PD 16-SEP-1999.
PA (META-) METAGEN GES GENOMFORSCHUNG MBH.
Query Match 9.5%; Score 61; DB 2; Length 66;
Best Local Similarity 33.3%; Pred. No. 46;
RESULT 1285
ID ABB88631 standard; peptide; 71 AA.
DE Conus masqu I-superfamily conotoxin peptide sequence SEQ:125.
PN WO200202590-A2.
PD 10-JAN-2002.
PA (UTAH) UNIV UTAH RES FOUND.
PA (COGN-) COGNETIX INC.
Query Match 9.5%; Score 61; DB 5; Length 71;

Best Local Similarity 38.9%; Pred. No. 51;
RESULT 1286
ID AAU60927 standard; protein; 76 AA.
DE Propionibacterium acnes immunogenic protein #21823.
PN WO200181581-A2.
PD 01-NOV-2001.
PA (CORI-) CORIXA CORP.
Query Match 9.5%; Score 61; DB 4; Length 76;
Best Local Similarity 27.1%; Pred. No. 55;
RESULT 1287
ID ABM57446 standard; protein; 76 AA.
DE Propionibacterium acnes predicted ORF-encoded polypeptide #22122.
PN WO2003033515-A1.
PD 24-APR-2003.
PA (CORI-) CORIXA CORP.
Query Match 9.5%; Score 61; DB 6; Length 76;
Best Local Similarity 27.1%; Pred. No. 55;
RESULT 1288
ID AAU40354 standard; protein; 130 AA.
DE Propionibacterium acnes immunogenic protein #1250.
PN WO200181581-A2.
PD 01-NOV-2001.
PA (CORI-) CORIXA CORP.
Query Match 9.5%; Score 61; DB 4; Length 130;
Best Local Similarity 24.2%; Pred. No. 1e+02;
RESULT 1289
ID ABM36873 standard; protein; 130 AA.
DE Propionibacterium acnes predicted ORF-encoded polypeptide #1549.
PN WO2003033515-A1.
PD 24-APR-2003.
PA (CORI-) CORIXA CORP.
Query Match 9.5%; Score 61; DB 6; Length 130;
Best Local Similarity 24.2%; Pred. No. 1e+02;
RESULT 1290
ID AAU62706 standard; protein; 133 AA.
DE Propionibacterium acnes immunogenic protein #23602.
PN WO200181581-A2.
PD 01-NOV-2001.
PA (CORI-) CORIXA CORP.
Query Match 9.5%; Score 61; DB 4; Length 133;
Best Local Similarity 29.8%; Pred. No. 1.1e+02;
RESULT 1291
ID ABM59225 standard; protein; 133 AA.
DE Propionibacterium acnes predicted ORF-encoded polypeptide #23901.
PN WO2003033515-A1.
PD 24-APR-2003.
PA (CORI-) CORIXA CORP.
Query Match 9.5%; Score 61; DB 6; Length 133;
Best Local Similarity 29.8%; Pred. No. 1.1e+02;
RESULT 1292
ID AAG03763 standard; protein; 136 AA.
DE Human secreted protein, SEQ ID NO: 7844.
PN EP1033401-A2.
PD 06-SEP-2000.
PA (GEST-) GENSET.
Query Match 9.5%; Score 61; DB 3; Length 136;
Best Local Similarity 24.7%; Pred. No. 1.1e+02;
RESULT 1293
ID AA30384 standard; protein; 138 AA.
DE Arabidopsis thaliana G2347 protein.
PN WO20027185-A2.
PD 03-OCT-2002.
PA (MENDEL-) MENDEL BIOTECHNOLOGY INC.
Query Match 9.5%; Score 61; DB 6; Length 138;
Best Local Similarity 25.8%; Pred. No. 1.1e+02;
RESULT 1294
ID ABG21912 standard; protein; 140 AA.
DE Novel human diagnostic protein #21903.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HVSE-) HVSEQ INC.
Query Match 9.5%; Score 61; DB 4; Length 140;
Best Local Similarity 31.6%; Pred. No. 1.1e+02;
RESULT 1295
ID AAU55085 standard; protein; 146 AA.
DE Propionibacterium acnes immunogenic protein #15981.
PN WO200181581-A2.
PD 01-NOV-2001.
PA (CORI-) CORIXA CORP.
Query Match 9.5%; Score 61; DB 4; Length 146;
Best Local Similarity 28.6%; Pred. No. 1.2e+02;
RESULT 1296
ID ABM51604 standard; protein; 146 AA.
DE Propionibacterium acnes predicted ORF-encoded polypeptide #16280.
PN WO2003033515-A1.
PD 24-APR-2003.
PA (CORI-) CORIXA CORP.
Query Match 9.5%; Score 61; DB 6; Length 146;
Best Local Similarity 28.6%; Pred. No. 1.2e+02;
RESULT 1297
ID AA325383 standard; protein; 155 AA.
DE Human NZMS-7 protein.
PN WO200246385-A2.
PD 13-JUN-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 9.5%; Score 61; DB 5; Length 155;
Best Local Similarity 26.0%; Pred. No. 1.3e+02;
RESULT 1298
ID AAG41559 standard; protein; 156 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 51722.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 9.5%; Score 61; DB 3; Length 156;
Best Local Similarity 25.8%; Pred. No. 1.3e+02;
RESULT 1299
ID AB081277 standard; protein; 161 AA.
DE Pseudomonas aeruginosa polypeptide #13452.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 9.5%; Score 61; DB 7; Length 161;
Best Local Similarity 24.8%; Pred. No. 1.3e+02;
RESULT 1300
ID AAM95503 standard; protein; 167 AA.
DE Human reproductive system related antigen SEQ ID NO: 4161.
PN WO200155320-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 9.5%; Score 61; DB 4; Length 167;
Best Local Similarity 30.9%; Pred. No. 1.4e+02;
RESULT 1301
ID AB96186 standard; protein; 167 AA.
DE Human testicular antigen SEQ ID NO: 1570.
PN WO200155317-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 9.5%; Score 61; DB 4; Length 167;
Best Local Similarity 30.9%; Pred. No. 1.4e+02;
RESULT 1302
ID AAU18158 standard; protein; 167 AA.
DE Novel human DNA-binding protein #5.
PN WO200155162-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 9.5%; Score 61; DB 4; Length 167;
Best Local Similarity 30.9%; Pred. No. 1.4e+02;
RESULT 1303
ID ABG92579 standard; protein; 167 AA.
DE Human DNA-binding protein #5.
PN US2002102638-A1.
PD 01-AUG-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 9.5%; Score 61; DB 5; Length 167;
Best Local Similarity 30.9%; Pred. No. 1.4e+02;

RESULT 1304
ID ADC25296 standard; protein; 167 AA.
DE Human extracellular matrix protein from gene 5.
PN US2003049650-A1.
PD 13-MAR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 9.5%; Score 61; DB 7; Length 167;
Best Local Similarity 30.9%; Pred. No. 1.4e+02;
RESULT 1305
ID RAY70953 standard; protein; 181 AA.
DE Arabidopsis SERK interacting protein #2 from clone 3B39.
PN WO200024914-A2.
PD 04-MAY-2000.
PA (NOVS) NOVARTIS-ERFINDUNGEN VERW GES MBH.
Query Match 9.5%; Score 61; DB 3; Length 181;
Best Local Similarity 25.8%; Pred. No. 1.5e+02;
RESULT 1306
ID AAG41558 standard; protein; 181 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 51721.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 9.5%; Score 61; DB 3; Length 181;
Best Local Similarity 25.8%; Pred. No. 1.5e+02;
RESULT 1307
ID AAU93175 standard; protein; 181 AA.
DE Arabidopsis transcription factor #213.
PN WO200215675-A1.
PD 28-FEB-2002.
PA (MEND-) MENDEL BIOTECHNOLOGY INC.
PA (PILG/) PILGRIM M.
PA (CREE/) CREELMAN R.
PA (DUBE/) DUBELL A J.
PA (HEAR/) HEARD J.
PA (JIAN/) JIANG C.
PA (KEDD/) KEDDIE J.
PA (ADAM/) ADAM L.
PA (RATC/) RATCLIFF O.
PA (REUB/) REUBER J L.
PA (RIEC/) RIECHMANN J L.
PA (YUGG/) YU G.
PA (PINE/) PINEDA O.
Query Match 9.5%; Score 61; DB 5; Length 181;
Best Local Similarity 25.8%; Pred. No. 1.5e+02;
RESULT 1308
ID ADD31087 standard; protein; 181 AA.
DE Plant yield-related protein from clone G2347.
PN WO2003013227-A2.
PD 20-FEB-2003.
PA (MEND-) MENDEL BIOTECHNOLOGY INC.
Query Match 9.5%; Score 61; DB 7; Length 181;
Best Local Similarity 25.8%; Pred. No. 1.5e+02;
RESULT 1309
ID ADI41969 standard; protein; 181 AA.
DE Plant transcription factor #216.
PN US2004019927-A1.
PD 29-JAN-2004.
PA (SHER/) SHERMAN B K.
PA (RIEC/) RIECHMANN J L.
PA (JIAN/) JIANG C.
PA (HEAR/) HEARD J E.
PA (HAAR/) HAAKE V.
PA (CREE/) CREELMAN R A.
PA (RATC/) RATCLIFFE O.
PA (ADAM/) ADAM L J.
PA (REUB/) REUBER T L.
PA (KEDD/) KEDDIE J.
PA (BROU/) BROUN P E.
PA (PILG/) PILGRIM M L.
PA (DUBE/) DUBELL A N.
PA (PINE/) PINEDA O.
PA (YUGG/) YU G.
Query Match 9.5%; Score 61; DB 8; Length 181;
Best Local Similarity 25.8%; Pred. No. 1.5e+02;
RESULT 1310
ID ADO2545 standard; protein; 181 AA.
DE Thalecress transcription factor protein #479.
PN US2004045049-A1.
PD 04-MAR-2004.
PA (ZHAN/) ZHANG J.
PA (FROM/) FROMM M E.
PA (HEAR/) HEARD J E.
PA (RIEC/) RIECHMANN J L.
PA (ADAM/) ADAM L J.
PA (BROU/) BROUN P E.
PA (PINE/) PINEDA O.
PA (REUB/) REUBER T L.
PA (KEDD/) KEDDIE J S.
PA (YUGG/) YU G.
PA (JIAN/) JIANG C.
PA (SAMA/) SAMAHA R S.
PA (PILG/) PILGRIM M L.
PA (CREE/) CREELMAN R A.
PA (DUBE/) DUBELL A N.
PA (RATC/) RATCLIFFE O.
PA (KUMI/) KUMIMOTO R.
PA (SHER/) SHERMAN B K.
Query Match 9.5%; Score 61; DB 8; Length 181;
Best Local Similarity 25.8%; Pred. No. 1.5e+02;
RESULT 1311
ID ADO3499 standard; protein; 181 AA.
DE Thalecress transcription factor protein #581.
PN US2004045049-A1.
PD 04-MAR-2004.
PA (ZHAN/) ZHANG J.
PA (FROM/) FROMM M E.
PA (HEAR/) HEARD J E.
PA (RIEC/) RIECHMANN J L.
PA (ADAM/) ADAM L J.
PA (BROU/) BROUN P E.
PA (PINE/) PINEDA O.
PA (REUB/) REUBER T L.
PA (KEDD/) KEDDIE J S.
PA (YUGG/) YU G.
PA (JIAN/) JIANG C.
PA (SAMA/) SAMAHA R S.
PA (PILG/) PILGRIM M L.
PA (CREE/) CREELMAN R A.
PA (DUBE/) DUBELL A N.
PA (RATC/) RATCLIFFE O.
PA (KUMI/) KUMIMOTO R.
PA (SHER/) SHERMAN B K.
Query Match 9.5%; Score 61; DB 8; Length 181;
Best Local Similarity 25.8%; Pred. No. 1.5e+02;
RESULT 1312
ID ABB70680 standard; protein; 184 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 38832.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 9.5%; Score 61; DB 4; Length 184;
Best Local Similarity 24.1%; Pred. No. 1.6e+02;
RESULT 1313
ID ADK34471 standard; protein; 191 AA.
DE Novel human polypeptide SeqID6553.
PN WO200216439-A2.
PD 28-FEB-2002.
PA (HYSE-) HYSEQ INC.
Query Match 9.5%; Score 61; DB 5; Length 191;
Best Local Similarity 29.9%; Pred. No. 1.6e+02;
RESULT 1314
ID AAG41557 standard; protein; 211 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 51720.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 9.5%; Score 61; DB 3; Length 211;


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Best Local Similarity 25.8%; Pred. No. 1.9e+02;
RESULT 1315
ID AAU32776 standard; protein; 219 AA.
DE Novel human secreted protein #3267.
PN WO200179449-A2.
PD 25-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 9.5%; Score 61; DB 4; Length 219;
RESULT 1316
ID AAU30328 standard; protein; 239 AA.
DE Novel human secreted protein #819.
PN WO200179449-A2.
PD 25-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 9.5%; Score 61; DB 4; Length 239;
RESULT 1317
ID ADY25086 standard; protein; 240 AA.
DE Plant full length insert polypeptide seqid 72870.
PN US2004034888-A1.
PD 19-FEB-2004.
PA (LIUJ/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABA/) TABASKA J E.
PA (CAOY/) CAO Y.
Query Match
Best Local Similarity 9.5%; Score 61; DB 8; Length 240;
RESULT 1318
ID AAM95499 standard; protein; 253 AA.
DE Human reproductive system related antigen SEQ ID NO: 4157.
PN WO200155320-A2.
PD 02-AUG-2001.
PA (HUNA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 9.5%; Score 61; DB 4; Length 253;
RESULT 1319
ID ABB96182 standard; protein; 253 AA.
DE Human testicular antigen SEQ ID NO: 1566.
PN WO200155317-A2.
PD 02-AUG-2001.
PA (HUNA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 9.5%; Score 61; DB 4; Length 253;
RESULT 1320
ID AAU18236 standard; protein; 253 AA.
DE Novel human DNA-binding protein #83.
PN WO200155162-A1.
PD 02-AUG-2001.
PA (HUNA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 9.5%; Score 61; DB 4; Length 253;
RESULT 1321
ID ABG92657 standard; protein; 253 AA.
DE Human DNA-binding protein #83.
PN US2002102638-A1.
PD 01-AUG-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match
Best Local Similarity 9.5%; Score 61; DB 5; Length 253;
RESULT 1322
ID ADC25374 standard; protein; 253 AA.
DE Human extracellular matrix protein from gene 83.
PN US2003049650-A1.
PD 13-MAR-2003.
PA (HUNA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 9.5%; Score 61; DB 7; Length 253;
RESULT 1323
ID ABB71139 standard; protein; 456 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 40209.
ID ABG05679 standard; protein; 261 AA.
DE Novel human diagnostic protein #5670.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 9.5%; Score 61; DB 4; Length 261;
RESULT 1324
ID ABG18016 standard; protein; 325 AA.
DE Novel human diagnostic protein #18007.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 9.5%; Score 61; DB 4; Length 325;
RESULT 1325
ID AAB25524 standard; protein; 339 AA.
DE Pinus radiata cell signalling involved protein SEQ ID NO:899.
PN WO200042171-A1.
PD 20-JUL-2000.
PA (GENE-) GENESIS RES & DEV CORP LTD.
Query Match
Best Local Similarity 9.5%; Score 61; DB 3; Length 339;
RESULT 1326
ID ABO59777 standard; protein; 374 AA.
DE Human genome derived single exon protein #6011.
PN US2003194704-A1.
PD 16-OCT-2003.
PA (PENN/) PENN S G.
PA (RANK/) RANK D R.
PA (HANZ/) HANZEL D K.
Query Match
Best Local Similarity 9.5%; Score 61; DB 8; Length 374;
RESULT 1327
ID ABG08725 standard; protein; 397 AA.
DE Novel human diagnostic protein #8716.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 9.5%; Score 61; DB 4; Length 397;
RESULT 1328
ID ADI24784 standard; protein; 399 AA.
DE Plant full length insert polypeptide seqid 72568.
PN US2004034888-A1.
PD 19-FEB-2004.
PA (LIUJ/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABA/) TABASKA J E.
PA (CAOY/) CAO Y.
Query Match
Best Local Similarity 9.5%; Score 61; DB 8; Length 399;
RESULT 1329
ID ABO77209 standard; protein; 428 AA.
DE Pseudomonas aeruginosa polypeptide #9384.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match
Best Local Similarity 9.5%; Score 61; DB 7; Length 428;
RESULT 1330
ID ADC37583 standard; protein; 429 AA.
DE Human nucleic acid associated protein, NAAP-50.
PN WO2003046151-A2.
PD 05-JUN-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match
Best Local Similarity 9.5%; Score 61; DB 7; Length 429;
RESULT 1331
ID ABB71139 standard; protein; 456 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 40209.
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PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 9.5%; Score 61; DB 4; Length 456;
Best Local Similarity 22.7%; Pred. No. 4.7e+02;
RESULT 1332
ID ABB06048 standard; protein; 468 AA.
DE Human NS protein sequence SEQ ID NO:140.
PN WO200206315-A2.
PD 24-JAN-2002.
PA (COMP-) COMPUGEN LTD.
Query Match 9.5%; Score 61; DB 5; Length 468;
Best Local Similarity 27.6%; Pred. No. 4.8e+02;
RESULT 1333
ID ADF32357 standard; protein; 491 AA.
DE T365 protein.
PN CN1394957-A.
PD 05-FEB-2003.
PA (GENE-) INST GENETICS CHINESE ACAD SCI.
Query Match 9.5%; Score 61; DB 7; Length 491;
Best Local Similarity 32.5%; Pred. No. 5.1e+02;
RESULT 1334
ID ABM89271 standard; protein; 498 AA.
DE Rice abiotic stress responsive polypeptide SEQ ID NO:7517.
PN WO2003008540-A2.
PD 30-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 9.5%; Score 61; DB 7; Length 498;
Best Local Similarity 25.0%; Pred. No. 5.2e+02;
RESULT 1335
ID ADX66627 standard; protein; 513 AA.
DE Plant full length insert polypeptide seqid 37470.
PN US2004034888-A1.
PD 19-FEB-2004.
PA (LIUJ/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABR/) TABASKA J E.
PA (CAOY/) CAO Y.
Query Match 9.5%; Score 61; DB 8; Length 513;
Best Local Similarity 32.5%; Pred. No. 5.4e+02;
RESULT 1336
ID ABM89036 standard; protein; 516 AA.
DE Rice abiotic stress responsive polypeptide SEQ ID NO:7282.
PN WO2003008540-A2.
PD 30-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 9.5%; Score 61; DB 7; Length 516;
Best Local Similarity 28.8%; Pred. No. 5.4e+02;
RESULT 1337
ID ABP62937 standard; protein; 558 AA.
DE Human polypeptide SEQ ID NO 374.
PN WO200218424-A2.
PD 07-MAR-2002.
PA (HYSE-) HYSEQ INC.
Query Match 9.5%; Score 61; DB 5; Length 558;
Best Local Similarity 22.3%; Pred. No. 5.9e+02;
RESULT 1338
ID ABB61808 standard; protein; 681 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 12216.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 9.5%; Score 61; DB 4; Length 681;
Best Local Similarity 23.9%; Pred. No. 7.5e+02;
RESULT 1339
ID ABB60096 standard; protein; 961 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 7080.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 9.5%; Score 61; DB 4; Length 961;

Best Local Similarity 22.7%; Pred. No. 1.1e+03;
RESULT 1340
ID AAU80188 standard; protein; 961 AA.
DE Human TSP1 domain containing protein encoded by cDNA FGO6969.
PN JP2002085059-A.
PD 26-MAR-2002.
PA (KAZU-) ZH KAZUSA DNA KENKYUSHO.
PA (YOSH) YOSHITOMI PHARM IND KK.
Query Match 9.5%; Score 61; DB 5; Length 961;
Best Local Similarity 26.4%; Pred. No. 1.1e+03;
RESULT 1341
ID AAY79165 standard; protein; 1014 AA.
DE Pneumocystis carinii major surface glycoprotein HMSGp1.
PN WO200009760-A1.
PD 24-FEB-2000.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
Query Match 9.5%; Score 61; DB 3; Length 1014;
Best Local Similarity 21.7%; Pred. No. 1.2e+03;
RESULT 1342
ID ABB61135 standard; protein; 1014 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 10197.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 9.5%; Score 61; DB 4; Length 1014;
Best Local Similarity 32.3%; Pred. No. 1.2e+03;
RESULT 1343
ID ABG11821 standard; protein; 1049 AA.
DE Novel human diagnostic protein #11812.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 9.5%; Score 61; DB 4; Length 1049;
Best Local Similarity 28.8%; Pred. No. 1.3e+03;
RESULT 1344
ID ADI82537 standard; protein; 1064 AA.
DE Human modifier of p21 (MP21) protein sequence SeqID103.
PN WO2004005486-A2.
PD 15-JAN-2004.
PA (EXEL-) EXELIXIS INC.
Query Match 9.5%; Score 61; DB 8; Length 1064;
Best Local Similarity 24.0%; Pred. No. 1.3e+03;
RESULT 1345
ID ABM80078 standard; protein; 1064 AA.
DE Tumour-associated antigenic target (TAT) polypeptide PRO60298, SEQ:203.
PN WO2004030615-A2.
PD 15-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 9.5%; Score 61; DB 8; Length 1064;
Best Local Similarity 24.0%; Pred. No. 1.3e+03;
RESULT 1346
ID ABB66149 standard; protein; 1320 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 25239.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 9.5%; Score 61; DB 4; Length 1320;
Best Local Similarity 24.5%; Pred. No. 1.7e+03;
RESULT 1347
ID ABG11841 standard; protein; 1492 AA.
DE Novel human diagnostic protein #11832.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 9.5%; Score 61; DB 4; Length 1492;
Best Local Similarity 28.8%; Pred. No. 1.9e+03;
RESULT 1348
ID AAB59827 standard; protein; 1592 AA.
DE Protein #4 encoded by TctD/E gene.
PN WO200072650-A2.
PD 07-DEC-2000.
PA (UYOH-) UNIV OHIO.
Query Match 9.5%; Score 61; DB 4; Length 1592;

Best Local Similarity 31.1%; Pred. No. 2.1e+03;
RESULT 1349
ID AD517495 standard; protein; 1799 AA.
DE Amino acid sequence of murine laminin beta-2.
PN WO2004079007-A2.
PD 16-SEP-2004.
PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
Query Match 9.5%; Score 61; DB 8; Length 1799;
Best Local Similarity 27.9%; Pred. No. 2.4e+03;
RESULT 1350
ID ADR97664 standard; protein; 1799 AA.
DE Murine laminin beta 2 chain protein, an actin acting substance SeqID 8.
PN WO2004079332-A2.
PD 16-SEP-2004.
PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
Query Match 9.5%; Score 61; DB 8; Length 1799;
Best Local Similarity 27.9%; Pred. No. 2.4e+03;
RESULT 1351
ID ADM44476 standard; protein; 1799 AA.
DE Murine laminin beta 2.
PN WO2005001090-A1.
PD 06-JAN-2005.
PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
Query Match 9.5%; Score 61; DB 9; Length 1799;
Best Local Similarity 27.9%; Pred. No. 2.4e+03;
RESULT 1352
ID ADY5710 standard; protein; 1799 AA.
DE Mouse laminin-2 beta chain protein.
PN WO2005021744-A1.
PD 10-WAR-2005.
PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
Query Match 9.5%; Score 61; DB 9; Length 1799;
Best Local Similarity 27.9%; Pred. No. 2.4e+03;
RESULT 1353
ID ADV32464 standard; protein; 1799 AA.
DE Mouse laminin beta chain protein.
PN JP2005052050-A.
PD 03-WAR-2005.
PA (DOKU-) DOKURITSU GYOSEI HOJIN SANGYO GIJUTSU SO.
Query Match 9.5%; Score 61; DB 9; Length 1799;
Best Local Similarity 27.9%; Pred. No. 2.4e+03;
RESULT 1354
ID AEB56264 standard; protein; 1799 AA.
DE Event sequencer related protein SEQ ID NO 8.
PN WO2005073890-A1.
PD 11-AUG-2005.
PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
Query Match 9.5%; Score 61; DB 9; Length 1799;
Best Local Similarity 27.9%; Pred. No. 2.4e+03;
RESULT 1355
ID AEF19266 standard; protein; 1799 AA.
DE Mouse laminin-2 beta chain.
PN WO2006001396-A1.
PD 05-JAN-2006.
PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
Query Match 9.5%; Score 61; DB 10; Length 1799;
Best Local Similarity 27.9%; Pred. No. 2.4e+03;
RESULT 1356
ID AEP16759 standard; protein; 1799 AA.
DE Mouse laminin-2 beta chain.
PN WO2006001397-A1.
PD 05-JAN-2006.
PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
Query Match 9.5%; Score 61; DB 10; Length 1799;
Best Local Similarity 27.9%; Pred. No. 2.4e+03;
RESULT 1357
ID ADO62867 standard; protein; 2068 AA.
DE Transcription factor G2990 orthologous sequence, SEQ ID 1334.
PN WO2004031349-A2.
PD 15-APR-2004.
PA (MEND-) MENDEL BIOTECHNOLOGY INC.
Query Match 9.5%; Score 61; DB 8; Length 2068;
Best Local Similarity 34.2%; Pred. No. 2.8e+03;

RESULT 1358
ID ABO79997 standard; protein; 90 AA.
DE Pseudomonas aeruginosa polypeptide #12172.
PN US551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 9.4%; Score 60.5; DB 7; Length 90;
Best Local Similarity 32.8%; Pred. No. 77;
RESULT 1359
ID AAG18562 standard; protein; 106 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 20021.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 9.4%; Score 60.5; DB 3; Length 106;
Best Local Similarity 21.2%; Pred. No. 93;
RESULT 1360
ID AAO21323 standard; protein; 106 AA.
DE Arabidopsis thaliana KCP-like protein, SEQ ID NO 78.
PN WO200222821-A2.
PD 21-WAR-2002.
PA (PION-) PIONEER HI-BRED INT INC.
Query Match 9.4%; Score 60.5; DB 5; Length 106;
Best Local Similarity 21.2%; Pred. No. 93;
RESULT 1361
ID ABM64904 standard; protein; 106 AA.
DE Propionibacterium acnes immunogenic polypeptide #29580.
PN WO2003033515-A1.
PD 24-APR-2003.
PA (CORI-) CORIXA CORP.
Query Match 9.4%; Score 60.5; DB 6; Length 106;
Best Local Similarity 29.6%; Pred. No. 93;
RESULT 1362
ID ADG74890 standard; protein; 106 AA.
DE Plant developmental pathway modulation-related RKS/ELS ligand protein 11.
PN EP1382682-A2.
PD 21-JAN-2004.
PA (EXPR-) EXPRESSIVE RES BV.
Query Match 9.4%; Score 60.5; DB 8; Length 106;
Best Local Similarity 21.2%; Pred. No. 93;
RESULT 1363
ID AAU60791 standard; protein; 109 AA.
DE Propionibacterium acnes immunogenic protein #21687.
PN WO200181581-A2.
PD 01-NOV-2001.
PA (CORI-) CORIXA CORP.
Query Match 9.4%; Score 60.5; DB 4; Length 109;
Best Local Similarity 26.5%; Pred. No. 96;
RESULT 1364
ID ABM57310 standard; protein; 109 AA.
DE Propionibacterium acnes predicted ORF-encoded polypeptide #21986.
PN WO2003033515-A1.
PD 24-APR-2003.
PA (CORI-) CORIXA CORP.
Query Match 9.4%; Score 60.5; DB 6; Length 109;
Best Local Similarity 26.5%; Pred. No. 96;
RESULT 1365
ID ADX66981 standard; protein; 112 AA.
DE Plant full length insert polypeptide seqid 37824.
PN US2004034888-A1.
PD 19-FEB-2004.
PA (LIUJ/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABA/) TABASKA J E.
PA (CAOY/) CAO Y.
Query Match 9.4%; Score 60.5; DB 8; Length 112;
Best Local Similarity 21.2%; Pred. No. 1e+02;
RESULT 1366
ID AAU53785 standard; protein; 118 AA.
DE Propionibacterium acnes immunogenic protein #14681.
PN WO200181581-A2.
PD 01-NOV-2001.

PA (CORI-) CORIXA CORP.
Query Match 9.4%; Score 60.5; DB 4; Length 118;
Best Local Similarity 26.4%; Pred. No. 1.1e+02;
RESULT 1367
ID ABM50304 standard; protein; 118 AA.
DE Propionibacterium acnes predicted ORF-encoded polypeptide #14980.
PN WO2003033515-A1.
PD 24-APR-2003.
PA (CORI-) CORIXA CORP.
Query Match 9.4%; Score 60.5; DB 6; Length 118;
Best Local Similarity 26.4%; Pred. No. 1.1e+02;
RESULT 1368
ID AAU67602 standard; protein; 122 AA.
DE Propionibacterium acnes immunogenic protein #28498.
PN WO200181581-A2.
PD 01-NOV-2001.
PA (CORI-) CORIXA CORP.
Query Match 9.4%; Score 60.5; DB 4; Length 122;
Best Local Similarity 29.6%; Pred. No. 1.1e+02;
RESULT 1369
ID ABM64121 standard; protein; 122 AA.
DE Propionibacterium acnes predicted ORF-encoded polypeptide #28797.
PN WO2003033515-A1.
PD 24-APR-2003.
PA (CORI-) CORIXA CORP.
Query Match 9.4%; Score 60.5; DB 6; Length 122;
Best Local Similarity 29.6%; Pred. No. 1.1e+02;
RESULT 1370
ID AAR78693 standard; protein; 162 AA.
DE Rat skeletal muscle stress protein, p20.
PN JP07181180-A.
PD 21-JUL-1995.
PA (KATO/) KATO K.
PA (IGAK-) IGAKU SEIBUTSUGAKU KENKYUSHO KK.
Query Match 9.4%; Score 60.5; DB 2; Length 162;
Best Local Similarity 23.4%; Pred. No. 1.5e+02;
RESULT 1371
ID ABG93942 standard; protein; 162 AA.
DE Rat polypeptide orthologous to DACC-9.
PN WO200264623-A1.
PD 22-AUG-2002.
PA (ADPP-) ADP PHARM PTY LTD.
PA (UNSY) UNIV SYDNEY.
Query Match 9.4%; Score 60.5; DB 5; Length 162;
Best Local Similarity 23.4%; Pred. No. 1.5e+02;
RESULT 1372
ID ADA34307 standard; protein; 162 AA.
DE Acinetobacter baumannii protein #1468.
PN US6562958-B1.
PD 13-MAY-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 9.4%; Score 60.5; DB 6; Length 162;
Best Local Similarity 23.1%; Pred. No. 1.5e+02;
RESULT 1373
ID ADE56085 standard; protein; 162 AA.
DE Rat Protein P97541, SEQ ID NO 1926.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 9.4%; Score 60.5; DB 7; Length 162;
Best Local Similarity 23.4%; Pred. No. 1.5e+02;
RESULT 1374
ID AAU49482 standard; protein; 175 AA.
DE Propionibacterium acnes immunogenic protein #10378.
PN WO200181581-A2.
PD 01-NOV-2001.
PA (CORI-) CORIXA CORP.
Query Match 9.4%; Score 60.5; DB 4; Length 175;
Best Local Similarity 27.1%; Pred. No. 1.7e+02;
RESULT 1375
ID ABM46001 standard; protein; 175 AA.
DE Propionibacterium acnes predicted ORF-encoded polypeptide #10677.

PN WO2003033515-A1.
PD 24-APR-2003.
PA (CORI-) CORIXA CORP.
Query Match 9.4%; Score 60.5; DB 6; Length 175;
Best Local Similarity 27.1%; Pred. No. 1.7e+02;
RESULT 1376
ID ADQ66278 standard; protein; 180 AA.
DE Novel human protein sequence #1251.
PN EP1440981-A2.
PD 28-JUL-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 9.4%; Score 60.5; DB 8; Length 180;
Best Local Similarity 39.6%; Pred. No. 1.8e+02;
RESULT 1377
ID ABO73633 standard; protein; 188 AA.
DE Pseudomonas aeruginosa polypeptide #5808.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 9.4%; Score 60.5; DB 7; Length 188;
Best Local Similarity 36.0%; Pred. No. 1.8e+02;
RESULT 1378
ID ADX68391 standard; protein; 194 AA.
DE Plant full length insert polypeptide seqid 39234.
PN US2004034888-A1.
PD 19-FEB-2004.
PA (LIUJ/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABA/) TABASKA J E.
PA (CAOY/) CAO Y.
Query Match 9.4%; Score 60.5; DB 8; Length 194;
Best Local Similarity 26.0%; Pred. No. 1.9e+02;
RESULT 1379
ID AAW40101 standard; protein; 210 AA.
DE Human herpesvirus 8 (HHV-8) dihydrofolate reductase.
PN WO9804284-A1.
PD 05-FEB-1998.
PA (UYJO) UNIV JOHNS HOPKINS.
Query Match 9.4%; Score 60.5; DB 2; Length 210;
Best Local Similarity 25.7%; Pred. No. 2.1e+02;
RESULT 1380
ID AAM82437 standard; protein; 210 AA.
DE KSHV DHR protein encoded by ORF 2.
PN US5849584-A.
PD 15-DEC-1998.
PA (UYCO) UNIV COLUMBIA NEW YORK.
Query Match 9.4%; Score 60.5; DB 2; Length 210;
Best Local Similarity 25.7%; Pred. No. 2.1e+02;
RESULT 1381
ID AAB93909 standard; protein; 217 AA.
DE Human protein sequence SEQ ID NO:13873.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 9.4%; Score 60.5; DB 4; Length 217;
Best Local Similarity 23.7%; Pred. No. 2.2e+02;
RESULT 1382
ID ABB70904 standard; protein; 231 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 39504.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 9.4%; Score 60.5; DB 4; Length 231;
Best Local Similarity 40.6%; Pred. No. 2.4e+02;
RESULT 1383
ID ADY13434 standard; protein; 259 AA.
DE Plant full length insert polypeptide seqid 69249.
PN US2004034888-A1.
PD 19-FEB-2004.
PA (LIUJ/) LIU J.
PA (ZHOU/) ZHOU Y.


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PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABA/) TABASKA J E.
PA (CAOY/) CAO Y.
Query Match
Best Local Similarity 9.4%; Score 60.5; DB 8; Length 259;
RESULT 1384
ID AAM41811 standard; protein; 272 AA.
DE Human polypeptide SEQ ID NO 6742.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 9.4%; Score 60.5; DB 4; Length 272;
RESULT 1385
ID AAM41810 standard; protein; 272 AA.
DE Human polypeptide SEQ ID NO 6741.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 9.4%; Score 60.5; DB 4; Length 272;
RESULT 1386
ID ADX72922 standard; protein; 275 AA.
DE Plant full length insert polypeptide seqid 42288.
PN US2004034888-A1.
PD 19-FEB-2004.
PA (LIUJ/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABA/) TABASKA J E.
PA (CAOY/) CAO Y.
Query Match
Best Local Similarity 9.4%; Score 60.5; DB 8; Length 275;
RESULT 1387
ID ABO72046 standard; protein; 278 AA.
DE Pseudomonas aeruginosa polypeptide #4221.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match
Best Local Similarity 9.4%; Score 60.5; DB 7; Length 278;
RESULT 1388
ID ABM89392 standard; protein; 278 AA.
DE Rice abiotic stress responsive polypeptide SEQ ID NO:7638.
PN WO2003008540-A2.
PD 30-JAN-2003.
PA (SYGN ) SYNGENTA PARTICIPATIONS AG.
Query Match
Best Local Similarity 9.4%; Score 60.5; DB 7; Length 278;
RESULT 1389
ID ABO69424 standard; protein; 297 AA.
DE Pseudomonas aeruginosa polypeptide #1599.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match
Best Local Similarity 9.4%; Score 60.5; DB 7; Length 297;
RESULT 1390
ID ADS29625 standard; protein; 322 AA.
DE Bacterial polypeptide #18650.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match
Best Local Similarity 9.4%; Score 60.5; DB 8; Length 322;
RESULT 1391
ID ADY22680 standard; protein; 324 AA.
DE Plant full length insert polypeptide seqid 70464.
PN US2004034888-A1.
PD 19-FEB-2004.
PA (LIUJ/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABA/) TABASKA J E.
PA (CAOY/) CAO Y.
Query Match
Best Local Similarity 9.4%; Score 60.5; DB 8; Length 324;
RESULT 1392
ID AAB93734 standard; protein; 325 AA.
DE Human protein sequence SEQ ID NO:13380.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match
Best Local Similarity 9.4%; Score 60.5; DB 4; Length 325;
RESULT 1393
ID ADR44482 standard; protein; 325 AA.
DE Human G protein beta subunit-like protein.
PN WO2004074448-A2.
PD 02-SEP-2004.
PA (WHED ) WHITEHEAD INST BIOMEDICAL RES.
Query Match
Best Local Similarity 9.4%; Score 60.5; DB 8; Length 325;
RESULT 1394
ID ADR44461 standard; protein; 326 AA.
DE Human G protein beta subunit-like protein.
PN WO2004074448-A2.
PD 02-SEP-2004.
PA (WHED ) WHITEHEAD INST BIOMEDICAL RES.
Query Match
Best Local Similarity 9.4%; Score 60.5; DB 8; Length 326;
RESULT 1395
ID ADR44439 standard; protein; 327 AA.
DE Human G protein beta subunit-like protein SEQ ID NO:6.
PN WO2004074448-A2.
PD 02-SEP-2004.
PA (WHED ) WHITEHEAD INST BIOMEDICAL RES.
Query Match
Best Local Similarity 9.4%; Score 60.5; DB 8; Length 327;
RESULT 1396
ID ADV17736 standard; protein; 327 AA.
DE PRO polypeptide SEQ ID NO 3542.
PN WO2005016962-A2.
PD 24-FEB-2005.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 9.4%; Score 60.5; DB 9; Length 327;
RESULT 1397
ID AAB41611 standard; protein; 332 AA.
DE Human OREF ORF1375 polypeptide sequence SEQ ID NO:2750.
PN WO200058473-A2.
PD 05-OCT-2000.
PA (CURA-) CURAGEN CORP.
Query Match
Best Local Similarity 9.4%; Score 60.5; DB 3; Length 332;
RESULT 1398
ID AAM40024 standard; protein; 332 AA.
DE Human polypeptide SEQ ID NO 3169.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 9.4%; Score 60.5; DB 4; Length 332;
RESULT 1399
ID AAM40025 standard; protein; 360 AA.
DE Human polypeptide SEQ ID NO 3170.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
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Query Match 9.4%; Score 60.5; DB 4; Length 360;
Best Local Similarity 23.7%; Pred. No. 4e+02;
RESULT 1400
ID ABO19957 standard; protein; 396 AA.
DE C elegans LMW-1 protein.
PN WO2003000861-A2.
PD 03-JAN-2003.
PA (REGC) UNIV CALIFORNIA.
Query Match 9.4%; Score 60.5; DB 6; Length 396;
Best Local Similarity 20.4%; Pred. No. 4.5e+02;
RESULT 1401
ID ABB70903 standard; protein; 410 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 39501.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 9.4%; Score 60.5; DB 4; Length 410;
Best Local Similarity 40.6%; Pred. No. 4.7e+02;
RESULT 1402
ID AAG39792 standard; protein; 452 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 49288.
PN EP1033485-A2.
PD 06-SEP-2000.
Query Match 9.4%; Score 60.5; DB 3; Length 452;
Best Local Similarity 26.5%; Pred. No. 5.3e+02;
RESULT 1403
ID ABO71664 standard; protein; 462 AA.
DE Pseudomonas aeruginosa polypeptide #3839.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 9.4%; Score 60.5; DB 7; Length 462;
Best Local Similarity 29.8%; Pred. No. 5.4e+02;
RESULT 1404
ID ABO70874 standard; protein; 471 AA.
DE Pseudomonas aeruginosa polypeptide #3049.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 9.4%; Score 60.5; DB 7; Length 471;
Best Local Similarity 25.5%; Pred. No. 5.5e+02;
RESULT 1405
ID AAB80627 standard; protein; 473 AA.
DE Environmental stress tolerant protein SEQ ID 40.
PN WO200105006-A1.
PD 25-JAN-2001.
PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.
Query Match 9.4%; Score 60.5; DB 4; Length 473;
Best Local Similarity 23.8%; Pred. No. 5.6e+02;
RESULT 1406
ID ABO80372 standard; protein; 487 AA.
DE Pseudomonas aeruginosa polypeptide #12547.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 9.4%; Score 60.5; DB 7; Length 487;
Best Local Similarity 29.1%; Pred. No. 5.8e+02;
RESULT 1407
ID ADM20100 standard; protein; 502 AA.
DE Protein encoded by novel human channel/transporter gene #174 clone 2.
PN WO200154472-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 9.4%; Score 60.5; DB 4; Length 502;
Best Local Similarity 23.7%; Pred. No. 6e+02;
RESULT 1408
ID ABO83526 standard; protein; 504 AA.
DE Pseudomonas aeruginosa polypeptide #15701.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 9.4%; Score 60.5; DB 7; Length 504;
Best Local Similarity 24.5%; Pred. No. 6e+02;

RESULT 1409
ID ABO79664 standard; protein; 535 AA.
DE Pseudomonas aeruginosa polypeptide #11839.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 9.4%; Score 60.5; DB 7; Length 535;
Best Local Similarity 22.3%; Pred. No. 6.4e+02;
RESULT 1410
ID ABO68460 standard; protein; 541 AA.
DE Pseudomonas aeruginosa polypeptide #635.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 9.4%; Score 60.5; DB 7; Length 541;
Best Local Similarity 27.3%; Pred. No. 6.5e+02;
RESULT 1411
ID AAB84687 standard; protein; 622 AA.
DE Amino acid sequence of a Drosophila hexosaminidase-2.
PN WO200142492-A1.
PD 14-JUN-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
PA (UYJO) UNIV JOHNS HOPKINS.
PA (UTEM) UNIV TEMPLE.
PA (UYWY-) UNIV WYOMING.
Query Match 9.4%; Score 60.5; DB 4; Length 622;
Best Local Similarity 21.2%; Pred. No. 7.7e+02;
RESULT 1412
ID ABB58485 standard; protein; 622 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 2247.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 9.4%; Score 60.5; DB 4; Length 622;
Best Local Similarity 21.2%; Pred. No. 7.7e+02;
RESULT 1413
ID AAE25828 standard; protein; 622 AA.
DE Fruit fly hexosaminidase-2 (Hex-2).
PN US2002055404-A1.
PD 30-MAY-2002.
PA (BETE/) BETENBAUGH M J.
PA (PALT/) PALTER K.
Query Match 9.4%; Score 60.5; DB 5; Length 622;
Best Local Similarity 21.2%; Pred. No. 7.7e+02;
RESULT 1414
ID ADJ49709 standard; protein; 626 AA.
DE Oil-associated gene related protein #1209.
PN US2004025202-A1.
PD 05-FEB-2004.
PA (LAUR/) LAURIE C C.
PA (RAVA/) RAVANELLO M.
PA (SAVA/) SAVAGE T.
PA (LEDE/) LEDEAUX J R.
PA (ROGE/) ROGERS J A.
Query Match 9.4%; Score 60.5; DB 8; Length 626;
Best Local Similarity 25.3%; Pred. No. 7.8e+02;
RESULT 1415
ID ADJ71063 standard; protein; 731 AA.
DE Human heat mitochondrial protein as a therapeutic target SeqID2869.
PN WO2003087768-A2.
PD 23-OCT-2003.
PA (MITO-) MITOKOR.
PA (BUCK-) BUCK INST AGE RES.
Query Match 9.4%; Score 60.5; DB 7; Length 731;
Best Local Similarity 24.0%; Pred. No. 9.3e+02;
RESULT 1416
ID ABB63043 standard; protein; 855 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 15921.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 9.4%; Score 60.5; DB 4; Length 855;
Best Local Similarity 18.5%; Pred. No. 1.1e+03;

RESULT 1417
ID ABO81651 standard; protein; 894 AA.
DE Pseudomonas aeruginosa polypeptide #13826.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 9.4%; Score 60.5; DB 7; Length 894;
Best Local Similarity 23.9%; Pred. No. 1.2e+03;
RESULT 1418
ID AAM43394 standard; protein; 1019 AA.
DE Singapore horseshoe crab factor C proenzyme (CrPC 21).
PN SG42456-A1.
PD 15-AUG-1997.
PA (UYSI-) UNIV SINGAPORE NAT.
Query Match 9.4%; Score 60.5; DB 2; Length 1019;
Best Local Similarity 24.8%; Pred. No. 1.4e+03;
RESULT 1419
ID AAY05750 standard; protein; 1019 AA.
DE Horseshoe crab Factor C.
PN WO9915676-A1.
PD 01-APR-1999.
PA (UYSI-) UNIV SINGAPORE NAT.
Query Match 9.4%; Score 60.5; DB 2; Length 1019;
Best Local Similarity 24.8%; Pred. No. 1.4e+03;
RESULT 1420
ID AAM94302 standard; protein; 1019 AA.
DE Horseshoe crab Factor C protein #2.
PN US5858706-A.
PD 12-JAN-1999.
PA (UYSI-) UNIV SINGAPORE NAT.
Query Match 9.4%; Score 60.5; DB 2; Length 1019;
Best Local Similarity 24.8%; Pred. No. 1.4e+03;
RESULT 1421
ID AAY42490 standard; protein; 1019 AA.
DE Recombinant N-terminally truncated Horseshoe crab Factor C protein.
PN US5985590-A.
PD 16-NOV-1999.
PA (UYSI-) UNIV SINGAPORE NAT.
Query Match 9.4%; Score 60.5; DB 3; Length 1019;
Best Local Similarity 24.8%; Pred. No. 1.4e+03;
RESULT 1422
ID AAB60935 standard; protein; 1019 AA.
DE Horseshoe crab recombinant Factor C #2.
PN WO200127289-A2.
PD 19-APR-2001.
PA (UYSI-) UNIV SINGAPORE NAT.
Query Match 9.4%; Score 60.5; DB 4; Length 1019;
Best Local Similarity 24.8%; Pred. No. 1.4e+03;
RESULT 1423
ID ABP72334 standard; protein; 1019 AA.
DE Horseshoe crab Factor C.
PN WO2003002976-A2.
PD 09-JAN-2003.
PA (WHIK) BIONEER INC.
Query Match 9.4%; Score 60.5; DB 6; Length 1019;
Best Local Similarity 24.8%; Pred. No. 1.4e+03;
RESULT 1424
ID ADM39099 standard; protein; 1019 AA.
DE Southeast Asian horseshoe crab Factor C.
PN WO2005003163-A1.
PD 13-JAN-2005.
PA (UYSI-) UNIV SINGAPORE NAT.
Query Match 9.4%; Score 60.5; DB 9; Length 1019;
Best Local Similarity 24.8%; Pred. No. 1.4e+03;
RESULT 1425
ID ABG07191 standard; protein; 2506 AA.
DE Novel human diagnostic protein #7182.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 9.4%; Score 60.5; DB 4; Length 2506;
Best Local Similarity 24.6%; Pred. No. 4.1e+03;
RESULT 1426
ID ABG30064 standard; protein; 2506 AA.
DE Novel human diagnostic protein #30055.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 9.4%; Score 60.5; DB 4; Length 2506;
Best Local Similarity 24.6%; Pred. No. 4.1e+03;
RESULT 1427
ID ADN73145 standard; protein; 5155 AA.
DE Thale cress protein upregulated in E2Fa/Dpa expressing plants SeqID 1040.
PN WO2004035798-A2.
PD 29-APR-2004.
PA (CROP-) CROPDESIGN NV.
Query Match 9.4%; Score 60.5; DB 8; Length 5155;
Best Local Similarity 36.8%; Pred. No. 9.6e+03;
RESULT 1428
ID AAU48414 standard; protein; 51 AA.
DE Propionibacterium acnes immunogenic protein #9310.
PN WO200181581-A2.
PD 01-NOV-2001.
PA (CORI-) CORIXA CORP.
Query Match 9.3%; Score 60; DB 4; Length 51;
Best Local Similarity 35.8%; Pred. No. 45;
RESULT 1429
ID ABM44933 standard; protein; 51 AA.
DE Propionibacterium acnes predicted ORF-encoded polypeptide #9609.
PN WO2003033515-A1.
PD 24-APR-2003.
PA (CORI-) CORIXA CORP.
Query Match 9.3%; Score 60; DB 6; Length 51;
Best Local Similarity 35.8%; Pred. No. 45;
RESULT 1430
ID AAU29306 standard; protein; 89 AA.
DE Human PRO polypeptide sequence #283.
PN WO200168848-A2.
PD 20-SEP-2001.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 60; DB 4; Length 89;
Best Local Similarity 40.5%; Pred. No. 87;
RESULT 1431
ID ABU58682 standard; protein; 89 AA.
DE Human PRO polypeptide #283.
PN US2003027272-A1.
PD 06-FEB-2003.
Query Match 9.3%; Score 60; DB 6; Length 89;
Best Local Similarity 40.5%; Pred. No. 87;
RESULT 1432
ID ABU88230 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO19680.
PN US2003032127-A1.
PD 13-FEB-2003.
Query Match 9.3%; Score 60; DB 6; Length 89;
Best Local Similarity 40.5%; Pred. No. 87;
RESULT 1433
ID ABU84545 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #283.
PN US2003032112-A1.
PD 13-FEB-2003.
Query Match 9.3%; Score 60; DB 6; Length 89;
Best Local Similarity 40.5%; Pred. No. 87;
RESULT 1434
ID ABR66419 standard; protein; 89 AA.
DE Human secreted polypeptide PRO19680, SEQ ID NO:566.
PN US2003027278-A1.
PD 06-FEB-2003.
Query Match 9.3%; Score 60; DB 6; Length 89;
Best Local Similarity 40.5%; Pred. No. 87;
RESULT 1435
ID ABR65809 standard; protein; 89 AA.
DE Human secreted polypeptide PRO19680, SEQ ID NO:566.
PN US2003036159-A1.
PD 20-FEB-2003.
Query Match 9.3%; Score 60; DB 6; Length 89;
Best Local Similarity 40.5%; Pred. No. 87;


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Best Local Similarity 40.5%; Pred. No. 87;
RESULT 1436
ID ABU99749 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #283.
PN US2003040070-A1.
PD 27-FEB-2003.
Query Match 9.3%; Score 60; DB 6; Length 89;
Best Local Similarity 40.5%; Pred. No. 87;
RESULT 1437
ID ABU82988 standard; protein; 89 AA.
DE Human PRO polypeptide #283.
PN US2003032113-A1.
PD 13-FEB-2003.
Query Match 9.3%; Score 60; DB 6; Length 89;
Best Local Similarity 40.5%; Pred. No. 87;
RESULT 1438
ID ABU90109 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO19680.
PN US2003036147-A1.
PD 20-FEB-2003.
Query Match 9.3%; Score 60; DB 6; Length 89;
Best Local Similarity 40.5%; Pred. No. 87;
RESULT 1439
ID ABR68358 standard; protein; 89 AA.
DE Human secreted polypeptide PRO19680, SEQ ID NO:566.
PN US2003027264-A1.
PD 06-FEB-2003.
Query Match 9.3%; Score 60; DB 6; Length 89;
Best Local Similarity 40.5%; Pred. No. 87;
RESULT 1440
ID ABU96411 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO19680.
PN US2003036144-A1.
PD 20-FEB-2003.
Query Match 9.3%; Score 60; DB 6; Length 89;
Best Local Similarity 40.5%; Pred. No. 87;
RESULT 1441
ID ABU92842 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #283.
PN US2003036149-A1.
PD 20-FEB-2003.
Query Match 9.3%; Score 60; DB 6; Length 89;
Best Local Similarity 40.5%; Pred. No. 87;
RESULT 1442
ID ABO08919 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #283.
PN US2003044923-A1.
PD 06-MAR-2003.
Query Match 9.3%; Score 60; DB 6; Length 89;
Best Local Similarity 40.5%; Pred. No. 87;
RESULT 1443
ID ABO02971 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #283.
PN US2003040062-A1.
PD 27-FEB-2003.
Query Match 9.3%; Score 60; DB 6; Length 89;
Best Local Similarity 40.5%; Pred. No. 87;
RESULT 1444
ID ABR75125 standard; protein; 89 AA.
DE Human secreted polypeptide PRO19680, SEQ ID NO:566.
PN US2003040056-A1.
PD 27-FEB-2003.
Query Match 9.3%; Score 60; DB 6; Length 89;
Best Local Similarity 40.5%; Pred. No. 87;
RESULT 1445
ID ABR94887 standard; protein; 89 AA.
DE Human secreted polypeptide PRO19680, SEQ ID NO:566.
PN US2003044926-A1.
PD 06-MAR-2003.
Query Match 9.3%; Score 60; DB 6; Length 89;
Best Local Similarity 40.5%; Pred. No. 87;
RESULT 1446
ID ABU85860 standard; protein; 89 AA.
DE Human PRO polypeptide #283.
PN US2003036140-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 9.3%; Score 60; DB 6; Length 89;
Best Local Similarity 40.5%; Pred. No. 87;
RESULT 1447
ID ABU99020 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO19680.
PN US2003013153-A1.
PD 16-JAN-2003.
Query Match 9.3%; Score 60; DB 6; Length 89;
Best Local Similarity 40.5%; Pred. No. 87;
RESULT 1448
ID ABU98235 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO19680.
PN US2003017544-A1.
PD 23-JAN-2003.
Query Match 9.3%; Score 60; DB 6; Length 89;
Best Local Similarity 40.5%; Pred. No. 87;
RESULT 1449
ID ABU91941 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO19680.
PN US2003027277-A1.
PD 06-FEB-2003.
Query Match 9.3%; Score 60; DB 6; Length 89;
Best Local Similarity 40.5%; Pred. No. 87;
RESULT 1450
ID ABU99634 standard; protein; 89 AA.
DE Human PRO polypeptide #283.
PN US2003036141-A1.
PD 20-FEB-2003.
Query Match 9.3%; Score 60; DB 6; Length 89;
Best Local Similarity 40.5%; Pred. No. 87;
RESULT 1451
ID ABU86475 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #283.
PN US2003036146-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 9.3%; Score 60; DB 6; Length 89;
Best Local Similarity 40.5%; Pred. No. 87;
RESULT 1452
ID ABU67688 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #283.
PN US2003036162-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 9.3%; Score 60; DB 6; Length 89;
Best Local Similarity 40.5%; Pred. No. 87;
RESULT 1453
ID ABU80716 standard; protein; 89 AA.
DE Human PRO protein #283.
PN US2003036137-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 9.3%; Score 60; DB 6; Length 89;
Best Local Similarity 40.5%; Pred. No. 87;
RESULT 1454
ID ABR99634 standard; protein; 89 AA.
DE Human secreted polypeptide PRO19680, SEQ ID NO:566.
PN US2003040063-A1.
PD 27-FEB-2003.
Query Match 9.3%; Score 60; DB 6; Length 89;
Best Local Similarity 40.5%; Pred. No. 87;
RESULT 1455
ID ABR99024 standard; protein; 89 AA.
DE Human secreted polypeptide PRO19680, SEQ ID NO:566.
PN US2003040064-A1.
PD 27-FEB-2003.
Query Match 9.3%; Score 60; DB 6; Length 89;
Best Local Similarity 40.5%; Pred. No. 87;
RESULT 1456
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ID ABO16547 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #283.
PN US2003027267-A1.
PD 06-FEB-2003.
Query Match 9.3%; Score 60; DB 6; Length 89;
Best Local Similarity 40.5%; Pred. No. 87;
RESULT 1457
ID ABR92447 standard; protein; 89 AA.
DE Human secreted polypeptide PRO19680, SEQ ID NO:566.
PN US2003036160-A1.
PD 20-FEB-2003.
Query Match 9.3%; Score 60; DB 6; Length 89;
Best Local Similarity 40.5%; Pred. No. 87;
RESULT 1458
ID ABO19088 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #283.
PN US2003044925-A1.
PD 06-MAR-2003.
Query Match 9.3%; Score 60; DB 6; Length 89;
Best Local Similarity 40.5%; Pred. No. 87;
RESULT 1459
ID ABR78509 standard; protein; 89 AA.
DE Human secreted polypeptide PRO19680, SEQ ID NO:566.
PN US2003054474-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 60; DB 6; Length 89;
Best Local Similarity 40.5%; Pred. No. 87;
RESULT 1460
ID ABU85245 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO19680.
PN US2003032114-A1.
PD 13-FEB-2003.
Query Match 9.3%; Score 60; DB 6; Length 89;
Best Local Similarity 40.5%; Pred. No. 87;
RESULT 1461
ID ABO00384 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO19680.
PN US2003032101-A1.
PD 13-FEB-2003.
Query Match 9.3%; Score 60; DB 6; Length 89;
Best Local Similarity 40.5%; Pred. No. 87;
RESULT 1462
ID ABO11716 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #283.
PN US2003036124-A1.
PD 20-FEB-2003.
Query Match 9.3%; Score 60; DB 6; Length 89;
Best Local Similarity 40.5%; Pred. No. 87;
RESULT 1463
ID ABO02361 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #283.
PN US2003040054-A1.
PD 27-FEB-2003.
Query Match 9.3%; Score 60; DB 6; Length 89;
Best Local Similarity 40.5%; Pred. No. 87;
RESULT 1464
ID ABU88935 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO19680.
PN US2003036133-A1.
PD 20-FEB-2003.
Query Match 9.3%; Score 60; DB 6; Length 89;
Best Local Similarity 40.5%; Pred. No. 87;
RESULT 1465
ID ABU83630 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #283.
PN US2003036134-A1.
PD 20-FEB-2003.
Query Match 9.3%; Score 60; DB 6; Length 89;
Best Local Similarity 40.5%; Pred. No. 87;
RESULT 1466
ID ABO06431 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO19680.

PN US2003022294-A1.
PD 30-JAN-2003.
Query Match 9.3%; Score 60; DB 6; Length 89;
Best Local Similarity 40.5%; Pred. No. 87;
RESULT 1467
ID ABR59467 standard; protein; 89 AA.
DE Human secreted polypeptide PRO19680, SEQ ID NO:566.
PN US2003027275-A1.
PD 06-FEB-2003.
Query Match 9.3%; Score 60; DB 6; Length 89;
Best Local Similarity 40.5%; Pred. No. 87;
RESULT 1468
ID ABO09529 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #283.
PN US2003027324-A1.
PD 06-FEB-2003.
Query Match 9.3%; Score 60; DB 6; Length 89;
Best Local Similarity 40.5%; Pred. No. 87;
RESULT 1469
ID ABO19393 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO19680.
PN US2003036118-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 60; DB 6; Length 89;
Best Local Similarity 40.5%; Pred. No. 87;
RESULT 1470
ID ABO11411 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #283.
PN US2003036123-A1.
PD 20-FEB-2003.
Query Match 9.3%; Score 60; DB 6; Length 89;
Best Local Similarity 40.5%; Pred. No. 87;
RESULT 1471
ID ABR67029 standard; protein; 89 AA.
DE Human secreted polypeptide PRO19680, SEQ ID NO:566.
PN US2003036148-A1.
PD 20-FEB-2003.
Query Match 9.3%; Score 60; DB 6; Length 89;
Best Local Similarity 40.5%; Pred. No. 87;
RESULT 1472
ID ABO16242 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #283.
PN US2003040060-A1.
PD 27-FEB-2003.
Query Match 9.3%; Score 60; DB 6; Length 89;
Best Local Similarity 40.5%; Pred. No. 87;
RESULT 1473
ID ABO13948 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #283.
PN US2003044916-A1.
PD 06-MAR-2003.
Query Match 9.3%; Score 60; DB 6; Length 89;
Best Local Similarity 40.5%; Pred. No. 87;
RESULT 1474
ID ABU65851 standard; protein; 89 AA.
DE Human secreted/transmembrane protein, SEQ ID 566.
PN US2003036156-A1.
PD 20-FEB-2003.
Query Match 9.3%; Score 60; DB 6; Length 89;
Best Local Similarity 40.5%; Pred. No. 87;
RESULT 1475
ID ABO07699 standard; protein; 89 AA.
DE Human PRO polypeptide #283.
PN US2003032117-A1.
PD 13-FEB-2003.
Query Match 9.3%; Score 60; DB 6; Length 89;
Best Local Similarity 40.5%; Pred. No. 87;
RESULT 1476
ID ABO03886 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #283.
PN US2003036128-A1.
PD 20-FEB-2003.

Query Match 9.3%; Score 60; DB 6; Length 89;
Best Local Similarity 40.5%; Pred. No. 87;
RESULT 1477
ID ABR67334 standard; protein; 89 AA.
DE Human secreted polypeptide PRO19680, SEQ ID NO:566.
PN US2003027266-A1.
PD 06-FEB-2003.
Query Match 9.3%; Score 60; DB 6; Length 89;
Best Local Similarity 40.5%; Pred. No. 87;
RESULT 1478
ID ABO15937 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #283.
PN US2003054483-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 60; DB 6; Length 89;
Best Local Similarity 40.5%; Pred. No. 87;
RESULT 1479
ID ABR56218 standard; protein; 89 AA.
DE Human secreted/transmembrane protein, PRO19680.
PN US2003022298-A1.
PD 30-JAN-2003.
Query Match 9.3%; Score 60; DB 6; Length 89;
Best Local Similarity 40.5%; Pred. No. 87;
RESULT 1480
ID ABR65546 standard; protein; 89 AA.
DE Human PRO polypeptide #283.
PN US2003032102-A1.
PD 13-FEB-2003.
Query Match 9.3%; Score 60; DB 6; Length 89;
Best Local Similarity 40.5%; Pred. No. 87;
RESULT 1481
ID ABR95491 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO19680.
PN US2003036117-A1.
PD 20-FEB-2003.
Query Match 9.3%; Score 60; DB 6; Length 89;
Best Local Similarity 40.5%; Pred. No. 87;
RESULT 1482
ID ABR71394 standard; protein; 89 AA.
DE Human PRO19680 protein.
PN US2003036143-A1.
PD 20-FEB-2003.
Query Match 9.3%; Score 60; DB 6; Length 89;
Best Local Similarity 40.5%; Pred. No. 87;
RESULT 1483
ID ABO08004 standard; protein; 89 AA.
DE Human PRO polypeptide #283.
PN US2003032130-A1.
PD 13-FEB-2003.
Query Match 9.3%; Score 60; DB 6; Length 89;
Best Local Similarity 40.5%; Pred. No. 87;
RESULT 1484
ID ABR70245 standard; protein; 89 AA.
DE Human secreted polypeptide PRO19680, SEQ ID NO:566.
PN US2003032138-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 60; DB 6; Length 89;
Best Local Similarity 40.5%; Pred. No. 87;
RESULT 1485
ID ABR69578 standard; protein; 89 AA.
DE Human secreted polypeptide PRO19680, SEQ ID NO:566.
PN US2003036132-A1.
PD 20-FEB-2003.
Query Match 9.3%; Score 60; DB 6; Length 89;
Best Local Similarity 40.5%; Pred. No. 87;
RESULT 1486
ID ABO01719 standard; protein; 89 AA.
DE Human PRO polypeptide #283.
PN US2003008353-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.

Query Match 9.3%; Score 60; DB 6; Length 89;
Best Local Similarity 40.5%; Pred. No. 87;
RESULT 1487
ID ABR81521 standard; protein; 89 AA.
DE Human PRO polypeptide #283.
PN US2003017542-A1.
PD 23-JAN-2003.
Query Match 9.3%; Score 60; DB 6; Length 89;
Best Local Similarity 40.5%; Pred. No. 87;
RESULT 1488
ID ABR60318 standard; protein; 89 AA.
DE Human secreted polypeptide PRO19680, SEQ ID NO:566.
PN US2003032137-A1.
PD 13-FEB-2003.
Query Match 9.3%; Score 60; DB 6; Length 89;
Best Local Similarity 40.5%; Pred. No. 87;
RESULT 1489
ID ABR68053 standard; protein; 89 AA.
DE Human secreted polypeptide PRO19680, SEQ ID NO:566.
PN US2003027269-A1.
PD 06-FEB-2003.
Query Match 9.3%; Score 60; DB 6; Length 89;
Best Local Similarity 40.5%; Pred. No. 87;
RESULT 1490
ID ABR65441 standard; protein; 89 AA.
DE Human secreted polypeptide PRO19680, SEQ ID NO:566.
PN US2003027268-A1.
PD 06-FEB-2003.
Query Match 9.3%; Score 60; DB 6; Length 89;
Best Local Similarity 40.5%; Pred. No. 87;
RESULT 1491
ID ABR68663 standard; protein; 89 AA.
DE Human secreted polypeptide PRO19680, SEQ ID NO:566.
PN US2003027274-A1.
PD 06-FEB-2003.
Query Match 9.3%; Score 60; DB 6; Length 89;
Best Local Similarity 40.5%; Pred. No. 87;
RESULT 1492
ID ABR72075 standard; protein; 89 AA.
DE Human secreted polypeptide PRO19680, SEQ ID NO:566.
PN US2003032135-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 60; DB 6; Length 89;
Best Local Similarity 40.5%; Pred. No. 87;
RESULT 1493
ID ABR85555 standard; protein; 89 AA.
DE Human PRO polypeptide #283.
PN US2003022295-A1.
PD 30-JAN-2003.
Query Match 9.3%; Score 60; DB 6; Length 89;
Best Local Similarity 40.5%; Pred. No. 87;
RESULT 1494
ID ABR89245 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #283.
PN US2003022297-A1.
PD 30-JAN-2003.
Query Match 9.3%; Score 60; DB 6; Length 89;
Best Local Similarity 40.5%; Pred. No. 87;
RESULT 1495
ID ABR83325 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #283.
PN US2003032105-A1.
PD 13-FEB-2003.
Query Match 9.3%; Score 60; DB 6; Length 89;
Best Local Similarity 40.5%; Pred. No. 87;
RESULT 1496
ID ABR95181 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO19680.
PN US2003032123-A1.
PD 13-FEB-2003.
Query Match 9.3%; Score 60; DB 6; Length 89;
Best Local Similarity 40.5%; Pred. No. 87;

RESULT 1497
ID ABU90729 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO19680.
PN US2003032108-A1.
PD 13-FEB-2003.
Query Match 9.3%; Score 60; DB 6; Length 89;
Best Local Similarity 40.5%; Pred. No. 87;
RESULT 1498
ID ABU84240 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #283.
PN US2003032111-A1.
PD 13-FEB-2003.
Query Match 9.3%; Score 60; DB 6; Length 89;
Best Local Similarity 40.5%; Pred. No. 87;
RESULT 1499
ID ABU93891 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO19680.
PN US2003032119-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 60; DB 6; Length 89;
Best Local Similarity 40.5%; Pred. No. 87;
RESULT 1500
ID ABR65136 standard; protein; 89 AA.
DE Human secreted polypeptide PRO19680, SEQ ID NO:566.
PN US2003027263-A1.
PD 06-FEB-2003.
Query Match 9.3%; Score 60; DB 6; Length 89;
Best Local Similarity 40.5%; Pred. No. 87;

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OM protein - protein search, using sw model

Run on: August 3, 2006, 09:56:18 ; Search time 16 Seconds
(without alignments)

715.612 Million cell updates/sec

Title: US-10-015-967-2

Perfect score: 644

Sequence: 1 MKVLISLLILLPLMLMSV.....SRACQQLKQCQLRSPALPL 119

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match: 0%

Maximum Match: 100%

Listing first 1500 summaries

Database :

PIR 80:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	77.5	12.0	477	2 T19801	hypothetical prote
2	77	12.0	2869	1 JQ1750	Genome polyprotein
3	74.5	11.6	448	2 I50451	vitamin D receptor
4	73.5	11.4	70	2 A60912	vitamin D receptor
5	71.5	11.1	108	2 G84522	similar to gibbere
6	71	11.0	411	2 S35333	steroid receptor p
7	71	11.0	2862	2 S16564	large protein L -
8	71	11.0	3190	2 T13828	CREB-binding prote
9	70.5	10.9	1283	2 T49804	hypothetical prote
10	70	10.9	543	2 A32693	steroid receptor p
11	70	10.9	746	2 B32693	steroid receptor p
12	70	10.9	1095	2 T24061	hypothetical prote
13	70	10.9	1620	2 T27283	hypothetical prote
14	69.5	10.8	221	2 C34768	ORF2 protein - Orf
15	69.5	10.8	575	1 THHUB	thrombomodulin pre
16	69	10.7	200	2 C83086	hypothetical prote
17	68.5	10.6	381	2 A46358	steroid/thyroid ho
18	68.5	10.6	422	2 PC4019	vitamin D receptor
19	68.5	10.6	423	2 A31761	1,25-dihydroxyvita
20	68.5	10.6	427	2 S24174	vitamin D receptor
21	68.5	10.6	427	2 A28200	vitamin D receptor
22	68.5	10.6	647	2 S36557	E1 protein - human
23	68.5	10.6	1066	2 S74992	hypothetical prote
24	68	10.6	283	2 S42393	G-box-binding prot
25	67	10.4	376	2 T48350	cysteine proteinase
26	67	10.4	475	2 E69643	histidine permease
27	67	10.4	1062	2 T14151	Inv protein - mous
28	67	10.4	1062	2 T30255	inversin - mouse
29	66.5	10.3	103	2 A72713	hypothetical prote

30	66.5	10.3	419	2 A57000	orphan receptor CO
31	66.5	10.3	422	2 I48305	gene COUP-TF1 prot
32	66.5	10.3	423	2 S02710	transcription fact
33	66	10.2	339	2 T36061	hypothetical prote
34	65.5	10.2	106	2 S60232	giberellin-regula
35	65.5	10.2	397	2 S26617	transcription fact
36	65.5	10.2	413	2 H82270	hypothetical prote
37	65.5	10.2	425	2 JC7230	vitamin D receptor
38	65.5	10.2	646	2 S36586	E1 protein - human
39	65.5	10.2	706	2 JE0164	frizzled-6 protein
40	65	10.1	363	2 JC4748	polygalacturonase
41	65	10.1	440	2 JS0374	hypothetical 51.6k
42	65	10.1	1797	2 A55677	laminin beta-2 cha
43	64.5	10.0	359	2 B29960	Balbani ring 2 ch
44	64.5	10.0	622	2 I48733	protein kinase rck
45	64	9.9	227	2 I39313	zinc-finger protei
46	64	9.9	334	2 T03556	probable D-ribose-
47	64	9.9	1798	2 S53869	laminin beta-2 cha
48	63.5	9.9	233	2 T09788	probable superoxid
49	63.5	9.9	262	2 T19323	hypothetical prote
50	63	9.8	160	2 I61899	eosinophil cation
51	63	9.8	330	2 S74255	homeotic protein s
52	63	9.8	371	1 S53442	DNA repair protein
53	63	9.8	462	2 T04437	hypothetical prote
54	62.5	9.7	410	2 I50689	orphan receptor CO
55	62.5	9.7	414	2 A37133	apolipoprotein A-I
56	62.5	9.7	414	2 I48975	apolipoprotein A-I
57	62.5	9.7	419	2 G82192	PqIA family protei
58	62.5	9.7	420	2 JC7229	vitamin D receptor
59	62.5	9.7	767	2 S41479	DNA-binding protei
60	62.5	9.7	840	2 T21333	hypothetical prote
61	62.5	9.7	2282	2 T42717	DNA-binding protei
62	62	9.6	235	2 T16916	hypothetical prote
63	62	9.6	346	2 B90620	NADH dehydrogenase
64	62	9.6	371	1 R65FM7	ribosomal protein
65	62	9.6	577	2 S33763	hormone receptor N
66	62	9.6	728	2 A48830	probable transcript
67	62	9.6	1453	2 G96613	hypothetical prote
68	62	9.6	1670	1 CGHU3B	collagen alpha 3(I
69	62	9.6	3026	2 T28431	variant surface pr
70	61.5	9.5	94	2 JH0787	transcription fact
71	61.5	9.5	369	2 A42565	interleukin-2 rece
72	61.5	9.5	403	2 S35334	steroid receptor p
73	61	9.5	138	2 T52567	squamosa promoter
74	61	9.5	181	2 T52607	squamosa promoter
75	61	9.5	183	2 A49905	protein secretion
76	61	9.5	346	2 T11168	NADH2 dehydrogenas
77	61	9.5	398	2 C91063	hypothetical prote
78	61	9.5	795	2 T34468	hypothetical prote
79	61	9.5	926	2 S58936	meiotic recombinat
80	61	9.5	1014	2 T30545	major surface glyc
81	61	9.5	1560	2 I54361	SMCX protein - hum
82	60.5	9.4	106	2 T49958	GAS44 - Arabidopsi
83	60.5	9.4	162	2 A53814	p20 protein - rat
84	60.5	9.4	256	2 F83194	polyamine transpor
85	60.5	9.4	322	2 F84343	pyruvate dehydroge
86	60.5	9.4	385	2 E96669	protein FLN19.19 [
87	60.5	9.4	393	2 A55859	regulatory protein
88	60.5	9.4	396	2 T27172	hypothetical prote
89	60.5	9.4	627	2 S76462	regulatory protei
90	60.5	9.4	640	2 S47865	regulatory protei
91	60.5	9.4	808	2 F64914	dimethylsulfoxide
92	60.5	9.4	808	2 F90915	probable oxidoredu
93	60.5	9.4	5138	2 B96695	hypothetical prote
94	60	9.3	67	2 B69830	hypothetical prote
95	60	9.3	346	2 S25423	NADH2 dehydrogenas
96	60	9.3	346	2 B90626	NADH dehydrogenase
97	60	9.3	363	2 JC4049	polygalacturonase
98	60	9.3	548	2 A70780	probable membrane
99	60	9.3	614	2 G81721	hypothetical prote
100	60	9.3	825	2 JC4163	DNA-binding protei
101	60	9.3	1033	2 I48775	Smcx protein (esca
102	60	9.3	1869	2 A59290	class V chitin syn

103	60	9.3	3161	2	T30342	protein HMP1 - Ye	176	58	9.0	998	2	I58351	receptor protein-t
104	59.5	9.2	104	1	R5PM25	ribosomal protein	177	58	9.0	998	2	JC5672	receptor tyrosine
105	59.5	9.2	180	1	R53814	p20 protein - huma	178	58	9.0	1639	1	MMFFB2	laminin gamma-1 ch
106	59.5	9.2	183	1	RSBY32	ribosomal protein	179	58	9.0	5376	2	T42215	zonadhesin - mouse
107	59.5	9.2	208	2	R89697	protein K02B9.4 [i	180	57.5	8.9	110	2	H86408	F3H9.8 precursor - A
108	59.5	9.2	210	2	BQIC2	Balbani ring-2 ch	181	57.5	8.9	111	2	JG0177	LEP precursor - Ko
109	59.5	9.2	226	2	T23233	hypothetical prote	182	57.5	8.9	134	2	T08710	hypothetical prote
110	59.5	9.2	343	2	S51392	hypothetical prote	183	57.5	8.9	274	2	S75320	hypothetical prote
111	59.5	9.2	359	2	A22891	fix2 protein - Rni	184	57.5	8.9	279	2	S75320	hypothetical prote
112	59.5	9.2	422	2	T10655	hypothetical prote	185	57.5	8.9	323	2	S38887	2S albumin - commo
113	59.5	9.2	427	2	JN0785	Carbon catabolite	186	57.5	8.9	339	2	G84444	protein C36E6.11 [
114	59.5	9.2	447	2	T12544	hypothetical prote	187	57.5	8.9	411	2	D84642	hypothetical prote
115	59.5	9.2	564	2	I48776	spermatogenesis re	188	57.5	8.9	433	2	D84335	hypothetical prote
116	59.5	9.2	633	2	F83028	DNA mismatch repai	189	57.5	8.9	475	2	I38597	zinc finger protei
117	59.5	9.2	946	2	S71168	Ca2+-transporting	190	57.5	8.9	535	2	A60531	probable estrase
118	59.5	9.2	1020	2	D86402	protein envelope C	191	57.5	8.9	535	2	S34576	D2 protein precurs
119	59.5	9.2	1020	2	T51926	Ca2+-transporting	192	57.5	8.9	1112	2	T40382	dna repair protein
120	59.5	9.2	1364	2	T00250	MEGF2 protein - hu	193	57.5	8.9	1216	2	T26104	hypothetical prote
121	59.5	9.2	2178	2	S29237	calcium channel pr	194	57.5	8.9	1417	2	P96613	hypothetical prote
122	59.5	9.2	2222	2	A37490	voltage-dependent	195	57	8.9	182	2	H87383	hypothetical prote
123	59.5	9.2	2251	2	B54972	voltage-dependent	196	57	8.9	225	2	T49759	hypothetical prote
124	59.5	9.2	2259	2	S29236	calcium channel pr	197	57	8.9	305	2	A46476	B cell-associated
125	59.5	9.2	2270	2	A54972	voltage-dependent	198	57	8.9	313	2	E72371	oligopeptide ABC t
126	59.5	9.2	2272	2	C54972	voltage-dependent	199	57	8.9	333	2	S61849	hrpV protein - Pae
127	59.5	9.2	3034	2	T14119	seven-pass transme	200	57	8.9	346	2	T12384	NADH2 dehydrogenas
128	59	9.2	157	2	T24380	hypothetical prote	201	57	8.9	362	2	T20573	hypothetical prote
129	59	9.2	160	2	I61896	eosinophil cationi	202	57	8.9	368	2	G84769	regulatory protein
130	59	9.2	162	2	JL0106	eosinophil cationi	203	57	8.9	416	2	A41694	hypothetical prote
131	59	9.2	346	2	B90616	NADH dehydrogenase	204	57	8.9	433	2	T19632	hypothetical prote
132	59	9.2	346	2	B90622	NADH dehydrogenase	205	57	8.9	480	2	T20154	hypothetical prote
133	59	9.2	361	2	I50505	gene wnt8 protein	206	57	8.9	514	2	B96986	sugar ABC-transport
134	59	9.2	402	2	S70703	carbon catabolite	207	57	8.9	531	2	E95358	probable L-sorbose
135	59	9.2	412	2	C86177	hypothetical prote	208	57	8.9	564	2	S59776	protein kinase DPF
136	59	9.2	437	2	T30897	hypothetical prote	209	57	8.9	592	2	JC7709	testis-specific ki
137	59	9.2	603	2	S22402	2-aminobenzoate-Co	210	57	8.9	692	2	S56849	probable membrane
138	59	9.2	716	2	S28185	phenylalanine ammo	211	57	8.9	754	2	S62561	ATP dependent RNA
139	59	9.2	730	2	R83951	translation initia	212	57	8.9	976	2	A36355	protein-tyrosine k
140	59	9.2	802	1	S48529	NAB3 protein - yea	213	57	8.9	1451	2	T33083	hypothetical prote
141	59	9.2	2101	2	S57245	insulin receptor (214	57	8.9	1557	2	G86419	probable reverse t
142	59	9.2	2135	2	T14602	variant-specific s	215	57	8.9	1790	1	MMFFB1	laminin beta-1 cha
143	58.5	9.1	115	2	T16069	hypothetical prote	216	57	8.9	2610	2	T20968	hypothetical prote
144	58.5	9.1	162	2	B72465	hypothetical prote	217	56.5	8.8	81	2	D95014	competence-induced
145	58.5	9.1	416	2	T02194	probable pectinase	218	56.5	8.8	106	2	E75371	hypothetical prote
146	58.5	9.1	738	2	I60486	gene trg protein -	219	56.5	8.8	139	2	B70049	flagellar protein
147	58.5	9.1	776	2	T20738	hypothetical prote	220	56.5	8.8	164	2	T00851	hypothetical prote
148	58.5	9.1	1019	2	A38738	coagulation factor	221	56.5	8.8	208	2	S28722	hypothetical prote
149	58.5	9.1	1083	2	C88854	protein FilA10.3 [222	56.5	8.8	220	2	S29195	antisikasin - Hydra
150	58.5	9.1	1238	2	T40120	C2H2 type zinc fin	223	56.5	8.8	249	2	T37920	hypothetical prote
151	58.5	9.1	1737	2	T00209	MEGF8 protein - hu	224	56.5	8.8	263	2	T25665	hypothetical prote
152	58.5	9.1	3051	2	S42373	hypothetical prote	225	56.5	8.8	304	2	T02125	chlorophyll a/b-bi
153	58	9.0	114	2	S75565	hypothetical prote	226	56.5	8.8	330	2	D71600	rifin PFB1035w - m
154	58	9.0	136	2	T48713	hypothetical prote	227	56.5	8.8	349	2	T36055	probable secreted
155	58	9.0	143	2	A72602	hypothetical prote	228	56.5	8.8	350	2	S63248	hypothetical prote
156	58	9.0	248	2	B84682	probable carbonic	229	56.5	8.8	356	2	E86934	benzoate X recepto
157	58	9.0	346	2	T11023	NADH2 dehydrogenas	230	56.5	8.8	388	2	JC7510	hypothetical prote
158	58	9.0	346	2	T12380	NADH2 dehydrogenas	231	56.5	8.8	408	2	E84743	cell wall-binding
159	58	9.0	346	2	T12381	NADH2 dehydrogenas	232	56.5	8.8	424	2	AD2017	hypothetical prote
160	58	9.0	346	2	B90612	NADH dehydrogenase	233	56.5	8.8	429	2	T26152	retrovirus-related
161	58	9.0	346	2	T12410	NADH2 dehydrogenase	234	56.5	8.8	445	2	C47757	hypothetical prote
162	58	9.0	346	2	T23383	NADH2 dehydrogenas	235	56.5	8.8	513	2	G84770	hypothetical prote
163	58	9.0	413	2	D71112	hypothetical prote	236	56.5	8.8	532	2	S22662	transcription fact
164	58	9.0	443	2	T48708	hypothetical prote	237	56.5	8.8	620	2	S56790	probable membrane
165	58	9.0	464	2	A28569	alpha-methyldopa-h	238	56.5	8.8	627	2	T04562	hypothetical prote
166	58	9.0	470	2	T22785	hypothetical prote	239	56.5	8.8	774	2	JC7265	neprilysin (SC 3.4
167	58	9.0	572	2	C42679	protein-tyrosine-p	240	56.5	8.8	905	2	A54654	centromere protein
168	58	9.0	603	2	E84744	hypothetical prote	241	56.5	8.8	994	2	S19595	chloride channel p
169	58	9.0	605	2	JC5673	receptor tyrosine	242	56.5	8.8	1246	2	JQ0406	hypothetical prote
170	58	9.0	610	2	I48612	developmental kina	243	56.5	8.8	1347	2	T45632	helicase homolog F
171	58	9.0	626	2	I48614	developmental kina	244	56.5	8.8	1513	2	T23681	hypothetical prote
172	58	9.0	685	1	Q3ECS7	hypothetical 77K p	245	56.5	8.8	1551	2	T18941	hypothetical prote
173	58	9.0	694	2	T10565	hypothetical prote	246	56.5	8.8	1876	2	T28627	vitellogenin - Rip
174	58	9.0	707	2	S50144	Gonyaulax-luciferi	247	56.5	8.8	2823	2	F87908	protein T22A3.8 li
175	58	9.0	811	2	S36109	osteoblast-specifi	248	56.5	8.8	2823	2	T23064	hypothetical prote

249	56.5	8.8	3102	2	T43291	laminin alpha chain	322	55	8.5	436	2	T36104	conserved hypotet
250	56	8.7	118	2	T49372	hypothetical prote	323	55	8.5	458	2	D70410	cytosolic axial fi
251	56	8.7	135	2	B38253	kappa-enhancer-bin	324	55	8.5	462	2	I38404	neu differentiation
252	56	8.7	135	2	E75078	hypothetical prote	325	55	8.5	533	1	A38228	dimethylalanine mo
253	56	8.7	135	2	P80328	polyprotein - hepa	326	55	8.5	531	2	B32891	finger protein 2,
254	56	8.7	135	2	P80327	polyprotein - hepa	327	55	8.5	715	4	TVMSMY	transforming prote
255	56	8.7	138	2	S67968	transition protein	328	55	8.5	862	2	B36786	hypothetical prote
256	56	8.7	145	2	A99583	SOS ribosomal prot	329	55	8.5	879	2	T22033	hypothetical prote
257	56	8.7	289	2	A48913	KRAB zinc finger p	330	55	8.5	891	2	G84693	probable proline-r
258	56	8.7	411	2	F97760	hypothetical prote	331	55	8.5	943	2	T16768	hypothetical prote
259	56	8.7	492	2	P80326	polyprotein - hepa	332	55	8.5	1139	2	T08421	resistance protein
260	56	8.7	516	2	G70149	hypothetical prote	333	55	8.5	1560	2	T42727	proliferation pote
261	56	8.7	597	2	D98186	adenine deaminase	334	55	8.5	4196	2	T43274	dynain heavy chain
262	56	8.7	597	2	AF3100	adenine deaminase	335	54.5	8.5	102	2	S33334	protamine P2 - ora
263	56	8.7	605	2	T05243	hypothetical prote	336	54.5	8.5	116	2	G85691	probable head-tail
264	56	8.7	653	2	C97768	hypothetical prote	337	54.5	8.5	116	2	A90876	probable head-tail
265	56	8.7	678	2	G98037	glycine-tRNA ligas	338	54.5	8.5	116	2	E90853	probable head-tail
266	56	8.7	716	2	JQ1366	polyprotein - hepa	339	54.5	8.5	116	2	F90909	probable head-tail
267	56	8.7	721	2	D83110	exodeoxyribonuclea	340	54.5	8.5	144	2	AF2695	conserved hypotet
268	56	8.7	735	2	T13646	hypothetical prote	341	54.5	8.5	144	2	F97477	hypothetical prote
269	56	8.7	794	2	T10519	pre-pro-legumin -	342	54.5	8.5	180	1	RKPM55	ribulose-bisphosph
270	56	8.7	857	2	T05352	hypothetical prote	343	54.5	8.5	182	2	S32748	even protein - zeb
271	56	8.7	944	2	S01909	hairy wing suppl	344	54.5	8.5	223	2	S43535	genome polyprotein
272	56	8.7	1020	2	T51925	Ca2+-transporting	345	54.5	8.5	232	2	A41551	vascular endotheli
273	56	8.7	1217	1	EGSM5G	epidermal growth f	346	54.5	8.5	255	2	T52352	hypothetical prote
274	56	8.7	1246	2	S56752	helicase SKI2W - h	347	54.5	8.5	255	2	A60637	merozoite antigen
275	56	8.7	1801	1	MMRTS	laminin beta-2 cha	348	54.5	8.5	284	2	S74256	homeotic protein s
276	56	8.7	2391	2	G89779	hypothetical prote	349	54.5	8.5	285	2	T27458	hypothetical prote
277	56	8.7	2416	2	T13825	adenomatous polypo	350	54.5	8.5	288	2	E86717	hypothetical prote
278	56	8.7	3011	1	GNWVC3	genome polyprotein	351	54.5	8.5	323	2	E72327	astb/chuk-related
279	56	8.7	3433	1	GNWVKY	genome polyprotein	352	54.5	8.5	340	2	T02120	hypothetical prote
280	55.5	8.6	131	2	T52597	squamosa promoter	353	54.5	8.5	344	2	F86267	.T6J4.6 protein - A
281	55.5	8.6	224	2	G70851	probable gid prote	354	54.5	8.5	364	2	H71440	hypothetical prote
282	55.5	8.6	244	2	A75408	triosephosphate is	355	54.5	8.5	377	2	B82370	phosphoribosylamin
283	55.5	8.6	252	2	B86422	FIN18.10 protein -	356	54.5	8.5	386	2	S68016	ATPase/RNA helicase
284	55.5	8.6	257	2	G82119	probable esterase/l	357	54.5	8.5	414	2	T15947	hypothetical prote
285	55.5	8.6	302	2	T45890	splicing factor-1	358	54.5	8.5	422	2	T24865	hypothetical prote
286	55.5	8.6	305	2	C39240	finger protein mfg	359	54.5	8.5	515	2	F88618	protein W06P12.2 (
287	55.5	8.6	319	2	T51280	hypothetical prote	360	54.5	8.5	543	2	H84724	probable ART-like
288	55.5	8.6	365	2	T22584	hypothetical prote	361	54.5	8.5	547	2	C96828	unknown protein F1
289	55.5	8.6	368	1	I39598	N-Acylamino acid r	362	54.5	8.5	562	2	T28242	hypothetical prote
290	55.5	8.6	376	2	AD2697	hypothetical prote	363	54.5	8.5	568	2	T26243	hypothetical prote
291	55.5	8.6	386	2	S41497	thyroid hormone re	364	54.5	8.5	571	2	S00566	convicillin precurs
292	55.5	8.6	494	2	T19550	hypothetical prote	365	54.5	8.5	598	2	A57040	T-cell nuclear rec
293	55.5	8.6	510	1	FOLJTM	gag polyprotein -	366	54.5	8.5	598	2	A46225	nuclear orphan rec
294	55.5	8.6	542	2	A45661	zinc finger protei	367	54.5	8.5	625	2	T48462	hypothetical prote
295	55.5	8.6	562	2	G88408	protein nhr-6 [imp	368	54.5	8.5	625	2	T48465	hypothetical prote
296	55.5	8.6	619	1	T43348	nuclear steroid ho	369	54.5	8.5	625	2	D87793	protein C27A12.2 l
297	55.5	8.6	700	2	B69667	ribonucleoside-dip	370	54.5	8.5	692	2	C81653	probable thiol-dis
298	55.5	8.6	707	2	S68958	finger protein - m	371	54.5	8.5	707	1	A64047	ribonucleoside-tri
299	55.5	8.6	728	2	H64346	hypothetical prote	372	54.5	8.5	729	2	T23972	hypothetical prote
300	55.5	8.6	749	2	A45294	Balbani ring 2.1	373	54.5	8.5	900	2	B87957	protein Y106G6D.7
301	55.5	8.6	1028	2	AF3286	Arp-dependent DNA	374	54.5	8.5	948	2	T26417	hypothetical prote
302	55.5	8.6	1371	2	T29019	hypothetical prote	375	54.5	8.5	1006	2	S20126	exoribonuclease RA
303	55.5	8.6	1808	2	T15099	hypothetical prote	376	54.5	8.5	1047	1	OYRTBR	atrial natriuretic
304	55.5	8.6	2195	2	T34264	hypothetical prote	377	54.5	8.5	1102	2	S55100	hypothetical prote
305	55.5	8.6	2337	2	T45115	N-type calcium cha	378	54.5	8.5	1678	2	D86481	189.6K hypotetica
306	55.5	8.6	2355	1	JQ1532	genome polyprotein	379	54.5	8.5	1700	2	S08167	Balbani ring 3 pr
307	55.5	8.6	2339	2	A42566	omega-conotoxin-se	380	54.5	8.5	3010	1	GNWVTW	genome polyprotein
308	55	8.5	56	2	T30739	hypothetical prote	381	54.5	8.5	3011	1	S40770	genome polyprotein
309	55	8.5	144	2	H75636	transposase-relate	382	54.5	8.5	4485	2	T08044	dynain gamma heavy
310	55	8.5	153	2	S75561	hypothetical prote	383	54.5	8.5	5149	2	F83345	probable non-ribos
311	55	8.5	155	2	A86765	mutator protein Wu	384	54	8.4	51	2	S00016	protamine 21 - sma
312	55	8.5	177	2	E64910	probable lysozyme	385	54	8.4	98	2	E64720	probable membrane
313	55	8.5	181	2	AF3291	5-formyltetrahydro	386	54	8.4	104	2	S57666	protamine 2 - rat
314	55	8.5	186	2	AF0248	conserved hypotet	387	54	8.4	105	2	B71672	ribosomal protein
315	55	8.5	214	2	S00832	finger protein (cl	388	54	8.4	129	2	H84749	probable squamosa-
316	55	8.5	246	2	T34067	hypothetical prote	389	54	8.4	167	2	E83743	4-hydroxybenzoyl-C
317	55	8.5	271	2	T48994	pirin-like protein	390	54	8.4	167	2	T52599	squamosa promoter
318	55	8.5	323	2	T31474	hypothetical prote	391	54	8.4	174	2	T52600	squamosa promoter
319	55	8.5	359	2	S28831	microtubule-associ	392	54	8.4	184	2	AB0635	conserved hypotet
320	55	8.5	388	2	T27645	hypothetical prote	393	54	8.4	205	2	F43719	uref protein - Pro
321	55	8.5	393	2	S62335	171-7 protein - fr	394	54	8.4	209	2	D90593	lipoprotein [impor

395	54	8.4	218	2	A40513	hypothetical prote	468	53.5	8.3	571	2	T20359	hypothetical prote
396	54	8.4	232	2	S42392	G-box-binding prot	469	53.5	8.3	602	2	T42401	ubiquitin thiolest
397	54	8.4	251	2	B39685	GRESAG protein 2.1	470	53.5	8.3	614	2	T19963	hypothetical prote
398	54	8.4	256	2	S57747	SURF-2 protein - h	471	53.5	8.3	619	1	OYB070	guanylate cyclase
399	54	8.4	257	2	T49701	hypothetical prote	472	53.5	8.3	619	1	OVRTB1	guanylate cyclase
400	54	8.4	275	2	C87634	conserved hypothet	473	53.5	8.3	619	2	S23097	guanylate cyclase
401	54	8.4	298	1	HLMS1	MHC class I histoc	474	53.5	8.3	619	2	A45625	phosphoenolpyruvat
402	54	8.4	332	2	S11714	transcription init	475	53.5	8.3	700	2	T77463	luteinizing hormon
403	54	8.4	346	2	B90614	NADH dehydrogenase	476	53.5	8.3	700	2	A49744	luteinizing-choriogon
404	54	8.4	354	2	T46014	squamosa promoter-	477	53.5	8.3	712	2	T30960	hypothetical prote
405	54	8.4	359	2	A49973	prostanoid EP race	478	53.5	8.3	729	2	T10692	polynucleotide ade
406	54	8.4	362	2	A53058	prostaglandin F2-a	479	53.5	8.3	731	2	B31383	hrpM protein - Pae
407	54	8.4	371	2	D52666	cell division prot	480	53.5	8.3	798	2	A40526	integrin beta-7 ch
408	54	8.4	405	2	T29639	hypothetical prote	481	53.5	8.3	811	2	AF0680	probable dimethyl
409	54	8.4	443	2	C88427	protein R07E5.6 [i	482	53.5	8.3	815	2	AC0394	probable acyl-CoA
410	54	8.4	478	2	S44249	bet protein - huma	483	53.5	8.3	885	2	JC4732	beta-N-acetylthexos
411	54	8.4	493	2	T48219	hypothetical prote	484	53.5	8.3	986	2	T52176	aldehyde oxidase (
412	54	8.4	495	2	T36043	probable integrase	485	53.5	8.3	1046	2	AD2959	AcrB/AcrD/AcrF fam
413	54	8.4	529	2	AH3554	sugar transport Ar	486	53.5	8.3	1046	2	B98324	probable rnd efflu
414	54	8.4	539	2	S50626	CKI3 protein - yea	487	53.5	8.3	1165	2	S27809	GTPase-activating
415	54	8.4	555	2	AE2208	hypothetical prote	488	53.5	8.3	1168	2	I56985	kalinin B1 - mouse
416	54	8.4	568	2	T17308	hypothetical prote	489	53.5	8.3	1268	2	B36502	insulin receptor-r
417	54	8.4	580	2	A37107	spermatogenesis pr	490	53.5	8.3	1332	2	D84669	aldehyde oxidase [
418	54	8.4	585	2	F33913	hypothetical prote	491	53.5	8.3	1721	1	I38902	retinoblastoma bin
419	54	8.4	588	1	FWCNAB	alpha-globulin B p	492	53.5	8.3	2531	2	A46019	notch-1 protein -
420	54	8.4	590	2	H71977	hypothetical prote	493	53.5	8.3	2706	2	T28155	variant-specific s
421	54	8.4	592	2	S43597	coiled-coil protei	494	53.5	8.3	3011	1	GNMVCH	genome polyprotein
422	54	8.4	620	2	T16166	hypothetical prote	495	53	8.2	57	2	H64023	hypothetical prote
423	54	8.4	632	2	J50631	alpha-amylase (EC	496	53	8.2	71	2	G72519	hypothetical prote
424	54	8.4	632	2	T32454	hypothetical prote	497	53	8.2	129	2	G72519	hypothetical prote
425	54	8.4	651	2	T32875	hypothetical prote	498	53	8.2	139	2	B39644	actin polymerizati
426	54	8.4	695	2	I54325	gene XE7 protein -	499	53	8.2	144	2	S23659	superoxide dismuta
427	54	8.4	779	2	S36111	osteoblast-specifi	500	53	8.2	152	2	S07505	endoxyribonucle
428	54	8.4	836	2	S36110	osteoblast-specifi	501	53	8.2	156	2	NRH01	pancreatic ribonuc
429	54	8.4	1191	2	S35305	zinc finger protei	502	53	8.2	159	2	T15298	hypothetical prote
430	54	8.4	1258	2	T14855	reverse transcript	503	53	8.2	174	2	B27748	hypothetical prote
431	54	8.4	1516	2	T01055	hypothetical prote	504	53	8.2	174	2	D83692	conserved hypothet
432	54	8.4	1584	2	T01055	brain-specific ang	505	53	8.2	184	2	AG0300	54K corneal protei
433	54	8.4	1963	1	MMKW	myosin heavy chain	506	53	8.2	196	2	PS0412	hypothetical prote
434	54	8.4	4976	2	T14165	peptide synthetase	507	53	8.2	203	2	T32346	conserved hypothet
435	53.5	8.3	115	2	S22588	V1 protein - tomat	508	53	8.2	216	2	AC0715	hemopoietic cell s
436	53.5	8.3	135	2	T15610	hypothetical prote	509	53	8.2	219	1	A37243	H+-transporting tw
437	53.5	8.3	136	2	T22959	hypothetical prote	510	53	8.2	225	2	T11279	bovine corneal pro
438	53.5	8.3	145	2	I54504	NGK5 secreted spli	511	53	8.2	239	2	T01406	hypothetical prote
439	53.5	8.3	174	2	A81080	single-strand bind	512	53	8.2	254	2	T20882	hypothetical prote
440	53.5	8.3	184	2	F75481	hypothetical prote	513	53	8.2	274	2	C84226	oligopeptide ABC t
441	53.5	8.3	225	1	MNNZP2	nonstructural prot	514	53	8.2	306	2	F97345	probable hydrolase
442	53.5	8.3	225	1	MNNZVT	nonstructural prot	515	53	8.2	324	2	B87196	flagellar M-ring p
443	53.5	8.3	232	2	B83732	hypothetical prote	516	53	8.2	341	2	B86598	flagellar m-ring p
444	53.5	8.3	251	2	I57668	luteinizing hormon	517	53	8.2	341	2	D72025	cysteine proteinas
445	53.5	8.3	252	2	T44299	hypothetical prote	518	53	8.2	343	2	D86198	thrombomodulin - b
446	53.5	8.3	291	2	A98322	alanine catabolic	519	53	8.2	356	2	A25918	hypothetical prote
447	53.5	8.3	291	2	A83231	conserved hypothet	520	53	8.2	359	2	T06604	hypothetical prote
448	53.5	8.3	298	2	B97186	probable glycosylt	521	53	8.2	382	2	T25538	transforming growt
449	53.5	8.3	324	2	S44956	lmb1 protein - Str	522	53	8.2	410	2	A41397	transforming growt
450	53.5	8.3	342	2	I77461	luteinizing hormon	523	53	8.2	410	2	A55706	transforming growt
451	53.5	8.3	345	2	S59236	SAE2 protein - yea	524	53	8.2	412	2	A36169	hypothetical prote
452	53.5	8.3	355	2	C38850	gamma-D-glutamyl-L	525	53	8.2	412	2	G83472	acid phosphatase (
453	53.5	8.3	360	2	B36470	Wnt-2 protein - mo	526	53	8.2	424	1	T21181	hypothetical prote
454	53.5	8.3	381	2	T29300	hypothetical prote	527	53	8.2	455	2	S65157	hypothetical prote
455	53.5	8.3	389	2	I49640	transcription fact	528	53	8.2	458	2	H75278	probable Na+/H+ an
456	53.5	8.3	390	2	S44285	EAR2 protein - mou	529	53	8.2	480	2	AH1481	beta-glucosidase h
457	53.5	8.3	395	2	T08350	hypothetical prote	530	53	8.2	490	2	S67581	STP4 protein - yea
458	53.5	8.3	399	2	S47071	finger protein HZF	531	53	8.2	497	2	S43745	phosphatidylinosit
459	53.5	8.3	403	2	S02709	ear-2 protein - hu	532	53	8.2	498	2	H85040	hypothetical prote
460	53.5	8.3	467	2	AC2015	hypothetical prote	533	53	8.2	531	2	T51922	hypothetical prote
461	53.5	8.3	477	2	T47753	hypothetical prote	534	53	8.2	554	1	TVVPHF	large T antigen -
462	53.5	8.3	492	2	T02458	hypothetical prote	535	53	8.2	577	2	T12536	hypothetical prote
463	53.5	8.3	530	2	T20360	hypothetical prote	536	53	8.2	583	2	A32861	type II site-speci
464	53.5	8.3	555	1	SVHQMA	malate synthase (E	537	53	8.2	612	2	T10727	protein kinase Xa2
465	53.5	8.3	558	2	GH3049	DNA repair protein	538	53	8.2	622	2	A34711	kinase-related pro
466	53.5	8.3	563	1	VCMVM7	env polyprotein -	539	53	8.2	629	2	T07426	probable polygalac
467	53.5	8.3	564	2	S92466	urocanate hydratase	540	53	8.2	670	2	T02019	callus-associated

541	53	8.2	710	2	I48668	zinc finger protei	614	52	8.1	67	2	T14467	pollen coat protei
542	53	8.2	782	2	S04047	finger protein zfy	615	52	8.1	113	2	S68936	probable membrane
543	53	8.2	783	2	A31491	sex-determining re	616	52	8.1	114	2	JC5238	galactosylceramide
544	53	8.2	822	2	JT0968	1,4-alpha-glucan b	617	52	8.1	141	2	A64536	hypothetical prote
545	53	8.2	884	2	TJ25205	hypothetical prote	618	52	8.1	156	2	JC5160	eosinophil-associa
546	53	8.2	952	2	T02751	DNA-directed RNA p	619	52	8.1	159	2	S37766	hypothetical prote
547	53	8.2	996	2	T10725	protein kinase Xa2	620	52	8.1	166	2	H75500	hypothetical prote
548	53	8.2	1002	2	T43236	carboxypeptidase C	621	52	8.1	192	2	I38022	hypothetical prote
549	53	8.2	1019	2	A80607	protein R52.2 (lmp	622	52	8.1	233	2	T26781	hypothetical prote
550	53	8.2	1025	1	A57676	protein kinase Xa2	623	52	8.1	241	2	T25886	hypothetical prote
551	53	8.2	1186	2	T33754	O/E-1-associated z	624	52	8.1	262	2	T02724	gag protein homolo
552	53	8.2	1365	2	S14871	suppressor two of	625	52	8.1	263	2	E97774	hypothetical prote
553	53	8.2	1538	2	H70846	hypothetical glyci	626	52	8.1	273	2	G84130	ABC transporter (p
554	53	8.2	1617	2	T28153	complement C4 - ch	627	52	8.1	275	2	A36415	32K protein - vacc
555	53	8.2	1732	2	E71442	hypothetical prote	628	52	8.1	276	2	S64103	hypothetical prote
556	53	8.2	1980	2	S54307	myosin heavy chain	629	52	8.1	279	2	T70612	hypothetical prote
557	53	8.2	2120	2	T30243	alpha tectorin - c	630	52	8.1	309	2	AH0946	probable lipase ST
558	53	8.2	2240	2	T37057	probable multi-dom	631	52	8.1	311	2	A82361	integrase/recombin
559	53	8.2	2703	1	A24420	notch protein - fr	632	52	8.1	320	2	T36823	probable integral
560	53	8.2	2895	2	T08437	hyperplastic discs	633	52	8.1	323	2	T47574	embryonic abundant
561	53	8.2	2910	2	T42214	otogelin - mouse	634	52	8.1	348	2	T08327	hypothetical prote
562	53	8.2	3430	1	GNWTWV	genome polyprotein	635	52	8.1	353	2	E81680	conserved hypotet
563	53	8.2	3795	2	T00831	hypothetical prote	636	52	8.1	354	2	S27013	GTP-binding regula
564	52.5	8.2	91	2	A83527	probable acylphosp	637	52	8.1	358	2	T17619	hypothetical prote
565	52.5	8.2	122	2	AD1092	hypothetical prote	638	52	8.1	377	2	T37403	35K myristylprotei
566	52.5	8.2	147	2	G86884	50S ribosomal prot	639	52	8.1	377	2	F72165	A17L protein - var
567	52.5	8.2	173	2	D83486	cobinamide kinase	640	52	8.1	377	2	T28558	hypothetical prote
568	52.5	8.2	183	2	C85439	probable cytoskele	641	52	8.1	378	2	I42518	A16L protein - vac
569	52.5	8.2	207	2	G83538	probable oxidoredu	642	52	8.1	408	2	S58791	bone morphogenetic
570	52.5	8.2	211	2	S56602	Yjfv protein - Esc	643	52	8.1	436	2	A38145	invariant surface
571	52.5	8.2	225	1	JQ2040	nonstructural prot	644	52	8.1	440	2	T24232	hypothetical prote
572	52.5	8.2	250	2	C86429	hypothetical prote	645	52	8.1	445	2	T49556	epithelial zinc-fi
573	52.5	8.2	252	2	E69034	hypothetical prote	646	52	8.1	448	2	A41725	integrase - Saccha
574	52.5	8.2	277	2	G87775	protein C24Al1.9 l	647	52	8.1	452	2	S47633	RXR protein - Afri
575	52.5	8.2	309	2	C65217	allose kinase (EC	648	52	8.1	468	2	JN0016	peripherin interme
576	52.5	8.2	348	2	A56197	nuclear hormone re	649	52	8.1	496	2	T33496	hypothetical prote
577	52.5	8.2	353	2	AI0036	conserved hypotet	650	52	8.1	503	2	E83490	probable MFS trans
578	52.5	8.2	361	2	S71182	probable polygalac	651	52	8.1	507	2	S52348	hypothetical prote
579	52.5	8.2	361	2	T01398	hypothetical prote	652	52	8.1	517	2	B40583	heat shock transcr
580	52.5	8.2	364	2	AF2459	hypothetical prote	653	52	8.1	521	2	S12152	gag polyprotein -
581	52.5	8.2	365	2	A53277	MHC class I histoc	654	52	8.1	551	2	A30342	interleukin-2 rece
582	52.5	8.2	367	2	AH0675	hydrogenase (EC 1.	655	52	8.1	559	2	T26141	hypothetical prote
583	52.5	8.2	369	2	S13721	Wnt-1 protein prec	656	52	8.1	560	2	G02753	steroid hormone re
584	52.5	8.2	417	2	T49847	hypothetical prote	657	52	8.1	568	2	G27874	testis specific ba
585	52.5	8.2	453	2	B88040	protein lin-42 (lm	658	52	8.1	578	2	T51888	asparagine synthas
586	52.5	8.2	453	2	S05573	deoxyribodipyrimid	659	52	8.1	589	2	E97276	sulfite reductase
587	52.5	8.2	478	2	T34338	hypothetical prote	660	52	8.1	589	2	AD2594	hypothetical prote
588	52.5	8.2	578	2	T51230	telomere repeat-bi	661	52	8.1	591	2	I49656	Fanconi anemia gro
589	52.5	8.2	599	2	I51405	protein-tyrosine-p	662	52	8.1	600	2	C69899	conserved hypotet
590	52.5	8.2	666	2	D82386	methyl-accepting c	663	52	8.1	627	2	D84494	probable Tail-like
591	52.5	8.2	676	1	A39379	hatching-suppress	664	52	8.1	657	1	W1WL18	El protein - human
592	52.5	8.2	715	2	B71418	hypothetical prote	665	52	8.1	662	2	A45155	mucin FIM-C.1 - Af
593	52.5	8.2	762	2	C96653	hypothetical prote	666	52	8.1	664	2	S60062	hevin precursor -
594	52.5	8.2	769	2	A41029	integrin beta-8 ch	667	52	8.1	665	2	S70706	probable protein x
595	52.5	8.2	788	2	AB1991	hypothetical prote	668	52	8.1	682	2	T10319	envelope protein E
596	52.5	8.2	806	2	G95362	probable [imported	669	52	8.1	701	1	S33709	DHR39-short protei
597	52.5	8.2	927	2	T47827	squamosa promoter	670	52	8.1	709	2	AE3468	diguanylate cyclas
598	52.5	8.2	1008	2	T32986	hypothetical prote	671	52	8.1	738	2	S40992	hypothetical prote
599	52.5	8.2	1023	2	T13068	CLOCK protein - fr	672	52	8.1	808	1	S33708	nuclear steroid/th
600	52.5	8.2	1045	2	S23570	pol polyprotein ho	673	52	8.1	886	2	T16536	hypothetical prote
601	52.5	8.2	1133	2	S54496	probable membrane	674	52	8.1	903	2	T20804	hypothetical prote
602	52.5	8.2	1323	2	B88257	protein let-23 (lm	675	52	8.1	905	2	T23510	hypothetical prote
603	52.5	8.2	1374	2	S70712	protein-tyrosine k	676	52	8.1	910	2	S40930	hypothetical prote
604	52.5	8.2	1616	2	G70668	polyketide synthas	677	52	8.1	910	2	A10796	NADH2 dehydrogenas
605	52.5	8.2	1898	1	A45973	trichohyalin - hum	678	52	8.1	971	2	T24866	hypothetical prote
606	52.5	8.2	1951	2	B43963	RNA viral polymera	679	52	8.1	993	2	D96812	protein F3F9.12 [1
607	52.5	8.2	2150	2	S13553	hypothetical prote	680	52	8.1	1045	2	T16275	hypothetical prote
608	52.5	8.2	2427	2	T16613	hypothetical prote	681	52	8.1	1091	1	PL0009	complement C3d/Eps
609	52.5	8.2	2531	2	T18188	notch protein homo	682	52	8.1	1113	2	S30301	exon repair pr
610	52.5	8.2	3033	1	GNWJ08	genome polyprotein	683	52	8.1	1135	2	T42368	DNA-directed RNA p
611	52.5	8.2	3396	2	T22613	hypothetical prote	684	52	8.1	1464	2	S58984	development protei
612	52.5	8.2	3796	2	T18514	lysosomal traffick	685	52	8.1	1847	2	T18308	probable vitellog
613	52.5	8.2	3856	2	T51174	ataxia-telangiecta	686	52	8.1	2207	2	T24629	glutamate synthase

687	52	8.1	3075	2	S14458	laminin alpha-1 ch	760	51.5	8.0	772	2	H86016	hypothetical prote
688	52	8.1	3163	2	AB0233	yersiniabactin bio	761	51.5	8.0	793	2	S73662	probable lipoprote
689	52	8.1	3163	2	T17440	probable polyketid	762	51.5	8.0	808	2	S45764	probable oxidoredu
690	52	8.1	3635	2	T10053	laminin alpha 5 ch	763	51.5	8.0	810	1	S45907	myb-related protei
691	51.5	8.0	103	2	S33337	protamine P2 - pig	764	51.5	8.0	836	2	AF3233	conserved hypothet
692	51.5	8.0	108	2	H81098	hypothetical prote	765	51.5	8.0	848	2	E85087	hypothetical prote
693	51.5	8.0	117	2	S54126	hypothetical 14.3K	766	51.5	8.0	884	2	T18649	hypothetical prote
694	51.5	8.0	122	2	S53234	globulin-10 - maiz	767	51.5	8.0	909	1	QXLL2	LDL receptor 2 pre
695	51.5	8.0	134	2	AG3208	hypothetical prote	768	51.5	8.0	1019	2	S96519	probable disease r
696	51.5	8.0	144	2	F90217	LSU ribosomal prot	769	51.5	8.0	1039	2	T22982	hypothetical prote
697	51.5	8.0	151	2	S43296	bone morphogenetic	770	51.5	8.0	1133	1	EGRT	epidermal growth f
698	51.5	8.0	161	2	I37034	eosinophil-derived	771	51.5	8.0	1184	2	A39800	calcium-activated
699	51.5	8.0	161	2	I61897	eosinophil-derived	772	51.5	8.0	1187	2	C84568	hypothetical prote
700	51.5	8.0	161	2	A33922	eosinophil-derived	773	51.5	8.0	1192	2	H88293	protein F59B10.1 [
701	51.5	8.0	169	1	Q8ECA1	cell division inhi	774	51.5	8.0	1244	2	T49632	hypothetical prote
702	51.5	8.0	169	2	H85622	hypothetical prote	775	51.5	8.0	1259	2	T16038	hypothetical prote
703	51.5	8.0	169	2	B90759	suppressor of lon	776	51.5	8.0	1416	2	E88550	protein ZC84.1 [im
704	51.5	8.0	170	2	T15991	hypothetical prote	777	51.5	8.0	1436	2	B1704	conserved hypothet
705	51.5	8.0	174	2	T08702	hypothetical prote	778	51.5	8.0	1454	2	S53398	hypothetical prote
706	51.5	8.0	177	2	E90971	probable endolysin	779	51.5	8.0	1476	2	A45773	kelch protein, lon
707	51.5	8.0	177	2	E85744	probable lysozyme	780	51.5	8.0	1560	2	T00080	hypothetical prote
708	51.5	8.0	188	2	T21208	hypothetical prote	781	51.5	8.0	1657	2	T19536	hypothetical prote
709	51.5	8.0	203	2	T49324	hypothetical prote	782	51.5	8.0	1693	2	T30867	Rho-guanine nucleo
710	51.5	8.0	208	2	T34626	probable polypeptid	783	51.5	8.0	1706	2	I84499	zinc finger protei
711	51.5	8.0	210	2	T05541	heat shock protein	784	51.5	8.0	1712	2	A38261	masking protein pr
712	51.5	8.0	217	2	S01358	salivary glue prot	785	51.5	8.0	2019	1	JQ1322	tenascin precursor
713	51.5	8.0	247	2	H86145	F22U4.7 protein -	786	51.5	8.0	2124	2	H83357	probable non-ribos
714	51.5	8.0	263	1	HLMSBK	H-2 class II histo	787	51.5	8.0	2844	2	S28291	hypothetical prote
715	51.5	8.0	280	2	A10190	probable hydrolase	788	51.5	8.0	3033	1	JQ1303	genome polyprotein
716	51.5	8.0	314	2	I37383	FAS soluble protei	789	51.5	8.0	3672	2	T23433	hypothetical prote
717	51.5	8.0	317	2	T24468	hypothetical prote	790	51.5	8.0	3704	2	T37316	probable laminin a
718	51.5	8.0	326	2	C95937	hypothetical expor	791	51.5	8.0	3712	2	S18253	laminin alpha-1 ch
719	51.5	8.0	335	2	A40036	hypothetical mediat	792	51.5	8.0	4845	2	T31067	BIR repeat contain
720	51.5	8.0	335	2	A53434	cell surface glyco	793	51	7.9	62	2	B58213	protamine I - Amer
721	51.5	8.0	338	2	C75607	conserved hypothet	794	51	7.9	73	2	AG1852	hypothetical prote
722	51.5	8.0	347	2	F90904	hypothetical prote	795	51	7.9	99	2	F90262	hypothetical prote
723	51.5	8.0	347	2	G85712	unknown protein en	796	51	7.9	106	2	D31201	hypothetical prote
724	51.5	8.0	360	2	JC6322	methyltransferase	797	51	7.9	115	2	S64490	hypothetical prote
725	51.5	8.0	361	1	F65012	hypothetical prote	798	51	7.9	128	1	TGHU	beta-thromboglobul
726	51.5	8.0	361	2	A91037	probable peptidase	799	51	7.9	134	2	B46178	probable transcrip
727	51.5	8.0	361	2	C85881	probable peptidase	800	51	7.9	139	2	S06550	finger protein (cl
728	51.5	8.0	367	2	F95159	prephenate dehydro	801	51	7.9	141	2	F71070	hypothetical prote
729	51.5	8.0	367	2	F98025	prephenate dehydro	802	51	7.9	142	2	JT0573	retinoic acid-indu
730	51.5	8.0	373	2	A5718	interleukin-2 rece	803	51	7.9	149	1	NRMS	pancreatic ribonuc
731	51.5	8.0	377	2	T32798	hypothetical prote	804	51	7.9	177	2	E75026	hypothetical prote
732	51.5	8.0	382	2	AG0188	histidinol-phospha	805	51	7.9	184	2	E87506	hypothetical prote
733	51.5	8.0	387	2	A86302	hypothetical prote	806	51	7.9	193	2	S26597	protein F3M18.20 [
734	51.5	8.0	391	2	T25211	hypothetical prote	807	51	7.9	204	2	B86410	hydroxyacylglutath
735	51.5	8.0	395	2	C88955	protein K04F1.10 [808	51	7.9	210	2	T36893	hypothetical prote
736	51.5	8.0	400	2	T46383	hypothetical prote	809	51	7.9	218	2	B33314	hypothetical prote
737	51.5	8.0	404	2	T50335	mating pheromone r	810	51	7.9	224	2	B81783	hypothetical prote
738	51.5	8.0	413	2	S59650	hypothetical prote	811	51	7.9	230	2	T30153	hypothetical prote
739	51.5	8.0	434	2	T11967	nodule-specific hy	812	51	7.9	236	2	T36446	hypothetical prote
740	51.5	8.0	443	2	T21499	hypothetical prote	813	51	7.9	241	2	F69165	ribosomal protein
741	51.5	8.0	454	2	T02593	hypothetical prote	814	51	7.9	247	1	JC6540	placenta specific-
742	51.5	8.0	471	2	G81156	transporter, Nadc	815	51	7.9	257	2	AH1072	conserved hypothet
743	51.5	8.0	471	2	A81948	probable transmemb	816	51	7.9	282	2	H89815	hypothetical prote
744	51.5	8.0	476	2	E97631	probable membrane	817	51	7.9	303	2	S41156	wingless protein -
745	51.5	8.0	476	2	S68965	legumin precursor	818	51	7.9	317	2	C38178	Te1B protein - pla
746	51.5	8.0	479	2	T40683	cell cycle protein	819	51	7.9	339	2	B34895	transcription fact
747	51.5	8.0	507	2	S56143	cell cycle protein	820	51	7.9	346	2	T11076	NADH2 dehydrogenas
748	51.5	8.0	519	1	F0UJG4	gag polyprotein -	821	51	7.9	377	2	H36849	Al61 protein - var
749	51.5	8.0	538	2	E96492	hypothetical prote	822	51	7.9	378	2	JH0134	creatinase [EC 3.5
750	51.5	8.0	556	1	S24395	protein-tyrosine-p	823	51	7.9	385	2	H89046	protein C10G8.8 [l
751	51.5	8.0	605	2	S06398	alpha-globulin typ	824	51	7.9	410	2	A44391	serum response ele
752	51.5	8.0	605	2	T74882	hypothetical prote	825	51	7.9	417	2	F90916	probable transport
753	51.5	8.0	610	2	G86407	hypothetical prote	826	51	7.9	417	2	F64915	membrane protein y
754	51.5	8.0	613	2	G82338	conserved hypothet	827	51	7.9	417	2	C85765	probable transport
755	51.5	8.0	620	2	T23522	hypothetical prote	828	51	7.9	418	2	S58776	failed axon connec
756	51.5	8.0	641	2	T17278	hypothetical prote	829	51	7.9	420	2	T14911	bZIP DNA-binding p
757	51.5	8.0	684	2	T40319	hypothetical prote	830	51	7.9	427	2	A32372	female-specific do
758	51.5	8.0	696	2	AB1566	hypothetical prote	831	51	7.9	434	2	F69081	sensory transducti
759	51.5	8.0	749	2	H91170	hypothetical membr	832	51	7.9	439	2	T31734	hypothetical prote

833	7.9	442	2	AF2539	manganese transpor	906	50.5	7.8	227	2	T11172	H+-transporting tw
834	7.9	446	2	E69899	L-amino acid oxida	907	50.5	7.8	227	2	PH1215	ig epsilon chain C
835	7.9	455	2	A36471	transcription fact	908	50.5	7.8	239	2	S65825	hypothetical prote
836	7.9	456	2	C82785	hypothetical prote	909	50.5	7.8	240	2	A39842	insulin-like growt
837	7.9	459	2	G71431	hypothetical prote	910	50.5	7.8	242	1	F75433	probable phosphoe
838	7.9	462	2	T40420	probable acid phos	911	50.5	7.8	243	2	G82163	leucyl/phenylalan
839	7.9	465	2	S23502	hepatocyte nuclea	912	50.5	7.8	246	2	D82078	conserved hypotet
840	7.9	469	2	F82085	glutamate synthase	913	50.5	7.8	250	1	A49053	CD27 antigen precu
841	7.9	489	2	F82985	conserved hypotet	914	50.5	7.8	256	2	JC4627	fibroblast growth
842	7.9	500	2	G01646	fusca protein homo	915	50.5	7.8	260	2	E71975	hypothetical prote
843	7.9	506	1	F0LJG3	gag polyprotein -	916	50.5	7.8	269	2	F71323	conserved hypotet
844	7.9	507	2	T11559	gag protein - simi	917	50.5	7.8	272	2	D83154	probable permease
845	7.9	507	2	S04237	gag polyprotein -	918	50.5	7.8	287	1	A28168	arylamine N-acetyl
846	7.9	521	1	F0LJCA	gag polyprotein -	919	50.5	7.8	324	2	S07735	probable malate de
847	7.9	521	1	S53091	gag polyprotein -	920	50.5	7.8	326	2	S09773	hypothetical prote
848	7.9	522	1	F0LJGG	gag polyprotein -	921	50.5	7.8	327	2	B84781	hypothetical prote
849	7.9	524	2	S38539	disintegrin-like m	922	50.5	7.8	339	2	S37920	MAR1 protein precu
850	7.9	532	2	S51130	dimethylalaniline m	923	50.5	7.8	352	2	JCS388	replication initia
851	7.9	549	2	B32372	male-specific doub	924	50.5	7.8	355	2	T50479	G protein alpha ch
852	7.9	560	2	A83155	probable medium-ch	925	50.5	7.8	360	2	A53611	interleukin-8 rece
853	7.9	561	2	T23722	hypothetical prote	926	50.5	7.8	368	1	W2WL6	E2 protein - human
854	7.9	573	1	HMM860	chaperonin groEL p	927	50.5	7.8	372	2	T47344	hypothetical prote
855	7.9	573	1	HHR760	chaperonin groEL p	928	50.5	7.8	373	2	S41452	glutamate-ammonia
856	7.9	573	2	A34173	mitochondrial prot	929	50.5	7.8	376	2	A49801	OGG1 protein - yea
857	7.9	582	2	I48673	matrix metalloprot	930	50.5	7.8	376	2	A48060	erythroid kruppel-
858	7.9	587	2	F83336	inner membrane cop	931	50.5	7.8	389	2	E49905	protein secretion
859	7.9	592	2	T13742	hypothetical prote	932	50.5	7.8	390	2	S73459	heat shock protein
860	7.9	616	2	T11850	DNA primase (EC 2.	933	50.5	7.8	409	2	D83326	probable acyl-CoA
861	7.9	647	2	S36575	E1 protein - human	934	50.5	7.8	423	2	T20857	hypothetical prote
862	7.9	670	2	I65967	disintegrin-like m	935	50.5	7.8	427	2	AC0203	chemotaxis MotB pr
863	7.9	696	2	T02832	long chain fatty a	936	50.5	7.8	434	2	S51644	secreted/adhesive
864	7.9	749	2	T10229	hypothetical prote	937	50.5	7.8	438	2	C86244	DnaJ homolog, 4706
865	7.9	768	2	T37601	probable transcript	938	50.5	7.8	444	2	T13155	linoleoyl-CoA desa
866	7.9	775	2	I49237	Azo protein - mous	939	50.5	7.8	467	2	A57627	p55 erythrocyte me
867	7.9	778	2	AG0906	aerobic respiratio	940	50.5	7.8	474	2	T20108	hypothetical prote
868	7.9	778	2	T43223	hypothetical prote	941	50.5	7.8	477	2	S33403	hypothetical prote
869	7.9	782	2	T45221	DNA damage checkp	942	50.5	7.8	480	2	S52306	zinc finger protei
870	7.9	788	1	S28302	ribonucleoside-dip	943	50.5	7.8	488	2	B75551	glutamate synthase
871	7.9	813	2	T04313	protein kinase Xa2	944	50.5	7.8	522	1	I37037	involucrin - commo
872	7.9	825	2	I46078	endothelin convert	945	50.5	7.8	531	2	B54096	flavin-containing
873	7.9	841	2	C87331	ISCC2, transposase	946	50.5	7.8	538	2	T50606	hypothetical prote
874	7.9	844	2	T52396	formin-binding pro	947	50.5	7.8	565	2	F70192	hypothetical prote
875	7.9	870	2	B82732	glycerol-3-phospha	948	50.5	7.8	565	2	D64058	outer membrane pro
876	7.9	884	1	IJMSCE	E-cadherin precurs	949	50.5	7.8	583	2	G84829	probable PRR2 fami
877	7.9	884	2	S34438	uvomorulin - mous	950	50.5	7.8	596	2	JC4299	orphan nuclear rec
878	7.9	899	2	B48586	suppressor of hair	951	50.5	7.8	596	2	I80177	TR4 orphan recepto
879	7.9	953	2	F96498	hypothetical prote	952	50.5	7.8	596	2	A57031	nuclear receptor T
880	7.9	961	2	H84787	probable receptor-	953	50.5	7.8	607	2	A47757	retrovirus-related
881	7.9	991	2	T25412	hypothetical prote	954	50.5	7.8	615	2	I59309	TR4 orphan recepto
882	7.9	998	1	QOBBB1	E1 protein - black	955	50.5	7.8	627	2	G86156	T14P4.5 protein -
883	7.9	998	2	S41397	protein A - flock	956	50.5	7.8	629	2	I54075	gene mTR2R1 protei
884	7.9	1106	2	T44598	hypothetical prote	957	50.5	7.8	639	2	S36551	E1 protein - human
885	7.9	1106	2	T13938	gene shuttle craft	958	50.5	7.8	686	2	T15795	hypothetical prote
886	7.9	1355	2	T00075	hypothetical prote	959	50.5	7.8	718	2	S06068	myeloperoxidase (E
887	7.9	1557	2	T13160	protein CNK - frui	960	50.5	7.8	726	2	S74514	hypothetical prote
888	7.9	1584	2	T22674	hypothetical prote	961	50.5	7.8	746	2	T28004	hypothetical prote
889	7.9	1588	2	T38660	probable transcrip	962	50.5	7.8	770	2	T01527	hypothetical prote
890	7.9	1722	2	E89753	protein Flic7.4 [1	963	50.5	7.8	779	2	D84866	hypothetical prote
891	7.9	2157	1	GNNY1B	genome polyprotein	964	50.5	7.8	800	2	D86712	glycogen phosphory
892	7.9	2224	1	KFHU5	coagulation factor	965	50.5	7.8	808	2	E64914	dimethylsulfoxide
893	7.9	2321	2	S78549	notch3 protein - h	966	50.5	7.8	808	2	E90915	probable oxidoredu
894	7.9	2452	1	RN202L	DNA-directed RNA p	967	50.5	7.8	808	2	B85764	probable oxidoredu
895	7.9	3014	1	JCS620	genome polyprotein	968	50.5	7.8	813	2	JCS785	ATP-dependent RNA
896	50.5	7.8	82	T10329	hypothetical prote	969	50.5	7.8	849	1	T09349	S-receptor kinase
897	50.5	7.8	113	B39437	exopolysaccharide	970	50.5	7.8	853	2	H70939	probable nirB prot
898	50.5	7.8	147	T30616	hypothetical prote	971	50.5	7.8	864	2	S61148	SBE2 protein - yea
899	50.5	7.8	160	I84444	eosinophil-derived	972	50.5	7.8	876	2	PC2219	polypeptide - hepa
900	50.5	7.8	174	A49181	alpha B-crystallin	973	50.5	7.8	880	2	T02245	hypothetical prote
901	50.5	7.8	184	A61196	genome polyprotein	974	50.5	7.8	893	2	T15183	hypothetical prote
902	50.5	7.8	194	A54317	probable nonstruct	975	50.5	7.8	909	1	QRXLL1	LDL receptor 1 pre
903	50.5	7.8	226	C25973	pertussis toxin ch	976	50.5	7.8	946	2	S28061	SCPI protein - rat
904	50.5	7.8	226	E95975	galactosyltransfer	977	50.5	7.8	955	2	E84845	probable villin 2
905	50.5	7.8	227	F90616	ATP synthase FO ch	978	50.5	7.8	956	2	A89153	protein C24B5.3 [1

979	50.5	7.8	963	2	T19140	hypothetical prote	1052	50	7.8	342	2	I47175	Ig alpha chain C r
980	50.5	7.8	976	2	T50669	villin 2 (imported	1033	50	7.8	354	2	JC7662	G protein alpha su
981	50.5	7.8	981	2	A12017	peptide synthetase	1034	50	7.8	361	2	JC7662	conserved hypothet
982	50.5	7.8	997	2	T01372	hypothetical prote	1055	50	7.8	363	2	JC5536	C-Fringe protein 1
983	50.5	7.8	993	2	S49461	synaptonemal compl	1056	50	7.8	363	2	A48338	hypothetical prote
984	50.5	7.8	1015	2	T13062	CLOCK protein - fr	1057	50	7.8	367	2	H83202	poly(beta-d-mannur
985	50.5	7.8	1027	2	T13071	CLOCK protein - fr	1058	50	7.8	368	2	JN0777	poly(beta-D-mannur
986	50.5	7.8	1047	1	OYHUBR	natruietic peptid	1059	50	7.8	371	2	S46335	env polyprotein -
987	50.5	7.8	1047	2	I45882	guanylate cyclase	1060	50	7.8	376	2	AD1621	heat shock protein
988	50.5	7.8	1077	2	T41146	probable cysteine-	1061	50	7.8	377	2	T43739	heat shock protein
989	50.5	7.8	1164	2	AC2136	multifunctional pe	1062	50	7.8	377	2	AH1258	heat shock protein
990	50.5	7.8	1167	2	T34020	zinc finger protei	1063	50	7.8	390	2	T48524	lysophospholipase-
991	50.5	7.8	1178	2	S78475	mannosylphosphoryl	1064	50	7.8	403	2	B88633	protein F56B3.9 [i
992	50.5	7.8	1182	2	G71607	probable integral	1065	50	7.8	411	2	A55610	corticotropin-rele
993	50.5	7.8	1236	1	VHWWE	structural polypro	1066	50	7.8	415	2	T35773	translation elonga
994	50.5	7.8	1292	2	T09229	galactose binding	1067	50	7.8	421	2	A35205	citrate synthase-1
995	50.5	7.8	1404	2	T13420	probable carboxype	1068	50	7.8	433	2	T31639	hypothetical prote
996	50.5	7.8	1406	2	T13421	probable carboxype	1069	50	7.8	440	2	JC4530	peroxisome prolif
997	50.5	7.8	1465	2	T23056	chromodomain helic	1070	50	7.8	451	2	A70539	hypothetical prote
998	50.5	7.8	1735	2	S54784	sex-limited protei	1071	50	7.8	454	2	T27249	hypothetical prote
999	50.5	7.8	1736	2	A29176	sex-limited protei	1072	50	7.8	463	2	C47301	virB6 homolog - Bo
1000	50.5	7.8	2180	2	T29764	hypothetical prote	1073	50	7.8	465	2	H86352	protein F2E2.2 [im
1001	50.5	7.8	2248	2	A35938	profilaggrin - hum	1074	50	7.8	474	2	T13575	hypothetical prote
1002	50.5	7.8	2453	2	S60254	nuclear receptor c	1075	50	7.8	480	2	T46925	hypothetical prote
1003	50.5	7.8	2870	2	H95974	cyclic beta 1-2 gl	1076	50	7.8	481	2	JC5378	protein disulfide-
1004	50.5	7.8	3010	1	A45573	genome polyprotein	1077	50	7.8	491	2	T01856	hypothetical prote
1005	50.5	7.8	3010	1	GNWVCJ	genome polyprotein	1078	50	7.8	500	2	A82127	two-component sens
1006	50.5	7.8	3010	1	GNWVCJ	genome polyprotein	1079	50	7.8	517	2	D84512	hypothetical prote
1007	50.5	7.8	3106	1	S53868	laminin alpha-2 ch	1080	50	7.8	521	1	FOLJST	gag polyprotein -
1008	50.5	7.8	4543	1	A53102	alpha-2-macroglobu	1081	50	7.8	521	2	S08435	gag polyprotein -
1009	50	7.8	56	2	I37964	zinc finger protei	1082	50	7.8	522	1	FOLJG2	gag polyprotein -
1010	50	7.8	103	2	PH1045	Ig light chain V r	1083	50	7.8	524	2	G84595	hypothetical prote
1011	50	7.8	105	2	T19159	hypothetical prote	1084	50	7.8	526	2	T20086	hypothetical prote
1012	50	7.8	116	2	B90822	probable head-tail	1085	50	7.8	561	2	T27318	hypothetical prote
1013	50	7.8	116	2	H85843	unknown protein en	1086	50	7.8	573	1	A32800	chaperonin GroEL p
1014	50	7.8	120	2	A97655	hypothetical prote	1087	50	7.8	578	2	T40984	transcription fact
1015	50	7.8	120	2	AG2878	conserved hypothet	1088	50	7.8	586	1	VCLJMP	env polyprotein -
1016	50	7.8	154	2	JQ2228	trans-activating p	1089	50	7.8	592	2	G89159	sensory transducti
1017	50	7.8	160	2	I37033	eosinophil cationi	1090	50	7.8	616	2	JQ1441	hypothetical 67K p
1018	50	7.8	169	2	T34520	hypothetical prote	1091	50	7.8	626	2	T27319	hypothetical prote
1019	50	7.8	185	2	JN0766	adrenomedullin pre	1092	50	7.8	630	2	H89056	protein K09H11.4 [
1020	50	7.8	186	2	T32656	hypothetical prote	1093	50	7.8	643	2	S36499	E1 protein - human
1021	50	7.8	189	2	E69743	hypothetical prote	1094	50	7.8	680	2	T25832	hypothetical prote
1022	50	7.8	190	2	AD2232	hypothetical prote	1095	50	7.8	680	2	T27078	hypothetical prote
1023	50	7.8	192	2	F70359	hypothetical prote	1096	50	7.8	682	2	S71476	homeotic protein H
1024	50	7.8	200	2	I51551	platelet-derived g	1097	50	7.8	686	2	AB2362	ribonuclease II [i
1025	50	7.8	215	2	S09220	platelet-derived g	1098	50	7.8	697	2	T03722	EXO70 protein - mo
1026	50	7.8	226	2	I51550	platelet-derived g	1099	50	7.8	705	2	S76729	hypothetical prote
1027	50	7.8	232	2	A60083	neural induction h	1100	50	7.8	748	2	S66129	disintegrin [EC 3.
1028	50	7.8	241	2	C97305	D-alanyl-D-alanine	1101	50	7.8	764	1	BBHU	complement factor
1029	50	7.8	251	2	T25820	hypothetical prote	1102	50	7.8	769	2	E56613	hypothetical prote
1030	50	7.8	254	2	AB0763	thiosulfate reduct	1103	50	7.8	772	2	JC4636	transcription elon
1031	50	7.8	254	2	C57143	thiosulfate-dithio	1104	50	7.8	807	2	T32463	hypothetical prote
1032	50	7.8	255	2	G64320	hypothetical prote	1105	50	7.8	816	2	C88196	protein ZK1127.7 [
1033	50	7.8	256	2	T24711	hypothetical prote	1106	50	7.8	820	2	G82168	trimethylamine-N-o
1034	50	7.8	264	2	T22054	hypothetical prote	1107	50	7.8	827	2	H83217	probable transcrip
1035	50	7.8	266	2	H83008	N-formylglutamate	1108	50	7.8	828	2	E81651	conserved hypothet
1036	50	7.8	271	2	F83081	hypothetical prote	1109	50	7.8	860	2	T27084	hypothetical prote
1037	50	7.8	278	2	D84492	hypothetical prote	1110	50	7.8	975	2	I48974	receptor-protein t
1038	50	7.8	282	2	T18608	hypothetical prote	1111	50	7.8	977	2	S49004	tyrosine kinase Mp
1039	50	7.8	286	2	T42610	probable immediate	1112	50	7.8	1020	2	H96793	unknown protein F1
1040	50	7.8	292	2	T28817	hypothetical prote	1113	50	7.8	1058	2	T30580	p-type ATPase - sl
1041	50	7.8	293	2	B26637	neurogenic repetit	1114	50	7.8	1110	2	T19673	hypothetical prote
1042	50	7.8	297	2	E84788	hypothetical prote	1115	50	7.8	1146	2	B35962	protein-tyrosine k
1043	50	7.8	308	2	S22930	ubiquinol-cytochr	1116	50	7.8	1182	2	A35962	protein-tyrosine k
1044	50	7.8	314	1	A35268	modulation protei	1117	50	7.8	1254	2	I48161	p-185 precursor -
1045	50	7.8	316	2	E81321	probable cation tr	1118	50	7.8	1284	2	T40879	probable helicase
1046	50	7.8	316	2	G65513	hypothetical prote	1119	50	7.8	1378	2	T47605	RING finger-like p
1047	50	7.8	318	2	AG0099	general secretion	1120	50	7.8	1462	2	S75142	sensory transducti
1048	50	7.8	325	2	E96620	protein T30E16.27	1121	50	7.8	1549	1	A40691	trichosyalin - she
1049	50	7.8	326	2	AB3100	hypothetical prote	1122	50	7.8	1615	2	JC6510	ras-responsive ele
1050	50	7.8	326	2	H98186	probable mikimopin	1123	50	7.8	1648	2	F94833	probable SNF2/SNF2
1051	50	7.8	341	2	B87011	conserved hypothet	1124	50	7.8	1813	2	T30564	resistance protein

1125	7.8	50	2139	2	A35672	crumbs protein - f	1198	49.5	7.7	407	2	T14909	bZIP DNA-binding p
1126	7.8	50	2182	2	T14320	calcineurin inhibi	1199	49.5	7.7	408	2	JC4938	hepatocyte nuclear
1127	7.8	50	2629	2	T32735	telomerase-associ	1200	49.5	7.7	409	2	S24460	probable membrane
1128	7.8	50	2871	2	A55567	fibrillin 1 - bovi	1201	49.5	7.7	410	2	S77844	alanine-tRNA ligas
1129	7.8	50	2907	2	A47271	fibrillin-1 precu	1202	49.5	7.7	419	2	D82067	UDP-N-acetylglucos
1130	7.8	50	3002	2	A57228	fibrillin 1 precu	1203	49.5	7.7	420	2	S71199	dnag protein homol
1131	49.5	7.7	50	2	T07556	hypothetical prote	1204	49.5	7.7	420	2	T49127	deltat6 fatty acid
1132	49.5	7.7	108	2	A83406	hypothetical prote	1205	49.5	7.7	444	2	JG0180	F5D14.3 protein -
1133	49.5	7.7	117	1	B59316	ghrelin precursor	1206	49.5	7.7	445	2	C86447	hepatocyte nuclear
1134	49.5	7.7	131	2	P64154	hypothetical prote	1207	49.5	7.7	465	2	JC4937	hepatocyte nuclear
1135	49.5	7.7	140	2	D72680	hypothetical prote	1208	49.5	7.7	465	2	S52074	BGR alpha transcri
1136	49.5	7.7	148	2	S09979	ferredoxin [2Fe-2S	1209	49.5	7.7	469	2	A57531	F22D16.15 protein
1137	49.5	7.7	150	2	A84488	hypothetical prote	1210	49.5	7.7	497	2	G86158	Hepaticocyte nuclear
1138	49.5	7.7	156	2	T02166	cysteine proteinas	1211	49.5	7.7	504	2	JC6096	Hepaticocyte nuclear
1139	49.5	7.7	161	1	S76604	hydrogenase-2 comp	1212	49.5	7.7	510	2	A53802	hypothetical prote
1140	49.5	7.7	162	2	A10884	Fur family protein	1213	49.5	7.7	511	2	D70507	IS3 family transpo
1141	49.5	7.7	163	2	D87293	cell division inhi	1214	49.5	7.7	512	2	AC3203	IS3 family transpo
1142	49.5	7.7	169	2	C29016	alpha-amylase inhi	1215	49.5	7.7	512	2	AD2835	IS3 family transpo
1143	49.5	7.7	171	2	S78525	hypothetical prote	1216	49.5	7.7	512	2	AD3049	probable transposa
1144	49.5	7.7	171	2	A99190	conserved hypotet	1217	49.5	7.7	512	2	G97612	probable transposa
1145	49.5	7.7	171	2	AH3096	hypothetical prote	1218	49.5	7.7	512	2	G98236	probable copper-bi
1146	49.5	7.7	173	2	A95864	hypothetical prote	1219	49.5	7.7	516	2	C64735	DNA repair protein
1147	49.5	7.7	174	2	S58758	alpha-crystallin c	1220	49.5	7.7	534	2	G82272	hypothetical prote
1148	49.5	7.7	174	2	S47069	finger protein HZF	1221	49.5	7.7	555	2	H96762	ENL (translocation
1149	49.5	7.7	187	1	Y0ECKS	KS71A fibrial pro	1222	49.5	7.7	559	2	B44265	outer membrane pro
1150	49.5	7.7	187	2	C43597	pilin type F7-1 pr	1223	49.5	7.7	565	2	B57148	netrin-2 precursor
1151	49.5	7.7	191	2	AE2559	hypothetical prote	1224	49.5	7.7	581	2	B54665	hypothetical prote
1152	49.5	7.7	193	2	AF1823	hypothetical prote	1225	49.5	7.7	583	2	T17326	protein F40E10.4 l
1153	49.5	7.7	207	1	A64915	ycdy protein homol	1226	49.5	7.7	601	2	D89711	hypothetical prote
1154	49.5	7.7	207	2	F85764	probable oxidoredu	1227	49.5	7.7	612	2	T22025	hypothetical prote
1155	49.5	7.7	207	2	A90916	probable oxidoredu	1228	49.5	7.7	612	2	T18848	hypothetical prote
1156	49.5	7.7	207	2	T50206	hypothetical zinc	1229	49.5	7.7	616	2	A95012	hypothetical prote
1157	49.5	7.7	209	2	B42687	neurotrophin-4 pre	1230	49.5	7.7	616	2	D97883	hypothetical prote
1158	49.5	7.7	212	2	A82128	thymidylate kinase	1231	49.5	7.7	665	2	A12733	NADH ubiquinone ox
1159	49.5	7.7	219	1	A39574	leukocyte antigen	1232	49.5	7.7	665	2	C97515	NADH-ubiquinone ox
1160	49.5	7.7	221	2	S65476	ras-homolog GTPase	1233	49.5	7.7	673	2	T40817	zinc finger protei
1161	49.5	7.7	233	2	B84237	hypothetical prote	1234	49.5	7.7	681	2	S36534	B1 protein - human
1162	49.5	7.7	236	2	F84586	hypothetical prote	1235	49.5	7.7	694	2	T01134	probable protein k
1163	49.5	7.7	241	1	HLMSTR	class I-related se	1236	49.5	7.7	730	2	T05345	hypothetical prote
1164	49.5	7.7	244	1	LNRTMC	mannose-binding le	1237	49.5	7.7	732	2	A35505	primosomal replica
1165	49.5	7.7	246	2	T28166	hypothetical prote	1238	49.5	7.7	744	2	T13429	hypothetical prote
1166	49.5	7.7	257	2	F75084	hypothetical prote	1239	49.5	7.7	749	2	T34090	hypothetical prote
1167	49.5	7.7	266	2	T15066	hypothetical prote	1240	49.5	7.7	758	2	E84933	5-methyltetrahydro
1168	49.5	7.7	268	2	T10304	inhibitor of apopt	1241	49.5	7.7	765	2	T15447	hypothetical prote
1169	49.5	7.7	268	2	A53989	apoptosis-inhibiti	1242	49.5	7.7	773	2	A83888	hypothetical prote
1170	49.5	7.7	269	2	T64151	hypothetical prote	1243	49.5	7.7	777	2	L48100	ADAM 5 protein pre
1171	49.5	7.7	280	2	T19363	hypothetical prote	1244	49.5	7.7	796	2	S57844	lethal(3)malignant
1172	49.5	7.7	287	2	A11072	conserved hypotet	1245	49.5	7.7	805	2	T34212	hypothetical prote
1173	49.5	7.7	294	2	G90032	hypothetical prote	1246	49.5	7.7	812	2	B97401	uridylyltransferas
1174	49.5	7.7	299	2	T15240	hypothetical prote	1247	49.5	7.7	827	2	A69793	conserved hypotet
1175	49.5	7.7	304	2	D83104	hypothetical prote	1248	49.5	7.7	862	2	E84567	probable carnitine
1176	49.5	7.7	306	2	E83197	transcription regu	1249	49.5	7.7	864	2	T49574	probable carnitine
1177	49.5	7.7	317	2	T13935	hypothetical prote	1250	49.5	7.7	880	2	AE0179	probable ATPase ch
1178	49.5	7.7	321	1	F87102	probable phosphoes	1251	49.5	7.7	882	2	AB0119	Clp ATPase [import
1179	49.5	7.7	322	2	A21125	MHC class I histoc	1252	49.5	7.7	915	2	A49874	metabotropic gluta
1180	49.5	7.7	325	2	S20045	MHC class I histoc	1253	49.5	7.7	942	2	AB2619	hypothetical prote
1181	49.5	7.7	326	2	T33343	hypothetical prote	1254	49.5	7.7	952	2	T18837	hypothetical prote
1182	49.5	7.7	343	2	T01475	env polyprotein -	1255	49.5	7.7	964	2	T52186	phosphoenolpyruvat
1183	49.5	7.7	375	2	A46345	B2 protein - human	1256	49.5	7.7	968	2	T52186	phosphoenolpyruvat
1184	49.5	7.7	376	2	S36535	hypothetical prote	1257	49.5	7.7	991	2	I49540	procollagen C-endo
1185	49.5	7.7	383	2	T30730	hypothetical prote	1258	49.5	7.7	1028	2	B24785	hypothetical prote
1186	49.5	7.7	383	2	T21946	hypothetical prote	1259	49.5	7.7	1141	2	T29104	Tbc1 protein - mou
1187	49.5	7.7	384	2	A46403	transcription fact	1260	49.5	7.7	1221	2	E83327	conserved hypotet
1188	49.5	7.7	387	2	D82134	benzoate transport	1261	49.5	7.7	1271	2	S37958	myosin heavy chain
1189	49.5	7.7	387	2	E82777	phage-related inte	1262	49.5	7.7	1311	2	C84528	hypothetical prote
1190	49.5	7.7	394	2	D65167	probable membrane	1263	49.5	7.7	1334	2	E86451	probable copia-typ
1191	49.5	7.7	397	2	AC3521	replication protei	1264	49.5	7.7	1372	2	T25933	hypothetical prote
1192	49.5	7.7	398	2	T26284	hypothetical prote	1265	49.5	7.7	1427	2	T39219	atp-binding casset
1193	49.5	7.7	399	2	AD2917	conserved hypotet	1266	49.5	7.7	1472	2	A26122	alpha-2-macroglobu
1194	49.5	7.7	399	2	G97691	hypothetical prote	1267	49.5	7.7	1490	2	F88311	protein T0608.10 l
1195	49.5	7.7	400	2	A92866	MFS permease [drug	1268	49.5	7.7	1490	2	T24502	hypothetical prote
1196	49.5	7.7	400	2	D97643	probable efflux pr	1269	49.5	7.7	1545	2	T14288	DNA (cytosine-5-) -
1197	49.5	7.7	406	2	F86454	CDS protein F9L11.	1270	49.5	7.7	1677	2	T18344	P-glycoprotein E -

1271	49.5	7.7	2150	2	S71629	sensory transducti	1344	49	7.6	410	2	H97597	hypothetical prote
1272	49.5	7.7	2210	1	RRXPLC	genome polyprotein	1345	49	7.6	430	2	S66671	neuron-derived rec
1273	49.5	7.7	2257	2	T18492	hypothetical prote	1346	49	7.6	431	2	I49149	CRP receptor - mou
1274	49.5	7.7	2895	2	H85362	hypothetical prote	1347	49	7.6	431	2	C86178	hypothetical prote
1275	49.5	7.7	3133	2	S52093	hemocytin - silkw	1348	49	7.6	433	2	T31511	hypothetical prote
1276	49.5	7.7	4544	1	S02392	alpha-2-macroglob	1349	49	7.6	434	2	A43252	probable transcrip
1277	49	7.6	69	2	S17518	opa protein - frui	1350	49	7.6	434	2	T01390	hypothetical prote
1278	49	7.6	87	2	S00180	spermatid protein	1351	49	7.6	437	1	A48051	translation releas
1279	49	7.6	94	2	S32939	AUA1 protein - yea	1352	49	7.6	437	1	S50853	probable transport
1280	49	7.6	95	2	S72980	hypothetical prote	1353	49	7.6	438	2	A83544	glutaconate CoA-tr
1281	49	7.6	96	2	AE1822	transcription regu	1354	49	7.6	447	2	F69399	probable CoA-tr
1282	49	7.6	101	2	D56272	probable pheromone	1355	49	7.6	459	2	A22842	finger protein esc
1283	49	7.6	102	2	A72507	hypothetical prote	1356	49	7.6	470	2	S33639	amino acid transpo
1284	49	7.6	105	1	JN0483	ribosomal protein	1357	49	7.6	472	2	JC7626	6-oxohexanoate deh
1285	49	7.6	105	2	G97825	30S ribosomal prot	1358	49	7.6	473	2	AG3537	hypothetical prote
1286	49	7.6	105	2	T08720	ribosomal protein	1359	49	7.6	476	2	T42692	hypothetical prote
1287	49	7.6	106	2	T36973	hypothetical prote	1360	49	7.6	483	2	T17346	hypothetical prote
1288	49	7.6	121	2	T28046	hypothetical prote	1361	49	7.6	495	1	I37062	involucrin S - gor
1289	49	7.6	128	2	A72678	hypothetical prote	1362	49	7.6	501	2	JC7877	toxin-60A - Okinaw
1290	49	7.6	130	1	RWMS58	T-cell receptor al	1363	49	7.6	513	2	A38193	phosphoprotein pho
1291	49	7.6	137	1	BGP62	spermatid transiti	1364	49	7.6	526	2	A86097	hypothetical prote
1292	49	7.6	137	2	AF0362	probable exported	1365	49	7.6	526	2	E91256	hypothetical prote
1293	49	7.6	147	2	A36790	hypothetical prote	1366	49	7.6	529	2	S46116	probable regulator
1294	49	7.6	152	2	A53274	complement factor	1367	49	7.6	530	2	F71445	hypothetical prote
1295	49	7.6	152	2	AE1812	hypothetical prote	1368	49	7.6	535	2	S44827	F54F2.2 protein -
1296	49	7.6	182	2	D82925	hypothetical prote	1369	49	7.6	538	1	S12570	homeotic protein b
1297	49	7.6	183	1	FRHUH	ferritin heavy cha	1370	49	7.6	538	2	G83653	oligopeptide ABC t
1298	49	7.6	188	2	F95322	hypothetical prote	1371	49	7.6	546	2	T24679	hypothetical prote
1299	49	7.6	203	2	T33864	hypothetical prote	1372	49	7.6	547	2	G83116	peroxochelin biosynth
1300	49	7.6	211	2	F86488	protein T32E20.33	1373	49	7.6	559	2	T12680	peroxisomal target
1301	49	7.6	217	2	T40730	probable rna-bindi	1374	49	7.6	578	2	D95400	probable oxidoredu
1302	49	7.6	222	2	T47742	hypothetical prote	1375	49	7.6	578	2	T50812	asparagine synthas
1303	49	7.6	224	2	C31201	GLI-related finger	1376	49	7.6	593	1	F70349	NADH2 dehydrogenas
1304	49	7.6	226	2	A70754	hypothetical prote	1377	49	7.6	595	2	F85438	nucleoporin-like p
1305	49	7.6	228	2	B72655	probable transcrip	1378	49	7.6	605	1	I37061	involucrin M - gor
1306	49	7.6	228	2	T47425	NAC domain-like pr	1379	49	7.6	612	2	S35471	NADH2 dehydrogenas
1307	49	7.6	234	2	C83097	InaA protein PA437	1380	49	7.6	613	2	T00077	gag-like protein -
1308	49	7.6	239	2	H84886	probable VAMP-asso	1381	49	7.6	619	2	A82638	DNA topoisomerase
1309	49	7.6	241	2	T34379	hypothetical prote	1382	49	7.6	625	2	S71930	neuron-derived rec
1310	49	7.6	247	2	S57136	probable ribosomal	1383	49	7.6	628	2	JC2493	neuron derived orp
1311	49	7.6	261	2	S29360	Fc gamma (IgG) rec	1384	49	7.6	632	2	T07587	probable polygalac
1312	49	7.6	273	2	D90819	probable antitermi	1385	49	7.6	635	1	I37060	involucrin L - gor
1313	49	7.6	273	2	B85627	probable antitermi	1386	49	7.6	640	1	UZADP7	terminal protein p
1314	49	7.6	277	2	S14324	platelet glycoprot	1387	49	7.6	643	1	S15616	E1 protein - human
1315	49	7.6	277	2	D84596	hypothetical prote	1388	49	7.6	643	2	A41120	prostaglandin tran
1316	49	7.6	298	2	G75140	hypothetical prote	1389	49	7.6	644	1	W1WL58	E1 protein - human
1317	49	7.6	305	2	T25117	hypothetical prote	1390	49	7.6	658	2	T16040	hypothetical prote
1318	49	7.6	306	2	A75316	hypothetical prote	1391	49	7.6	669	2	T08827	hypothetical prote
1319	49	7.6	311	2	T12500	hypothetical prote	1392	49	7.6	681	2	I38755	transcription fact
1320	49	7.6	315	1	B69812	ferrichrome ABC tr	1393	49	7.6	682	2	G86300	F19K19.13 protein
1321	49	7.6	346	2	S10188	NADH2 dehydrogenas	1394	49	7.6	694	2	S32938	probable membrane
1322	49	7.6	346	2	T11194	NADH2 dehydrogenas	1395	49	7.6	732	2	AF0938	primosomal protein
1323	49	7.6	346	2	B90624	NADH2 dehydrogenas	1396	49	7.6	740	2	S61568	probable membrane
1324	49	7.6	348	2	T13817	NADH2 dehydrogenas	1397	49	7.6	744	2	S70619	finger protein bow
1325	49	7.6	354	1	WNECPW	glycine betaine/L-	1398	49	7.6	749	2	G86186	hypothetical prote
1326	49	7.6	354	2	AB0842	glycine betaine/L-	1399	49	7.6	755	2	S24262	hypothetical prote
1327	49	7.6	354	2	E91071	hypothetical prote	1400	49	7.6	788	2	A37057	structural polypro
1328	49	7.6	354	2	H85915	hypothetical prote	1401	49	7.6	789	2	A39564	integrin beta-6 ch
1329	49	7.6	364	2	S28771	polygalacturonase	1402	49	7.6	790	2	A35797	transcription repr
1330	49	7.6	366	2	I53488	prostaglandin F2 a	1403	49	7.6	793	2	S68238	probable DNA-bindi
1331	49	7.6	366	2	S51281	F2-alpha receptor	1404	49	7.6	810	2	I38361	trp-1 protein - hu
1332	49	7.6	367	2	AC1135	B. subtilis floN p	1405	49	7.6	833	1	T24682	hypothetical prote
1333	49	7.6	372	2	AD1493	conserved hypothet	1406	49	7.6	835	1	I57441	hypothetical prote
1334	49	7.6	374	2	T35581	probable O-sialogl	1407	49	7.6	838	2	T20125	lipoxigenase (EC 1
1335	49	7.6	379	2	S88457	ubiquinol-cytochro	1408	49	7.6	859	1	JQ2267	LDL receptor precu
1336	49	7.6	381	2	F87197	probable anion tra	1409	49	7.6	860	1	QRHULD	trehalose-6-phosph
1337	49	7.6	396	2	T23767	hypothetical prote	1410	49	7.6	865	2	H71447	env polyprotein -
1338	49	7.6	398	2	B86298	protein F309.11 [i	1411	49	7.6	877	2	C46356	hypothetical prote
1339	49	7.6	401	2	T51493	stearoyl-acyl carr	1412	49	7.6	886	2	S07132	env polyprotein pr
1340	49	7.6	401	2	D87368	imidazolonepropion	1413	49	7.6	904	1	VCLJBT	hypothetical prote
1341	49	7.6	408	1	BMHU4	bone morphogenetic	1414	49	7.6	905	2	T23229	excinuclease ABC c
1342	49	7.6	409	2	S70704	carbon catabolite	1415	49	7.6	935	2	A64608	excinuclease ABC c
1343	49	7.6	410	2	AH2819	cyclopropane-fatty	1416	49	7.6	941	2	H71906	

C06G4.1 protein - 1417 957 2 S44748
immediate-early pr 1418 2 B49284
hypothetical prote 1419 2 B82557
probable DNA misa 1420 2 B85295
mah3 protein homol 1421 2 T05793
hypothetical prote 1422 2 T44232
DNA mismatch repa 1423 2 T51613
AF17 protein - hum 1424 2 T38533
hypothetical 119.5 1425 2 JQ0405
hypothetical prote 1426 2 T00715
pol polyprotein - 1427 2 S70393
protein-cytosine k 1428 2 TVRNU
viral mRNA transla 1429 2 S55954
hypothetical prote 1430 2 S62419
natural killer cel 1431 2 B47328
hypothetical prote 1432 2 T04464
hypothetical prote 1433 2 T46095
resistance protein 1434 2 T30562
myosin-IXb [simila 1435 2 A59256
fibronectin precu 1436 2 FNUH
gp330 protein prec 1437 2 T42737
potassium channel 1438 2 S33268
protamine St2a - h 1439 2 S10754
hypothetical prote 1440 2 C91290
collipase B precurs 1441 2 XLHOB
protamine P2 - rhe 1442 2 S33336
hypothetical prote 1443 2 H81841
Ig lambda chain v 1444 2 S13726
hypothetical prote 1445 2 S25839
conserved hypotet 1446 2 A28272
id747 (AF322013) [1447 2 D97648
hypothetical prote 1448 2 F86496
hypothetical prote 1449 2 G72127
hypothetical prote 1450 2 D86159
phospholipase A2 (1451 2 S62781
Ig lambda chain pr 1452 2 S70444
hypothetical prote 1453 2 AE1031
cysteine proteinas 1454 2 S27239
polyprotein - hepa 1455 2 PS0329
hypothetical prote 1456 2 A84072
hypothetical prote 1457 2 T22005
alpha-amylase inhi 1458 2 S16031
alpha-amylase inhi 1459 2 S10029
hypothetical prote 1460 2 H91248
hypothetical prote 1461 2 F86506
hypothetical prote 1462 2 F72115
hypothetical prote 1463 2 T51065
probable endolysin 1464 2 D90820
probable endolysin 1465 2 B90902
probable endolysin 1466 2 B85819
probable endolysin 1467 2 E85579
probable endolysin 1468 2 C90911
probable endolysin 1469 2 D90874
probable endolysin 1470 2 H90851
probable endolysin 1471 2 H90765
probable endolysin 1472 2 B87516
probable endolysin 1473 2 E90780
probable endolysin 1474 2 H90999
probable endolysin 1475 2 C85845
hypothetical prote 1476 2 C87614
hypothetical prote 1477 2 T08768
nonstructural prot 1478 2 S06067
probable transcrip 1479 2 T35727
hypothetical prote 1480 2 T19264
endothelin 1 precu 1481 2 S20609
cold-regulated pro 1482 2 A55112
hypothetical prote 1483 2 A03863
heme exporter prot 1484 2 H83462
hypothetical prote 1485 2 T33891
ATP synthase fo ch 1486 2 F90614
Ig lambda chain - 1487 2 S25748
transcription fact 1488 2 T46203
hypothetical prote 1489 2 T34545

1490 48.5 7.5 247 2 F84420
1491 48.5 7.5 256 2 A32373
1492 48.5 7.5 258 2 B83044
1493 48.5 7.5 259 2 G48652
1494 48.5 7.5 259 2 T36219
1495 48.5 7.5 264 2 A31638
1496 48.5 7.5 268 1 UHMS2
1497 48.5 7.5 270 2 T50058
1498 48.5 7.5 275 2 AF1160
1499 48.5 7.5 275 2 AF1519
1500 48.5 7.5 280 2 S35623
hypothetical prote
transformer-2 prot
hypothetical prote
regulatory protein
regulatory protein
transformer-2 sex-
interleukin-2 rece
probable serine ac
motility protein (
motility protein (
beta-glucosyl-HMC-

ALIGNMENTS

RESULT 1

T18801
hypothetical protein ZK131.11 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 31-Dec-2004
C;Accession: T18801; T27746
R;Percy, C.
submitted to the EMBL Data Library, March 1997
A;Reference number: Z19024
A;Accession: T18801
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-477 <WIL>
A;Cross-references: UNIPROT:O62022; UNIPARC:UPI00001640DD; EMBL:Z93373; PIDN:CAB07552.1;
A;Experimental source: clone C0189
R;Steward, C.
submitted to the EMBL Data Library, December 1996
A;Reference number: Z20413
A;Accession: T27746
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-477 <W12>
A;Cross-references: UNIPARC:UPI00001640DD; EMBL:Z83245; PIDN:CAB05840.1; GSPDB:GN000020;
A;Experimental source: clone ZK131
C;Genetics:
A;Gene: CESP:ZK131.11
A;Map position: 2
A;Introns: 20/2; 49/2; 113/1; 169/1; 260/2; 375/3; 432/3

Query Match 12.0%; Score 77.5; DB 2; Length 477;
Best Local Similarity 34.7%; Pred. No. 2.4;
Matches 25; Conservative 6; Mismatches 32; Indels 9; Gaps 3;

QY 46 GGQCECKDWFLRAPRR---KEMTVSGLPKQ--CPDHPKGNVKKTRHQHRRKPKNCHS 100
DB 290 GGNAESNTTFLRATYKRFKKIYTSATLPKQNSTMDNFKQSSVFFEDTAHHNPNWDG 349
QY 101 RACQQLKQCOL 112
DB 350 R----ILKKAPL 357

RESULT 2

JQ1750
genome polyprotein - simian paramyxovirus SV41 (strain Toshiba/Chanock)
N;Alternate names: RNA nucleotidyltransferase (RNA-directed); RNA replicase
N;Contains: RNA-directed RNA polymerase (EC 2.7.7.48)
C;Species: simian paramyxovirus SV41
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C;Accession: JQ1750
R;Ogawa, M.; Mutsaers, N.; Tsurudome, M.; Kawano, M.; Matsuura, H.; Kusagawa, S.; Komada, J.
J. Gen. Virol. 73, 2743-2750, 1992
A;Title: Nucleotide sequence analysis of the simian virus 41 gene encoding the large (L)
A;Reference number: JQ1750; MUID:93019033; PMID:1328485
A;Accession: JQ1750
A;Molecule type: mRNA
A;Residues: 1-2269 <OGA>


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A:Cross-references: UNIPROT:P35341; UNIPARC:UPI00001344PD; EMBL:X64275; NID:G433516; PID:
C:Genetics:
A:Gene: L
C:Superfamily: parainfluenza virus RNA-directed RNA polymerase
C:Keywords: ATP; nucleotidyltransferase; RNA biosynthesis; RNA replication

Query Match      12.0%; Score 77; DB 1; Length 2269;
Best Local Similarity 27.5%; Pred. No. 11;
Matches 30; Conservative 12; Mismatches 31; Indels 36; Gaps 6;

Qy 13 PLMLSMVSSSLNPGVARGHRDRGQAS-----RRWLQ-----EGQGECE--CK 53
Db 422 PLSLPQNAKSL-----IELHDNSISVEYTLRHKELSLIEFKKCFDPDPEELSLIPWK 477
Qy 54 DWFLRAPRRKFTVMTVSGLPKKQCPDHFKNVKKTRHQRH-RKPNKHSR 101
Db 478 DKAISAPKEDWMSV-----FRKSLIKQRHQRHIMPMPNPNR 514

RESULT 3
I50451
A:Title: D receptor isoform A - Japanese quail
C:Species: Coturnix coturnix japonica (Japanese quail)
C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 05-Oct-2004
C:Accession: I50451
R:Elaroussi, M.A.; Prahl, J.W.; Deluca, H.F.
Proc. Natl. Acad. Sci. U.S.A. 91, 11596-11600, 1994
A:Title: The avian vitamin D receptors; primary structures and their origins.
A:Reference number: I50451; MUID:95062315; PMID:7972109
A:Accession: I50451
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-448 <ELA>
A:Cross-references: UNIPROT:P49701; UNIPARC:UPI00001382C2; EMBL:U12641; NID:G595500; PID:
C:Superfamily: Vitamin D3 receptor (VDR)
C:Keywords: zinc finger
F:42-362/Domain: erba transforming protein homology <ERBA>

Query Match      11.6%; Score 74.5; DB 2; Length 448;
Best Local Similarity 32.9%; Pred. No. 4.7;
Matches 24; Conservative 11; Mismatches 15; Indels 23; Gaps 6;

Qy 50 CE-CKDWFLRAPRRKFTVMTVSGLPKKQCPDHFKNVKKTRHQRHHRKPNKHSRACQOFLK 108
Db 61 CEGCKGFFRRSMKRAMFT-----CP----FSGDKITKONR-----RHCQACR--LK 102

Qy 109 QC-----QLRSPAL 117
Db 103 RCVDIGMKKEFTL 115

RESULT 4
A60912
A:Title: D receptor - chicken (fragment)
C:Species: Gallus gallus (chicken)
C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 31-Dec-2004
C:Accession: A60912
R:McDonnell, D.P.; Mangelsdorf, D.J.; Pike, J.W.; Haussler, M.R.; O'Malley, B.W.
Science 235, 1214-1217, 1987
A:Title: Molecular cloning of complementary DNA encoding the avian receptor for vitamin
A:Reference number: A60912; MUID:87149040; PMID:3029866
A:Accession: A60912
A:Status: nucleic acid sequence not shown; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-70 <MCD>
A:Cross-references: UNIPROT:Q42392; UNIPARC:UPI000017A1EE
C:Keywords: DNA binding; zinc finger
F:1-70/Domain: erba transforming protein homology (fragment) <ERBA>

Query Match      11.4%; Score 73.5; DB 2; Length 70;
Best Local Similarity 35.5%; Pred. No. 1.2;
Matches 22; Conservative 9; Mismatches 12; Indels 19; Gaps 5;
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Qy 50 CE-CKDWFLRAPRRKFTVMTVSGLPKKQCPDHFKNVKKTRHQRHHRKPNKHSRACQOFLK 108
Db 20 CEGCKGFFRRSMKRAMFT-----CP----FNGDKITKONR-----RHCQACR--LK 61

Qy 109 QC 110
Db 62 RC 63

RESULT 5
G84522
A:Title: gibberellin-regulated proteins [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C:Accession: G84522
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.;
eusa, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
Nature 402, 761-768, 1999
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: AB4420; MUID:20083487; PMID:10617197
A:Accession: G84522
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-108 <STO>
A:Cross-references: UNIPROT:O82328; UNIPARC:UPI000000BE2C; GB:AE002093; NID:G3650032; PID:
C:Genetics:
A:Gene: At2g14900
A:Map position: 2
A:Superfamily: gibberellin-regulated protein GAS2

Query Match      11.1%; Score 71.5; DB 2; Length 108;
Best Local Similarity 25.9%; Pred. No. 2.8;
Matches 29; Conservative 18; Mismatches 38; Indels 27; Gaps 7;

Qy 1 MKVLISLLLL-LPLMLSMVSSSLNPGVARG-----HRDRGQASRRWLQEGGQGECE-- 51
Db 1 MKIIVSLVLASLLLSLSSLASATISDAFGSGAVAPQSKDGPALKWC---GQKCEGR 57

Qy 52 CKDWFLRAPRRKFTVMTVSGLPKKQCPDHFKNVKKTRHQRHHRKPNKHSRAC 103
Db 58 CKE---AGMKDRCLKYCGICCKDCQC-----VPSGTY-----GNKHECAC 94

RESULT 6
S35333
A:Title: steroid receptor protein svp44 - zebra fish
C:Species: Brachydanio rerio (zebra fish)
C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 05-Oct-2004
C:Accession: S35333
R:Fjose, A.; Nornes, S.; Weber, U.; Mlodzik, M.
EMBO J. 12, 1403-1414, 1993
A:Title: Functional conservation of vertebrate seven-up related genes in neurogenesis and
A:Reference number: S35333; MUID:93223680; PMID:8467797
A:Accession: S35333
A:Molecule type: mRNA
A:Residues: 1-411 <FOO>
A:Cross-references: UNIPROT:Q06725; UNIPARC:UPI000013628E; EMBL:X70299; NID:G296418; PID:
C:Genetics:
A:Gene: svp44
C:Keywords: DNA binding; steroid hormone receptor; zinc finger
F:74-320/Domain: erba transforming protein homology <ERBA>
F:76-96/Region: zinc finger
F:112-136/Region: zinc finger

Query Match      11.0%; Score 71; DB 2; Length 411;
Best Local Similarity 26.3%; Pred. No. 9.9;
Matches 26; Conservative 14; Mismatches 27; Indels 32; Gaps 6;

Qy 26 PGVA--RGHRDRGQASRR-----WLOEGQGECE-CKDWFLRAPRRKFTVMTVSGLP 71
Db 56 PGTAGDKGSQNSGQSQHQHIECVCCDKSSGKHGYQFTCEGCKSPFKRSVRRN-LTYTCRA 114
```


C;Accession: T49804
R;Schulte, U.; Align, V.; Hoheisel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura,
submitted to the Protein Sequence Database, May 2000
A;Reference number: Z25022
A;Accession: T49804
A;Status: preliminary
A:Molecule type: DNA
A;Residues: 1-1283 <SCH>
A;Cross-references: UNIPROT:Q96UA3; UNIPARC:UPI000017B451; EMBL:AL356834; GSPDB:GN00116;
A;Experimental source: BAC clone B11B22; strain OR74A
C;Genetics:
A;Gene: NCSP:B11B22.60
A;Map position: 6
A;Introns: 856/2

Query Match 10.9%; Score 70.5; DB 2; Length 1283;
Best Local Similarity 24.5%; Pred. No. 30;
Matches 26; Conservative 18; Mismatches 31; Indels 31; Gaps 6;

Qy 33 RDGQASRWLOEGQECEKDWFLRAPRRKFTWVS---GLPKQCPCDHFPGNVKK--T 87
Db 454 RKMKWKQKWQEGSKSGK-----LRAPESAMPPVSVVMGSPRAWPLPRMQGHIRGDV 508
Qy 88 RHQRHHR-----KPNKHSRACQF--LKQCQLRSFA 116
Db 509 GHOSHNOHYMDEGVYRLMWSEKLEPH----QQFARLRKAELALIYA 550

RESULT 10
A32693
steroid receptor protein svp 1 - fruit fly (*Drosophila melanogaster*)
C;Species: *Drosophila melanogaster*
C;Date: 22-Jun-1990 #sequence_revision 22-Jun-1990 #text_change 31-Dec-2004
C;Accession: A32693
R;Midzik, M.; Hiromi, Y.; Weber, U.; Goodman, C.S.; Rubin, G.M.
Cell 60, 211-224, 1990
A;Title: The *Drosophila* seven-up gene, a member of the steroid receptor gene superfamily
A;Reference number: A32693; PMID:90124631; PMID:2105166
A;Accession: A32693
A;Status: preliminary
A:Molecule type: mRNA
A;Residues: 1-543 <MLQ>
A;Cross-references: UNIPROT:P16375; UNIPARC:UPI00001245E6; GB:M28863; NID:g158518; PIDN:
C;Genetics:
A;Gene: FlyBase:svp
A;Cross-references: FlyBase:FBgn0003651
C;Keywords: alternative splicing; DNA binding; steroid hormone receptor; transcription r
F;136-452/Domain: erba transforming protein homology <ERBA>
F;200-220/Region: zinc finger
F;236-260/Region: zinc finger

Query Match 10.9%; Score 70; DB 2; Length 543;
Best Local Similarity 26.7%; Pred. No. 16;
Matches 27; Conservative 12; Mismatches 28; Indels 34; Gaps 5;

Qy 21 SSSLNPG-----VARGHRDRGQASRWLQEGQECEKDWFLRAPRRKFTWVG 69
Db 183 SQSSNSGSQIDSQNIECVCGDKSGKHGYQTCEG----CKSPFKRSVRRN-LTYSC 236

Qy 70 LPKQCPCDHFPGNVKKTRHQHRRKPNKHSRACQCFLLKOC 110
Db 237 RGRNRCPID-----QHRRNQCCQYCR-----LKKC 260

RESULT 11
B32693
steroid receptor protein svp 2 - fruit fly (*Drosophila melanogaster*)
C;Species: *Drosophila melanogaster*
C;Date: 22-Jun-1990 #sequence_revision 22-Jun-1990 #text_change 31-Dec-2004
C;Accession: B32693
R;Midzik, M.; Hiromi, Y.; Weber, U.; Goodman, C.S.; Rubin, G.M.
Cell 60, 211-224, 1990
A;Title: The *Drosophila* seven-up gene, a member of the steroid receptor gene superfamily

A;Reference number: A32693; MUID:90124631; PMID:2105166

A;Accession: B32693

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-746 <MLO>

A;Cross-references: UNIPROT:P16376; UNIPARC:UPI0000124PA1; GB:M28863; GB:M28864

C;Genetics:

A;Gene: FlyBase:svp

A;Cross-references: FlyBase:FBgn0003651

C;Keywords: alternative splicing; DNA binding; steroid hormone receptor; transcription

F;198-452/Domain: erba transforming protein homology <ERBA>

F;200-220/Region: zinc finger

F;236-260/Region: zinc finger

Query Match 10.9%; Score 70; DB 2; Length 746;

Best Local Similarity 26.7%; Pred. No. 21;

Matches 27; Conservative 12; Mismatches 28; Indels 34; Gaps 5;

QY 21 SSSINPG-----VARGHRDQGASRWLQEGGQCECKDWFLLRAPRRKFWTVSG 69

DB 183 SQSSNSGQIDSKQIECVCGDKSGKHGYQFTCEG-----CKSFPRKSVRRN-LTYSC 236

QY 70 LPKQPCPDHFGKGVKTRHQRHHRKPNKHSRACQQLKQC 110

DB 237 RGRNCPID-----QHRRNQCYCR-----LKKC 260

RESULT 12

T24061

hypothetical protein R09A8.1 - Caenorhabditis elegans

C;Species: Caenorhabditis elegans

C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

C;Accession: T24061

R;Wilkinson, J.

submitted to the EMBL Data Library, November 1995

A;Reference number: Z19836

A;Accession: T24061

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-1095 <WIL>

A;Cross-references: UNIPROT:Q21852; UNIPARC:UPI000007CD18; EMBL:Z68009; PIDN:CAA92003.1;

A;Experimental source: clone R09A8

C;Genetics:

A;Gene: CESP:R09A8.1

A;Map position: X

A;Introns: 48/2; 189/1; 285/3; 347/3; 402/3; 543/3; 619/1; 693/1; 771/1; 835/1; 1

Query Match

Best Local Similarity 10.9%; Score 70; DB 2; Length 1095;

Matches 24; Conservative 10; Mismatches 32; Indels 10; Gaps 3;

QY 20 VSSSLNPGVARGHRDQGASRWLQEGGQCECKDWFLLRAPRRKFWTVSGLPKQPCDH 79

DB 305 VOSSLVNGNRSTDVRVA-QRFASGTGFVEKECRWDQLVEKKQ-----KKEVNSDH 355

QY 80 FKGKGVKTRHQRHHRK 95

DB 356 KKAN-RITSHLEHNR 370

RESULT 13

T27283

hypothetical protein Y64GI0A.f - Caenorhabditis elegans

C;Species: Caenorhabditis elegans

C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999

C;Accession: T27283

R;Ainscough, R.

submitted to the EMBL Data Library, September 1999

A;Reference number: Z20336

A;Accession: T27283

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-1620 <WIL>

A;Cross-references: UNIPARC:UPI000017BCB4; EMBL:AL110498; NID:e1542303; PIDN:CAB54471.1;

A;Experimental source: clone Y64GI0A

C;Genetics:

A;Gene: CESP:Y64GI0A.f

A;Introns: 77/1; 116/1; 198/1; 282/1; 365/1; 425/1; 466/1; 548/1; 559/1; 601/1; 625/1; 71

Query Match 10.9%; Score 70; DB 2; Length 1620;

Best Local Similarity 30.0%; Pred. No. 42;

Matches 21; Conservative 10; Mismatches 35; Indels 4; Gaps 3;

QY 46 GGQCECKDWF-LRAPRRKFWTVSGLPKQPCDHFKGNVKKTRH--QRHHRKPNKHSRA 102

DB 261 GRAQCQYPGFHLSDRRSCVDIDECAKN--GCEHFCENVAGTYRCKREGQLGRDGR 319

QY 103 COQFLKQCQL 112

DB 320 CEEMLGCCQV 329

RESULT 14

C34768

ORF2 protein - Orf virus (strain N22)

C;Species: Orf virus

C;Date: 23-Aug-1991 #sequence_revision 23-Aug-1991 #text_change 09-Jul-2004

C;Accession: C34768

R;Fraser, K.W.; Hill, D.F.; Mercer, A.A.; Robinson, A.J.

Virolgy 176, 379-389, 1990

A;Title: Sequence analysis of the inverted terminal repetition in the genome of the para

A;Reference number: A34768; MUID:90266454; PMID:2129563

A;Accession: C34768

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-221 <FRA>

A;Cross-references: UNIPROT:Q85299; UNIPARC:UPI00000F1366; GB:M30023; EMBL:M37623; NID:g

Query Match 10.8%; Score 69.5; DB 2; Length 221;

Best Local Similarity 29.2%; Pred. No. 8.3;

Matches 33; Conservative 8; Mismatches 37; Indels 35; Gaps 6;

QY 26 PGVARGHRDQGASRWLQEGGQCECKDWFLLRAPRRKFWTVSGLPKK-----QCP 76

DB 83 PAAARGARRCCARRARGGGWP---RRWRPRAARRG---SGPPARAPAAALAPDQAP 135

QY 77 CDHFKGNVKKTR-----HQR--HHRKPNKHSRACQQLKQCQLRS 114

DB 136 ----RSKYKQDLAVETLPPQPTPTHTLPPARRQHRSQQAQTPRRRCSARS 184

RESULT 15

THHUB

thrombomodulin precursor [validated] - human

C;Species: Homo sapiens (man)

C;Date: 31-Dec-1998 #sequence_revision 12-May-1995 #text_change 09-Jul-2004

C;Accession: A14442; A28307; A29680; A27073; JX0264; S38954

R;Shirai, T.; Shiojiri, S.; Ito, H.; Yamamoto, S.; Kusumoto, H.; Deyashiki, Y.; Maruyama,

J. Biochem. 103, 281-285, 1988

A;Title: Gene structure of human thrombomodulin, a cofactor for thrombin-catalyzed activa

A;Reference number: A41442; MUID:88227901; PMID:2836377

A;Accession: A41442

A;Molecule type: DNA

A;Residues: 1-575 <SHI>

A;Cross-references: UNIPROT:P07204; UNIPARC:UPI00000498FB; DBJ:000210; NID:g220126; PIDN

R;Jackman, R.W.; Beeler, D.L.; Fritze, L.; Soff, G.; Rosenberg, R.D.

Proc. Natl. Acad. Sci. U.S.A. 84, 6425-6429, 1987

A;Title: Human thrombomodulin gene is intron depleted: nucleic acid sequences of the cDN

A;Reference number: A28307; MUID:87317665; PMID:2819876

A;Accession: A28307

A;Molecule type: DNA; mRNA

A;Residues: 1-472,'A',474-575 <JAC>

A;Cross-references: UNIPARC:UPI000000002BD; GB:J02973; NID:g339658; PIDN:AAAG1175.1; PID:g

R;Suzuki, K.; Kusumoto, H.; Deyashiki, Y.; Nishioaka, J.; Maruyama, I.; Zushi, M.; Kawahar

EMBO J. 6, 1891-1897, 1987

A;Title: Structure and expression of human thrombomodulin, a thrombin receptor on endoth

A;Reference number: A29680; PMID:88004395; PMID:2820710
A;Accession: A29680
A;Molecule type: mRNA
A;Residues: 1-575 <SUZ>
A;Cross-references: UNIPARC:UPI00000498FB; GB:X05495; NID:g37123; PIDN:CAA29045.1; PID:9
A;Experimental source: lung endothelium
A;Note: Part of this sequence, including the amino end of the mature protein, were deter
R;Wen, D.; Dittman, W.A.; Ye, R.D.; Deaven, L.L.; Majerus, P.W.; Sadler, J.E.
Biochemistry 26, 4350-4357, 1987
A;Title: Human thrombomodulin: complete cDNA sequence and chromosome localization of the
A;Reference number: A27073; PMID:88024950; PMID:2822087
A;Accession: A27073
A;Molecule type: mRNA
A;Residues: 1-472, 'A', 474-575 <WEN>
A;Cross-references: UNIPARC:UPI00000002BD; GB:M16552; NID:g339656; PIDN:AAB59508.1; PID:
A;Experimental source: placenta
A;Note: Parts of this sequence were determined by protein sequencing
R;Yamamoto, S.; Mizoguchi, T.; Tamaki, T.; Ohkuchi, M.; Kimura, S.; Aoki, N.
J. Biochem. 113, 433-440, 1993.
A;Title: Urinary thrombomodulin, its isolation and characterization.
A;Reference number: JX0264; PMID:93293792; PMID:8390446
A;Accession: JX0264
A;Molecule type: protein; mRNA
A;Residues: 19-472, 'A', 474-486 <YAM>
A;Cross-references: UNIPARC:UPI0000173341
A;Experimental source: urine
A;Note: the urinary form appears to be identical with that circulating in plasma
R;Gerlitz, B.; Hassell, T.; Vlahos, C.J.; Parkinson, J.F.; Bang, N.U.; Grinnell, B.W.
Biochem. J. 295, 131-140, 1993
A;Title: Identification of the predominant glycosaminoglycan-attachment site in soluble
serine.
A;Reference number: S38954; PMID:94029900; PMID:8216207
A;Accession: S38954
A;Molecule type: protein
A;Residues: 475-491, 'X', 493-494 <GER>
A;Cross-references: UNIPARC:UPI0000173342
A;Note: the residue designated 'X' was determined to be a Ser with covalently bound chon
R;Meininger, D.P.; Komives, E.A.
submitted to the Brookhaven Protein Data Bank, September 1995
A;Reference number: A67369; PDB:2ZAQ
A;Contents: annotation; conformation and disulfide bond assignments by (1)H-NMR, residue
R;Tullinsky, A.; Mathews, I.I.
submitted to the Brookhaven Protein Data Bank, August 1994
A;Reference number: A52804; PDB:1HLT
A;Contents: annotation; X-ray crystallography, 3.0 angstroms, residues 426-442
R;Hrabal, R.; Komives, E.A.; Ni, F.
submitted to the Brookhaven Protein Data Bank, November 1995
A;Reference number: A65583; PDB:1FGD
A;Contents: annotation; conformation by (1)H-NMR, residues 427-444
R;Hrabal, R.; Komives, E.A.; Ni, F.
Protein Sci. 5, 195-203, 1996
A;Title: Structural resiliency of an EGF-like subdomain bound to its target protein, thr
A;Reference number: A58595; PMID:96276211; PMID:8745396
A;Contents: annotation; conformation by (1)H-NMR
C;Genetics:
A;Gene: GDB:THBD
A;Cross-references: GDB:119613; OMIM:188040
A;Map position: 20p11.2-20p11.2
A;Introns: #status absent
C;Complex: homodimer, urinary form
C;Function:
A;Description: inhibits thrombin activation of fibrinogen; cofactor for thrombin activat
A;Pathway: blood coagulation moderation
A;Note: the membrane-bound form is located on the endothelium luminal surface of arterie
A;Note: thrombin complexed with the membrane-bound form is subject to endocytosis
C;Superfamily: thrombomodulin; C-type lectin homology; EGF homology
C;Keywords: anticoagulant; beta-hydroxyasparagine; beta-hydroxyaspartic acid; blood coag
e protein
F;1-18/Domain: signal sequence #status predicted <SIG>
F;19-575/Product: thrombomodulin, membrane-bound form #status predicted <MAT>
F;19-513/Domain: extracellular #status predicted <EXT>
F;19-486/Product: thrombomodulin, urinary form #status experimental <MAU>
F;24-167/Domain: C-type lectin homology <LCH>

F;177-199/Region: PEST sequence
F;201-233/Region: PEST sequence
F;245-280/Domain: EGF homology <EG1>
F;288-323/Domain: EGF homology <EG2>
F;329-362/Domain: EGF homology <EG3>
F;369-404/Domain: EGF homology <EG4>
F;408-439/Domain: EGF homology <EG5>
F;445-480/Domain: EGF homology <EG6>
F;485-513/Region: PEST sequence
F;517-539/Domain: transmembrane #status predicted <TMN>
F;540-575/Domain: intracellular #status predicted <INT>
F;47,115,116,382,409/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;174,225,411,504/Binding site: carbohydrate (Thr) (covalent) #status predicted
F;245-256,252-265,267-280,288-296,292-308,310-323,329-340,336-349,351-362,369-378,374-388
F;334,498/Binding site: carbohydrate (Ser) (covalent) #status predicted
F;342/Modified site: erythro-beta-hydroxyasparagine (Asn) #status experimental
F;490,492/Binding site: chondroitin sulfate (Ser) (covalent) (partial) #status experimental

Query Match 10.8%; Score 69.5; DB 1; Length 575;
Best Local Similarity 23.5%; Pred. No. 19;
Matches 24; Conservative 11; Mismatches 26; Indels 41; Gaps 5;
QY 5 ISSLLLLLPMLMSVSSSLNPGVARGHRDRGQASRRW---LQEGGQCECKDWFLRAPR 61
DB 209 VGSSAAVAFGLQLMCTAP--PGAQVGHAR-EAPGAWDCSVENGCCERACN----- 257
QY 62 RKFMVTYSGLPKKQCP-----CDHF 80
DB 258 ----AIPGAPRCQCPAGALQADGRSCTASATQSCNDLCEHP 295

Search completed: August 3, 2006, 09:57:13

Job time : 48 secs

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GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: August 3, 2006, 09:56:38 ; Search time 299 Seconds

(without alignments)

368.150 Million cell updates/sec

Title: US-10-015-967-2

Perfect score: 644

Sequence: 1 MKVLISLLLLPLMLMSV.....SRACQFLKQCQLRSFALPL 119

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 92501592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

Database :

UniProt 7.2.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	644	100.0	119	2	Q6UXB2 HUMAN
2	456	70.8	119	2	Q5UW37 MOUSE
3	322	50.0	128	2	Q8R3U6 MOUSE
4	81	12.6	170	2	Q52VJ8 CIOIN
5	81	12.6	170	2	Q52VK0 CIOIN
6	81	12.6	397	2	Q52VK2 CIOIN
7	81	12.6	487	2	Q3CNY9 ALTAT
8	80.5	12.5	188	2	Q32PK5 BRARE
9	80.5	12.5	188	2	Q5RHD0 BRARE
10	80.5	12.5	613	2	Q5RHD1 BRARE
11	80	12.4	844	2	Q4BU62 BURVI
12	79.5	12.3	662	2	Q61TA9 CAEBR
13	77.5	12.0	170	2	Q52VJ5 CIOIN
14	77.5	12.0	192	2	Q6NDV5 RHOPA
15	77.5	12.0	337	2	Q62022 CAEBL
16	77.5	12.0	398	2	Q52VK3 CIOIN
17	77.5	12.0	449	2	Q810M4 CAEBL
18	77	12.0	335	2	Q74EB4 GEOSL
19	77	12.0	2269	1	L SV41
20	76.5	11.9	411	2	Q9W745 XENLA
21	76.5	11.9	825	2	Q4SAD2 TETNG
22	76	11.8	376	2	Q5AH87 CANAL
23	75.5	11.7	323	2	Q6BJ36 DEBHA
24	75	11.6	373	2	Q5SHK7 THET8
25	75	11.6	373	2	Q72HX1 THET2
26	75	11.6	413	2	Q4FZU0 RAT
27	75	11.6	1817	2	Q7XW82 ORYSA
28	75	11.6	1835	2	Q3WGB8 SACTO
29	74.5	11.6	373	2	Q5A2C5 CANAL
30	74.5	11.6	448	1	VDR COTJA
31	74.5	11.6	451	1	VDR_CHICK

32	74	11.5	145	2	Q4RDG3 TETNG
33	74	11.5	169	2	Q89B64 BRAJA
34	74	11.5	311	2	Q2JRM6 CYAN
35	74	11.5	356	2	Q4IQ10 GIBZE
36	74	11.5	662	2	Q3JVR4 BURP1
37	74	11.5	1501	2	Q2M1B4 DROPS
38	73	11.3	209	2	Q2WBP5 HYDMA
39	73	11.3	217	2	Q524A7 ORYSA
40	73	11.3	564	2	Q7SCU8 NEUCR
41	73	11.3	797	2	Q2OTM6 ORYSA
42	72.5	11.3	246	2	Q2UT28 ASPOR
43	72.5	11.3	289	2	Q5FUS3 GLUOX
44	72.5	11.3	783	2	Q60T21 CAEBR
45	72.5	11.3	3313	1	CELR3 RAT
46	72	11.2	278	2	Q89VG7 BRAJA
47	72	11.2	1575	2	Q6TXJ1 RAT
48	71.5	11.1	108	2	Q82328 ARATH
49	71.5	11.1	483	2	Q5SNF1 CRINE
50	71.5	11.1	483	2	Q5KBT7 CRINE
51	71	11.0	188	2	Q8TEV2 HUMAN
52	71	11.0	410	2	Q6PHF2 BRARE
53	71	11.0	411	1	NR2FL BRARE
54	71	11.0	601	2	Q5ZMB1 CHICK
55	71	11.0	1798	1	LAMB2 HUMAN
56	71	11.0	2262	1	L PI2HT
57	71	11.0	2263	2	Q4R4G3 PI2H
58	71	11.0	3190	2	Q01368 DROME
59	71	11.0	3276	2	Q9W321 DROME
60	70.5	10.9	160	2	Q9SQH1 ARAHY
61	70.5	10.9	383	2	Q6AN18 DESPS
62	70.5	10.9	747	2	Q53LB6 ORYSA
63	70.5	10.9	1104	2	Q443W5 SOLUS
64	70.5	10.9	1290	2	Q96UA3 NEUCR
65	70	10.9	117	2	Q6RUI8 HUMAN
66	70	10.9	131	2	Q4S580 TETNG
67	70	10.9	331	2	Q6DG16 BRARE
68	70	10.9	543	1	7UP1 DROME
69	70	10.9	743	2	Q97120 SCHMA
70	70	10.9	746	1	7UP2 DROME
71	70	10.9	1095	2	Q21852 CAEBL
72	70	10.9	1851	2	Q9TVQ2 CAEBL
73	69.5	10.8	221	2	Q85299 9POKV
74	69.5	10.8	310	2	Q62436 ORYSA
75	69.5	10.8	324	2	Q4S635 TETNG
76	69.5	10.8	575	1	TREM HUMAN
77	69.5	10.8	575	1	TREM SAISC
78	69.5	10.8	575	2	Q81V29 HUMAN
79	69.5	10.8	595	2	Q88ZE7 LACPL
80	69.5	10.8	617	2	Q5BBX3 EMENI
81	69.5	10.8	653	2	Q8JTG6 9PAPI
82	69.5	10.8	706	2	Q2T9G7 HUMAN
83	69.5	10.8	1116	2	Q381X0 9TRYP
84	69.5	10.8	1325	1	UBF42 HUMAN
85	69.5	10.8	1387	2	Q4RKM6 TETNG
86	69	10.7	111	2	Q9FWV9 ORYSA
87	69	10.7	125	2	Q5BJC5 BRARE
88	69	10.7	174	1	Y4473 PSEAE
89	69	10.7	191	2	Q872V4 NEUCR
90	69	10.7	210	2	Q5K943 CRINE
91	69	10.7	314	1	SIX3 CHICK
92	69	10.7	378	1	GLR1 ASPAC
93	69	10.7	400	2	Q8LEL2 ARATH
94	69	10.7	413	2	Q9C8W2 ARATH
95	69	10.7	454	2	Q90ZE8 ONCMA
96	69	10.7	527	2	Q9SKW4 ARATH
97	69	10.7	599	2	Q5NI25 FRATT
98	69	10.7	1077	2	Q8N279 HUMAN
99	69	10.7	1081	2	Q9BE73 MACFA
100	68.5	10.6	154	2	Q6VVH1 ANOGA
101	68.5	10.6	198	2	Q5JKU3 ORYSA
102	68.5	10.6	336	2	Q3HYJ9 STRPU
103	68.5	10.6	356	2	Q58114 HORSE
104	68.5	10.6	381	2	Q26641 STRPU

Q4rdg3	tetraodon n
Q89b64	bradyrhizob
Q2jrm6	cyanoabacter
Q4iq10	gibberella
Q3jvr4	burkholderi
Q2m1b4	drosophila
Q2wbp5	hydra magni
Q524a7	oryza sativ
Q7scu8	neurospora
Q2otm6	oryza sativ
Q2ut28	aspergillus
Q5fus3	gluconobact
Q60t21	caenorhabdi
Q88t78	rattus norv
Q89vg7	bradyrhizob
Q6txj1	rattus norv
Q82328	arabidopsis
Q5snf1	cryptococcu
Q5kbt7	cryptococcu
Q8tev2	homo sapien
Q6phf2	brachydanio
Q6725	brachydanio
Q5zmb1	gallus gall
F55268	homo sapien
P26676	h large str
Q4r4g3	human parai
Q01368	drosophila
Q9w321	drosophila
Q9sqh1	arachis hyp
Q6an18	desulfotale
Q53lb6	oryza sativ
Q443w5	solibacter
Q96ua3	neurospora
Q6ru18	homo sapien
Q4s580	tetraodon n
Q6dg16	brachydanio
P16375	drosophila
Q97120	schistosoma
P16376	drosophila
Q21852	caenorhabdi
Q9tvq2	caenorhabdi
Q85299	orf virus
Q62436	oryza sativ
Q4s635	tetraodon n
P7204	homo sapien
Q71u07	salmi sci
Q81v29	homo sapien
Q88ze7	lactobacill
Q5bbx3	aspergillus
Q8jtg6	human papil
Q2t9g7	homo sapien
Q381x0	trypanosoma
Q9bf44	homo sapien
Q4rk6	tetraodon n
Q9fwv9	oryza sativ
Q5bjc5	brachydanio
Q9hv08	pseudomonas
Q872v4	neurospora
Q5k943	cryptococcu
Q42406	gallus gall
Q74213	aspergillus
Q81e12	arabidopsis
Q9c8w2	arabidopsis
Q90ze8	oncorhynch
Q9skw4	arabidopsis
Q5ni25	franciseila
Q8n279	homo sapien
Q9be73	macaca fasc
Q6vvh1	anopheles g
Q5jku3	oryza sativ
Q3hyj9	strongyloce
Q58114	equus cabal
Q26641	strongyloce

105	68.5	10.6	381	2	Q5R8V3_PONPY	Q5T8V3_pongo pygma	178	66.5	10.3	1772	2	Q4Q8V1_LEIMA	Q4Q8V1_leishmania
106	68.5	10.6	405	2	Q7X17_XENLA	Q7x17 xenopus lae	179	66.5	10.3	2571	1	STAB1_MOUSE	Q8T4Y4_mus musculus
107	68.5	10.6	405	2	Q9P579_9PIPI	Q9p579 xenopus. xc	180	66.5	10.3	3301	1	CELK3_MOUSE	Q9i210_mus musculus
108	68.5	10.6	422	1	VDR_MOUSE	P4B281_mus musculus	181	66	10.2	181	2	Q6IKZ4_DROME	Q6ikz4_drosophila
109	68.5	10.6	422	1	VDR_XENLA	Q13124 xenopus lae	182	66	10.2	255	2	Q84B45_9BACT	Q84b45_uncultured
110	68.5	10.6	422	1	Q3UJ07_MOUSE	Q3u0j7 mus musculus	183	66	10.2	256	2	Q7QHL6_ANOGA	Q7qhl6_anopheles g
111	68.5	10.6	422	2	Q4FJVB_MOUSE	Q4fjv8 mus musculus	184	66	10.2	301	2	Q82XU4_NITEU	Q82xu4_nitrosomona
112	68.5	10.6	422	2	Q4FJVB_MOUSE	Q4fjv8 mus musculus	185	66	10.2	339	2	Q9ZBX7_STRCO	Q9zbx7_streptomyce
113	68.5	10.6	423	1	Q922X0_MOUSE	P122X0 m vitamin d	186	66	10.2	375	2	Q526Q1_ORYSA	Q526q1_oryza sativ
114	68.5	10.6	424	1	VDR_RAT	Q91303 rattus norv	187	66	10.2	432	2	Q5BC72_EMENI	Q5bc72_aspergillus
115	68.5	10.6	424	1	VDR_BOVIN	Q28037 bos taurus	188	66	10.2	452	2	Q5UCM5_ORYSA	Q5ucm5_oncorhynch
116	68.5	10.6	427	1	VDR_HUMAN	P11473 homo sapien	189	66	10.2	454	2	Q98SW7_ONCMY	Q98sw7_oncorhynch
117	68.5	10.6	427	1	VDR_SAGOE	Q95mh5 seguinus oe	190	66	10.2	551	2	Q5VP90_ORYSA	Q5vp90_oryza sativ
118	68.5	10.6	473	2	Q5U626_HUMAN	Q5u626 homo sapien	191	66	10.2	558	2	Q32SR8_BRARE	Q32s8r brachydanio
119	68.5	10.6	647	1	VE1_HPV40	P36727 human papil	192	66	10.2	577	2	Q7T0V3_XENLA	Q7t0v3 xenopus lae
120	68.5	10.6	1006	2	P73012_SYNY3	P73012 synechocyst	193	66	10.2	736	2	Q3TYB3_MOUSE	Q3tyb3 mus musculus
121	68.5	10.6	1168	2	Q60XC0_CAEBR	Q60xc0 caenorhabdi	194	66	10.2	799	2	Q95P95_CRAGI	Q95p95_crassostrea
122	68.5	10.6	1186	2	Q553F8_DICDI	Q553f8 dictyosteli	195	66	10.2	1034	2	Q4P583_USTMA	Q4p583_ustilago ma
123	68	10.6	189	2	Q93IU7_922Z	Q93iu7 uncultured	196	66	10.2	116	2	Q7SP44_ALV	Q7sp44_avian leuko
124	68	10.6	209	2	Q683L7_HYDMA	Q683l7 hydra magni	197	66	10.2	182	2	Q4D179_TRYCR	Q4d179_trypanosoma
125	68	10.6	283	2	Q43508_LYCES	Q43508 lycopersico	198	66	10.2	1535	1	JAD1D_PANTR	Q5xun4_pan troglod
126	68	10.6	291	2	Q91AK3_XENLA	Q91ak3 xenopus lae	199	66	10.2	1539	1	JAD1D_HUMAN	Q9y966_homo sapien
127	68	10.6	482	2	Q49BF8_SCHMD	Q49bf8 schmidtea m	200	66	10.2	3135	2	Q813B5_PLAF7	Q813b5_plasmodium
128	68	10.6	539	2	Q9XHV3_ORYSA	Q9xhv3_oryza sativ	201	65.5	10.2	116	2	Q9D2T8_MOUSE	Q9d2t8 mus musculus
129	68	10.6	559	2	Q4J5V9_AZOVI	Q4j5v9 azotobacter	202	65.5	10.2	156	2	Q7SP44_ALV	Q7sp44_avian leuko
130	68	10.6	618	2	Q60K76_CAEBR	Q60k76 caenorhabdi	203	65.5	10.2	182	2	Q4D179_TRYCR	Q4d179_trypanosoma
131	68	10.6	773	2	Q6C1L1_ERWCT	Q6cyl1 erwinia car	204	65.5	10.2	279	2	Q47GP0_DECAR	Q47gp0_dechloromon
132	68	10.6	914	2	Q40UV8_KINRA	Q40uv8 kinococcus	205	65.5	10.2	326	2	Q8BNG8_MOUSE	Q8bng8 mus musculus
133	67.5	10.5	1343	2	Q65W9X_ORYSA	Q65w9x_oryza sativ	206	65.5	10.2	353	2	Q2PCF0_CUPSA	Q2pcf0_cupienius
134	67.5	10.5	158	2	Q52VK1_CIOIN	Q52vk1 ciona intes	207	65.5	10.2	397	2	Q91720_XENLA	Q91720 xenopus lae
135	67.5	10.5	199	2	Q61GJ3_DROME	Q61gj3 drosophila	208	65.5	10.2	413	2	Q9KTP1_VIBCH	Q9ktp1_vibrio chol
136	67.5	10.5	211	2	Q447Z5_SOLUS	Q447z5 solibacter	209	65.5	10.2	425	2	Q31B74_PAROL	Q31b74_paralichthy
137	67.5	10.5	262	2	Q60U59_CAEBR	Q60u59 caenorhabdi	210	65.5	10.2	638	2	Q3M224_9DELIT	Q3m224_syntrophoba
138	67.5	10.5	374	2	Q5DVI8_CYPCA	Q5dvi8 cyprinus ca	211	65.5	10.2	646	1	VE1_HPV07	Q05133_human papil
139	67.5	10.5	439	2	Q671M5_9HYFL	Q671m5 chlorella v	212	65.5	10.2	679	2	Q60UD9_CAEBR	Q60ud9_caenorhabdi
140	67.5	10.5	443	2	Q86GV5_BRAFL	Q86gv5 brachioosto	213	65.5	10.2	706	2	F2ZD6_HUMAN	Q60353_homo sapien
141	67.5	10.5	453	2	Q9PTN2_BRARE	Q9ptn2 brachydanio	214	65.5	10.2	706	2	Q6N0A5_HUMAN	Q6n0a5_homo sapien
142	67.5	10.5	454	2	Q52V43_CIOIN	Q52v43 ciona intes	215	65.5	10.2	707	2	Q8WXR9_HUMAN	Q8wxr9_homo sapien
143	67.5	10.5	473	2	Q75CK9_ASHGO	Q75ck9 ashbya goss	216	65.5	10.2	711	2	Q338K3_ORYSA	Q338k3_oryza sativ
144	67.5	10.5	567	2	Q7X2R0_XENLA	Q7x2r0 xenopus lae	217	65.5	10.2	712	1	F2ZD6_CANPA	Q8wmus_canis famli
145	67.5	10.5	672	2	Q4FYC7_LEIMA	Q4fyc7 leishmania	218	65.5	10.2	768	2	Q629D7_CAEBR	Q629d7_caenorhabdi
146	67	10.4	1069	2	Q9BP82_BOMMO	Q9bp82 bombyx mori	219	65.5	10.2	1218	2	Q5H8C5_COPCI	Q5h8c5_coprinus ci
147	67	10.4	331	2	Q4KRX6_CRAVI	Q4kxr6 crassostrea	220	65.5	10.2	1428	2	Q6L634_COPCI	Q6l634_coprinus ci
148	67	10.4	376	1	CPR2_AEATH	Q91xw3 arabidopsis	221	65.5	10.2	1497	2	Q86BF5_DROME	Q86bf5_drosophila
149	67	10.4	452	2	Q3UMM8_MOUSE	Q3umm8 mus musculus	222	65.5	10.2	2087	2	Q86BF6_DROME	Q86bf6_drosophila
150	67	10.4	454	2	Q8QGE2_SALSA	Q8qge2 salmo salar	223	65.5	10.2	2111	1	GLT1_SCHPO	Q9c102_schizosacch
151	67	10.4	529	1	HUTM_BACSU	P42087 bacillus su	224	65	10.1	142	2	Q43F42_9CHLB	Q43f42_chlorobium
152	67	10.4	537	2	Q55KG5_CRYNE	Q9ulm2 homo sapien	225	65	10.1	150	2	Q2XSW8_SESIN	Q2xsw8_sesamum ind
153	67	10.4	743	2	Q83111_ADEMI	Q55kg5 cryptococcu	226	65	10.1	152	2	Q9H807_HUMAN	Q9h8q7_homo sapien
154	67	10.4	1062	1	INVS_MOUSE	Q83111 murine aden	227	65	10.1	155	2	Q9JKG2_MUSCR	Q9jkg2_mus caroli
155	66.5	10.3	103	2	Q9YCC2_AERPE	Q9yc22 aeropyrum p	228	65	10.1	251	2	Q526R3_ORYSA	Q526r3_oryza sativ
156	66.5	10.3	155	2	Q4WIY8_ASPFU	Q4wiy8 aspergillus	229	65	10.1	345	2	P79353_HORSE	Q00446_colletotric
157	66.5	10.3	297	2	Q5N8V8_ORYSA	Q5n8v8_oryza sativ	230	65	10.1	363	1	PLGL1_COLLN	P15627_soybean chl
158	66.5	10.3	304	2	Q5NKR5_AZOSE	Q5nkr5 azoarcus ap	231	65	10.1	441	1	COAT_SOCMV	Q82r20_mus musculus
159	66.5	10.3	368	2	Q2XIA1_PSEPU	Q2xial pseudomonas	232	65	10.1	450	2	Q8R250_MOUSE	Q8r250_mus musculus
160	66.5	10.3	398	2	Q74LP3_LACJO	Q74lp3 lactobacilli	233	65	10.1	563	2	Q2QTR1_ORYSA	Q2qtr1_oryza sativ
161	66.5	10.3	407	2	Q54TF7_DICDI	Q54tf7 dictyosteli	234	65	10.1	564	2	Q3UJY9_MOUSE	Q3ujy9_mus musculus
162	66.5	10.3	419	2	Q626M1_RAT	Q626m1 rattus norv	235	65	10.1	574	2	Q3UKZ9_MOUSE	Q3ukz9_m_blastocys
163	66.5	10.3	420	2	Q32NY6_MOUSE	Q32ny6 mus musculus	236	65	10.1	594	2	Q5R8L9_PONPY	Q5r8l9_pongo pygma
164	66.5	10.3	422	1	COT1_MOUSE	Q60632 mus musculus	237	65	10.1	623	1	Q3UJ62_MOUSE	Q3uj62_mus musculus
165	66.5	10.3	422	2	COT1_MOUSE	Q60632 mus musculus	238	65	10.1	623	2	ASH2L_MOUSE	Q91x20_mus musculus
166	66.5	10.3	423	1	COT1_HUMAN	Q91430 brachydanio	239	65	10.1	623	2	Q3UIF9_MOUSE	Q3uif9_mus musculus
167	66.5	10.3	424	1	COT1_BOVIN	P10589 homo sapien	240	65	10.1	678	1	ASH2L_HUMAN	Q9ub13_homo sapien
168	66.5	10.3	444	2	Q2TCL1_CHICK	Q9trt8 bos taurus	241	65	10.1	682	2	Q9VLG5_DROME	Q9vlg5_drosophila
169	66.5	10.3	552	2	Q4DZ60_TRYCR	Q2tcl1 gallus gall	242	65	10.1	715	2	Q4DLG2_TRYCR	Q4dlg2_trypanosoma
170	66.5	10.3	571	2	Q2LZ77_DROPS	Q4dz60 trypanosoma	243	65	10.1	878	2	Q7NXY3_CHRVO	Q7nxy3_chromobacte
171	66.5	10.3	579	2	Q6NZC6_MOUSE	Q2l277 drosophila	244	65	10.1	1064	1	JMW2A_PONPY	Q5td88_pongo pygma
172	66.5	10.3	606	2	Q3RVF4_RALME	Q6nzc6 mus musculus	245	65	10.1	1096	1	PHF2_MOUSE	Q9wtu0_mus musculus
173	66.5	10.3	731	2	Q7Z4S7_HUMAN	Q3rvf4 ralstonia m	246	65	10.1	1096	2	Q4VXB9_HUMAN	Q4vxb9_homo sapien
174	66.5	10.3	746	2	Q4REU2_TETNG	Q7z4s7 homo sapien	247	65	10.1	1101	1	PHF2_HUMAN	Q75151_homo sapien
175	66.5	10.3	777	2	Q8BV42_MOUSE	Q4reu2 tetraodon n	248	64.5	10.0	30	2	Q9S871_MOMCH	Q9s871_monordica c
176	66.5	10.3	1020	2	Q2CMX9_ORYSA	Q8bv42 mus musculus	249	64.5	10.0	46	2	Q42535_BRARE	Q42535_brachydanio
177	66.5	10.3	1043	2	Q4IKM0_GIBZE	Q2cmx9_oryza sativ	250	64.5	10.0	81	1	LCR41_ARATH	P82756_arabidopsis

251	64.5	10.0	121	2	Q4TFN0_TETNG	Q4tfn0 tetraodon n	324	63.5	9.9	456	2	Q4HT9_CIOIN	Q4ht29 ciona intes
252	64.5	10.0	140	2	Q8L694_MOMCH	Q8l694 momordica c	325	63.5	9.9	464	2	Q5VT39_HUMAN	Q5vt39 homo sapien
253	64.5	10.0	161	2	Q8T8D3_BOMMO	Q8t8d3 bombyx mori	326	63.5	9.9	464	2	Q96BR6_HUMAN	Q96br6 homo sapien
254	64.5	10.0	227	1	CPSP5_BOVIN	CPsp5 bos taurus	327	63.5	9.9	464	2	Q9H9Q6_HUMAN	Q9h9q6 homo sapien
255	64.5	10.0	227	1	CPSP5_HUMAN	Q3zca2 bos taurus	328	63.5	9.9	570	2	Q9DLK5_ALV	Q9dlk5 avian leuko
256	64.5	10.0	227	1	CPSP5_HUMAN	Q43809 h cleavage	329	63.5	9.9	625	2	Q4F6E6_USTMA	Q4f6e6 ustilago ma
257	64.5	10.0	227	1	CPSP5_PONPY	Q9cqi3 mus musculus	330	63.5	9.9	762	2	Q4R497_MACFA	Q4r497 macaca fasc
258	64.5	10.0	227	1	CPSP5_RAT	Q5rai8 pongo pygma	331	63.5	9.9	912	2	Q4E2Q6_TRYCR	Q4e2q6 trypanosoma
259	64.5	10.0	230	2	Q3LZT2_LEICH	Q3lzt2 leishmania	332	63.5	9.9	927	2	Q6Z635_ORYSA	Q6z635 oryza sativ
260	64.5	10.0	251	2	Q50J67_BRARE	Q50j67 brachydanio	333	63.5	9.9	1040	2	Q699V1_SIVCZ	Q699v1 chimpanzee
261	64.5	10.0	277	2	Q93863_MYCCE	Q93863 mycobacteri	334	63.5	9.9	1100	2	Q3JU50_BURP1	Q3ju50 burkholderi
262	64.5	10.0	359	2	Q23772_CHITE	Q23772 chironomus	335	63.5	9.9	1100	2	Q63VH9_BURPS	Q63vhn9 burkholderi
263	64.5	10.0	369	2	Q3BJL2_MACMU	Q3bjl2 macaca mula	336	63.5	9.9	1136	2	Q604F4_9TELE	Q604f4 sternopygus
264	64.5	10.0	386	2	Q5FNW1_GLUOX	Q5fnw1 gluconobact	337	63.5	9.9	2405	2	Q5T1R5_HUMAN	Q5t1r5 homo sapien
265	64.5	10.0	389	2	Q70VZ9_CIOIN	Q70vz9 ciona intes	338	63.5	9.9	2406	2	Q5T1R4_HUMAN	Q5t1r4 homo sapien
266	64.5	10.0	397	2	Q5DTZ6_MOUSE	Q5dtz6 mus musculus	339	63.5	9.9	2406	2	Q9BZS0_HUMAN	Q9bzso0 homo sapien
267	64.5	10.0	419	2	Q7QXL3_GIALA	Q7qxl3 giardia lam	340	63.5	9.9	2414	2	Q9HCL7_HUMAN	Q9hcl7 homo sapien
268	64.5	10.0	421	2	Q9G9A9_BOMMO	Q9g9a9 bombyx mori	341	63	9.8	146	2	Q58L11_9CAUD	Q58l11 cyanophage
269	64.5	10.0	431	2	Q8U5W7_AGR75	Q8u5w7 agrobacteri	342	63	9.8	160	1	ECF_PANTR	P47780 pan troglod
270	64.5	10.0	499	2	Q4RTT7_TETNG	Q4rtt7 tetraodon n	343	63	9.8	174	2	Q95LE0_CANFA	Q95le0 canis famli
271	64.5	10.0	530	2	Q5D5L4_ALV	Q5d5l4 avian leuko	344	63	9.8	244	2	Q8AVH6_XENLA	Q8avh6 xenopus lae
272	64.5	10.0	534	1	ZN397_HUMAN	Q8nf99 homo sapien	345	63	9.8	244	2	Q9PMD9_XENLA	Q9pmd9 xenopus lae
273	64.5	10.0	615	2	Q7XG33_ORYSA	Q7xg33 oryza sativ	346	63	9.8	245	2	Q5FYZ2_BRARE	Q5fyz2 brachydanio
274	64.5	10.0	615	2	Q94I17_ORYSA	Q94i17 oryza sativ	347	63	9.8	245	2	Q7T3G8_BRARE	Q7t3g8 brachydanio
275	64.5	10.0	622	1	MAK_MOUSE	Q04859 mus musculus	348	63	9.8	246	1	SIX6_HUMAN	Q95475 homo sapien
276	64.5	10.0	741	2	Q6K9F7_ORYSA	Q6k9f7 oryza sativ	349	63	9.8	246	1	SIX6_HUMAN	Q9qz28 mus musculus
277	64.5	10.0	796	2	Q4TBV7_TETNG	Q4tbv7 tetraodon n	350	63	9.8	246	2	Q6NT42_HUMAN	Q6nt42 homo sapien
278	64.5	10.0	1081	2	Q6AHT3_PNECA	Q6aht3 pneumocysti	351	63	9.8	266	2	Q4SYA8_TETNG	Q4syas8 tetraodon n
279	64.5	10.0	1500	2	Q5TUT2_ANOGA	Q5tut2 anopheles g	352	63	9.8	273	2	Q5WIZ7_BACSK	Q5wiz7 bacillus cl
280	64.5	10.0	1530	2	Q7PRV6_ANOGA	Q7prv6 anopheles g	353	63	9.8	292	2	Q4OOR2_DESAC	Q4oar2 desulfuromo
281	64	9.9	179	2	Q2KM69_STRIN	Q2km69 streptococc	354	63	9.8	298	2	Q5M8S8_HUMAN	Q5m8s8 homo sapien
282	64	9.9	201	2	Q5HXK1_GLUOX	Q5hsk1 gluconobact	355	63	9.8	305	2	Q6P051_HUMAN	Q6p051 homo sapien
283	64	9.9	246	1	SIX6_CHICK	Q93307 gallus gall	356	63	9.8	332	1	SIX3_HUMAN	Q95343 homo sapien
284	64	9.9	260	2	Q2SNZ4_9GAMM	Q2snz4 habella che	357	63	9.8	332	2	Q53T42_HUMAN	Q53t42 homo sapien
285	64	9.9	282	2	Q61D23_CABER	Q61d23 caenorhabdi	358	63	9.8	333	1	SIX3_MOUSE	Q62233 mus musculus
286	64	9.9	317	2	Q31QV7_SYNP7	Q31qv7 synchococc	359	63	9.8	333	2	Q4QQQ3_MOUSE	Q4qqq3 mus musculus
287	64	9.9	317	2	Q5N3D9_SYNP6	Q5n3d9 synchococc	360	63	9.8	337	2	Q9ET75_RAT	Q9et75 rattus norv
288	64	9.9	334	2	Q68119_RHOCA	Q68119 rhodobacter	361	63	9.8	342	2	Q7Z2T4_BUFMA	Q7z2t4 bufo marinu
289	64	9.9	345	2	Q32R13_EPTBU	Q32r13 eptatretus	362	63	9.8	346	2	Q955U6_TRATE	Q955u6 tragopan te
290	64	9.9	357	2	Q3XSB3_9PROT	Q3xsb3 magnetococc	363	63	9.8	347	2	Q52KB8_MOUSE	Q52kb8 mus musculus
291	64	9.9	417	2	Q681B0_ARATH	Q681b0 arabidopsis	364	63	9.8	348	2	Q343V0_RHOFA	Q343v0 rhodopseudo
292	64	9.9	418	2	Q67ZU1_ARATH	Q67zu1 arabidopsis	365	63	9.8	371	1	RAD14_YEAST	P28519 saccharomyc
293	64	9.9	431	2	Q6LUA2_PHOPR	Q6lua2 photobacter	366	63	9.8	376	2	Q8LAC2_ARATH	Q8lac2 arabidopsis
294	64	9.9	454	2	Q6SES0_SALSA	Q6ses0 salmo salar	367	63	9.8	377	2	Q3UQ14_MOUSE	Q3uq14 mus musculus
295	64	9.9	472	2	Q5WNE1_CABER	Q5wne1 caenorhabdi	368	63	9.8	395	2	Q98DM3_RHTLO	Q98dm3 rhizobium l
296	64	9.9	540	2	Q8XHG9_CLOPE	Q8xhg9 clostridium	369	63	9.8	413	2	Q2PQ08_GLOMR	Q2pq08 glossina mo
297	64	9.9	552	2	Q4SAQ4_TETNG	Q4saq4 tetraodon n	370	63	9.8	447	2	Q8NZL6_HUMAN	Q8nzl6 homo sapien
298	64	9.9	811	2	Q8S7P4_ORYSA	Q8s7p4 oryza sativ	371	63	9.8	453	2	Q304A5_ARATH	Q304a5 arabidopsis
299	64	9.9	856	2	Q3POM6_NITHA	Q3pom6 nitrobacter	372	63	9.8	462	2	Q49674_ARATH	Q49674 arabidopsis
300	64	9.9	915	2	Q75G97_ORYSA	Q75g97 oryza sativ	373	63	9.8	464	2	Q7FAG5_ORYSA	Q7fag5 oryza sativ
301	64	9.9	952	2	Q5KBF3_CRYNE	Q5kbf3 cryptococcu	374	63	9.8	464	2	Q9JQJ3_MOUSE	Q9jqj3 mus musculus
302	64	9.9	1290	2	Q4DIT1_TRYCR	Q4dit1 trypanosoma	375	63	9.8	473	2	Q60SZ8_CABER	Q60sz8 caenorhabdi
303	64	9.9	2040	2	Q4S5I1_TETNG	Q4s5i1 tetraodon n	376	63	9.8	475	2	Q4SCV3_TETNG	Q4scv3 tetraodon n
304	63.5	9.9	215	2	Q8N930_HUMAN	Q8n930 homo sapien	377	63	9.8	488	2	Q8VS81_PARVE	Q8vs81 paracoccus
305	63.5	9.9	218	2	Q69CH9_9VIRU	Q69ch9 infectious	378	63	9.8	490	2	Q9XEV7_ORYSA	Q9xev7 oryza sativ
306	63.5	9.9	218	2	Q69C12_9VIRU	Q69c12 infectious	379	63	9.8	493	2	Q9BMU6_AEDAE	Q9bmue6 aedes aegyp
307	63.5	9.9	223	2	Q3EDS5_ARATH	Q3eds5 arabidopsis	380	63	9.8	509	2	Q7OCB4_ANOGA	Q7ocb4 anopheles g
308	63.5	9.9	233	2	Q42672_CARPA	Q42672 carica papa	381	63	9.8	536	2	Q5SBA8_DICDI	Q5sba8 dictyosteli
309	63.5	9.9	262	1	UTP11_CABEL	Q09462 caenorhabdi	382	63	9.8	556	2	Q36EAB_9GAMM	Q36eab shewanella
310	63.5	9.9	303	2	Q2UBY6_ASPOR	Q2uby6 aspergillus	383	63	9.8	603	1	FBX46_MOUSE	Q8bg80 mus musculus
311	63.5	9.9	315	2	Q8UW70_XENLA	Q8uw70 xenopus lae	384	63	9.8	603	2	Q4KLY2_RAT	Q4kly2 rattus norv
312	63.5	9.9	326	1	ZN773_HUMAN	Q43830 homo sapien	385	63	9.8	646	1	FBX46_HUMAN	Q6p161 homo sapien
313	63.5	9.9	334	2	Q6NTM2_XENLA	Q6ntm2 xenopus lae	386	63	9.8	689	2	Q583T7_9TRYP	Q583t7 trypanosoma
314	63.5	9.9	335	2	Q4V7Y2_XENOPUS	Q4v7y2 xenopus lae	387	63	9.8	721	2	Q4SQB3_TETNG	Q4sqb3 tetraodon n
315	63.5	9.9	342	2	Q61580_DROSL	Q61580 drosophila	388	63	9.8	954	2	Q7RZU4_NEUCR	Q7rrzu4 neurospora
316	63.5	9.9	343	2	Q5GVW7_XANOR	Q5gvw7 xanthomonas	389	63	9.8	972	1	PARG_RAT	Q9qym2 rattus norv
317	63.5	9.9	350	2	Q3KDP9_XENLA	Q3kdp9 xenopus lae	390	63	9.8	1068	2	Q69ZG6_MOUSE	Q69zge6 mus musculus
318	63.5	9.9	361	2	Q8FED6_ECUL6	Q8fed6 escherichia	391	63	9.8	1120	2	Q7XNT5_ORYSA	Q7xnt5 oryza sativ
319	63.5	9.9	378	2	Q5VT38_HUMAN	Q5vt38 homo sapien	392	63	9.8	1175	2	Q4RER3_TETNG	Q4rer3 tetraodon n
320	63.5	9.9	391	2	Q3GRG2_9GAMM	Q3grg2 psychrobact	393	63	9.8	1650	2	Q4DB09_TRYCR	Q4db09 trypanosoma
321	63.5	9.9	397	2	Q4PSE7_ARATH	Q4pse7 arabidopsis	394	63	9.8	2096	2	Q2R0G5_ORYSA	Q2r0g5 oryza sativ
322	63.5	9.9	404	2	Q6P115_BRARE	Q6p115 brachydanio	395	62.5	9.7	116	2	Q8C336_MOUSE	Q8c336 mus musculus
323	63.5	9.9	454	2	Q6Q247_CHICK	Q6q247 gallus gall	396	62.5	9.7	119	2	Q9DAL9_MOUSE	Q9dal9 mus musculus

397	62.5	9.7	148	2	Q6H5T8_ORYSA	Q6H5T8	oryza sativ	470	62	9.6	297	2	Q5B1S4_EMENI	Q5B1S4	aspergillus
398	62.5	9.7	156	1	RNAS7_HUMAN	Q9H1E1	homo sapien	471	62	9.6	310	2	Q3H4L3_9ACTO	Q3H4L3	nocardioides
399	62.5	9.7	156	2	Q546N3_HUMAN	Q546N3	homo sapien	472	62	9.6	316	2	Q39D11_BURS3	Q39D11	burkholderi
400	62.5	9.7	191	2	Q89KH5_BRAJA	Q89KH5	bradyrhizob	473	62	9.6	332	2	Q5F3E3_CHICK	Q5F3E3	gallus gall
401	62.5	9.7	192	2	Q8VJR4_MYCTU	Q8VJR4	mycobacteri	474	62	9.6	332	2	Q8HHF1_9TYRA	Q8HHF1	pachyrhampu
402	62.5	9.7	202	2	Q5BYW7_SCHJA	Q5BYW7	schistosoma	475	62	9.6	332	2	Q8HHF2_9TYRA	Q8HHF2	tityra caya
403	62.5	9.7	218	2	Q621H9_BURMA	Q621H9	burkholderi	476	62	9.6	346	2	Q392V2_BURS3	Q392V2	burkholderi
404	62.5	9.7	221	2	Q4SSA9_TETNG	Q4SSA9	tetradodon n	477	62	9.6	346	2	Q958E3_TINMA	Q958E3	tinamus maj
405	62.5	9.7	223	2	Q5D9Q3_SCHJA	Q5D9Q3	schistosoma	478	62	9.6	371	1	RN02_YEAST	RN02	saccharomyc
406	62.5	9.7	227	1	CPSP5_XENLA	Q6JFE4	xenopus lae	479	62	9.6	390	2	Q6LGC9_POPR	Q6LGC9	photobacter
407	62.5	9.7	228	1	CPSP5_XENLA	Q7C3C6	brachydanio	480	62	9.6	464	2	Q5WN10_CABBR	Q5WN10	caenorhabdi
408	62.5	9.7	229	2	Q4SIH0_TETNG	Q4SIH0	tetradodon n	481	62	9.6	488	2	Q7R740_PLAYO	Q7R740	plasmodium
409	62.5	9.7	259	2	Q8KW83_9RHOB	Q8KW83	ruesgeria sp	482	62	9.6	519	2	Q4R6H6_NACFA	Q4R6H6	macaca fasc
410	62.5	9.7	292	2	Q82PK3_STRAW	Q82PK3	streptomyce	483	62	9.6	559	2	Q3UP18_MOUSE	Q3UP18	mus musculus
411	62.5	9.7	326	2	Q84NF7_9CONI	Q84NF7	callitropi	484	62	9.6	559	2	Q31WM0_MOUSE	Q31WM0	mus musculus
412	62.5	9.7	326	2	Q4QRA0_RAT	Q4QRA0	rattus norv	485	62	9.6	564	2	Q3P2U9_9GAMM	Q3P2U9	shewanella
413	62.5	9.7	326	2	Q8C882_MOUSE	Q8C882	mus musculus	486	62	9.6	567	2	Q2UUM4_ASPOR	Q2UUM4	aspergillus
414	62.5	9.7	326	2	Q9DCJ1_MOUSE	Q9DCJ1	m adult mal	487	62	9.6	577	1	NR4A2_XENLA	NR4A2	xenopus lae
415	62.5	9.7	326	2	Q9JJK6_MOUSE	Q9JJK6	mus musculus	488	62	9.6	577	1	Q61NV4_XENLA	Q61NV4	xenopus lae
416	62.5	9.7	326	2	Q922K5_RAT	Q922K5	rattus norv	489	62	9.6	587	2	Q5KNM4_CRYNE	Q5KNM4	cryptococu
417	62.5	9.7	328	2	Q59V90_CANAL	Q59V90	candida alb	490	62	9.6	587	2	Q322X6_MOUSE	Q322X6	mus musculus
418	62.5	9.7	339	2	Q7YRQ3_BOVIN	Q7YRQ3	bos taurus	491	62	9.6	655	2	Q2R0U5_ORYSA	Q2R0U5	oryza sativ
419	62.5	9.7	340	2	Q3WEG6_9ACTO	Q3WEG6	frankia sp.	492	62	9.6	728	2	Q06054_MOUSE	Q06054	mus musculus
420	62.5	9.7	355	2	Q9CVN0_MOUSE	Q9CVN0	mus musculus	493	62	9.6	782	2	Q4CQL3_TRYCR	Q4CQL3	trypanosoma
421	62.5	9.7	366	2	Q8WT79_9NEOP	Q8WT79	chimarra ro	494	62	9.6	803	2	Q4CNG7_TRYCR	Q4CNG7	trypanosoma
422	62.5	9.7	367	2	Q8BWF5_MOUSE	Q8BWF5	mus musculus	495	62	9.6	803	2	Q4CUS4_TRYCR	Q4CUS4	trypanosoma
423	62.5	9.7	388	2	Q6POE6_BRARE	Q6POE6	brachydanio	496	62	9.6	817	2	Q5DZB6_VIBF1	Q5DZB6	vibrio fusc
424	62.5	9.7	389	2	Q6PH18_BRARE	Q6PH18	brachydanio	497	62	9.6	954	2	Q6AWQ1_DROME	Q6AWQ1	drosophila
425	62.5	9.7	404	2	Q6DCH6_XENLA	Q6DCH6	xenopus lae	498	62	9.6	954	2	Q9VU43_DROME	Q9VU43	drosophila
426	62.5	9.7	410	1	COT2_CHICK	Q97073	gallus gall	499	62	9.6	1161	2	Q7EYV1_ORYSA	Q7EYV1	oryza sativ
427	62.5	9.7	414	1	COT2_BOVIN	Q9T1T7	bos taurus	500	62	9.6	1483	2	Q9VB40_DROME	Q9VB40	drosophila
428	62.5	9.7	414	1	COT2_HUMAN	P24468	homo sapien	501	62	9.6	1483	2	Q5C6F9_ARATH	Q5C6F9	arabidopsis
429	62.5	9.7	414	1	COT2_MOUSE	Q9018	mus musculus	502	62	9.6	1670	1	CO4A3_HUMAN	CO4A3	homo sapien
430	62.5	9.7	414	1	COT2_RAT	Q9018	rattus norv	503	62	9.6	2098	2	Q3QG46_9GAMM	Q3QG46	shewanella
431	62.5	9.7	414	1	Q3UST6_MOUSE	Q3UST6	mus musculus	504	62	9.6	2135	2	Q4SZ58_TETNG	Q4SZ58	tetradodon n
432	62.5	9.7	419	2	Q9KRY3_VIBCH	Q9KRY3	vibrio chol	505	62	9.6	3026	2	Q26030_PLAFA	Q26030	plasmodium
433	62.5	9.7	420	2	Q6H817_SALSA	Q6H817	salmo salar	506	62	9.6	4796	2	Q4Q363_LEIMA	Q4Q363	leishmania
434	62.5	9.7	420	2	Q91B71_PAROL	Q91B71	paralichthy	507	61.5	9.5	107	2	Q37U65_SPHAR	Q37U65	novosphingo
435	62.5	9.7	440	2	Q46W12_RALEJ	Q46W12	raistonia e	508	61.5	9.5	115	2	Q2XSV6_GEMI	Q2XSV6	tomato yell
436	62.5	9.7	450	2	Q8BW19_MOUSE	Q8BW19	mus musculus	509	61.5	9.5	122	2	Q3QJN5_9GAMM	Q3QJN5	shewanella
437	62.5	9.7	450	2	Q8C178_MOUSE	Q8C178	mus musculus	510	61.5	9.5	127	2	Q7XZ60_GRIJA	Q7XZ60	griffithsia
438	62.5	9.7	472	2	Q3WE50_9ACTO	Q3WE50	frankia sp.	511	61.5	9.5	138	2	Q3ENG5_BACTI	Q3ENG5	bacillus th
439	62.5	9.7	550	2	Q4D876_TRYCR	Q4D876	trypanosoma	512	61.5	9.5	167	2	Q6Q2J3_XENLA	Q6Q2J3	xenopus lae
440	62.5	9.7	550	2	Q8CDL5_MOUSE	Q8CDL5	mus musculus	513	61.5	9.5	169	2	Q89G37_BRAJA	Q89G37	bradyrhizob
441	62.5	9.7	563	2	Q4ASA4_BACFR	Q4ASA4	bacteroides	514	61.5	9.5	201	2	Q4P089_USTMA	Q4P089	ustilago ma
442	62.5	9.7	565	2	Q3KQV3_HUMAN	Q3KQV3	homo sapien	515	61.5	9.5	209	2	Q8RG09_9VIRU	Q8RG09	hyposoter d
443	62.5	9.7	720	2	Q9N003_MACFA	Q9N003	macaca fasc	516	61.5	9.5	219	2	Q5VYT7_HUMAN	Q5VYT7	homo sapien
444	62.5	9.7	752	2	Q61V72_HUMAN	Q61V72	homo sapien	517	61.5	9.5	239	2	Q53K64_ORYSA	Q53K64	oryza sativ
445	62.5	9.7	766	2	Q6P0Z1_BRARE	Q6P0Z1	brachydanio	518	61.5	9.5	243	2	Q5L4A0_9FLAV	Q5L4A0	cy1014 viru
446	62.5	9.7	766	2	Q6TELS_BRARE	Q6TELS	brachydanio	519	61.5	9.5	253	2	Q5U3Z5_RAT	Q5U3Z5	rattus norv
447	62.5	9.7	840	2	Q19777_CAEEL	Q19777	caenorhabdi	520	61.5	9.5	300	2	Q7MBY5_BORPA	Q7MBY5	bordetella
448	62.5	9.7	982	2	Q4D985_TRYCR	Q4D985	trypanosoma	521	61.5	9.5	300	2	Q7WPI1_BORBR	Q7WPI1	bordetella
449	62.5	9.7	1026	2	Q6PFI5_BRARE	Q6PFI5	brachydanio	522	61.5	9.5	300	2	Q7T3B4_BRARE	Q7T3B4	brachydanio
450	62.5	9.7	1060	2	Q3SPX7_9BRAD	Q3SPX7	bradyrhizob	523	61.5	9.5	306	2	Q2TV48_BABBO	Q2TV48	babesia bov
451	62.5	9.7	1232	2	Q41ZHO_AZOVI	Q41ZHO	azotobacter	524	61.5	9.5	326	2	Q803V5_BRARE	Q803V5	brachydanio
452	62.5	9.7	1612	2	Q416D6_GIBZE	Q416D6	gibberella	525	61.5	9.5	347	2	Q58BR6_BRARE	Q58BR6	brachydanio
453	62.5	9.7	1614	2	Q3ZTP0_MICMU	Q3ZTP0	microcebus	526	61.5	9.5	352	2	Q58DN5_BOVIN	Q58DN5	bos taurus
454	62.5	9.7	2038	2	Q4E222_TRYCR	Q4E222	trypanosoma	527	61.5	9.5	361	2	Q8UYW1_GEMI	Q8UYW1	squash leaf
455	62.5	9.7	2282	2	Q6SNP9_MOUSE	Q6SNP9	mus musculus	528	61.5	9.5	369	1	IL2RG_HUMAN	IL2RG	homo sapien
456	62	9.6	48	2	Q53RM8_HUMAN	Q53RM8	homo sapien	529	61.5	9.5	382	2	Q4I0P5_GIBZE	Q4I0P5	gibberella
457	62	9.6	88	2	Q9TF10_ARATH	Q9TF10	arabidopsis	530	61.5	9.5	398	2	Q5MGH5_LONON	Q5MGH5	lonomia obl
458	62	9.6	93	2	Q61IG3_DROME	Q61IG3	drosophila	531	61.5	9.5	398	2	Q8A3G3_BACTN	Q8A3G3	bacteroides
459	62	9.6	135	2	Q6FFY4_ACIAD	Q6FFY4	acinetobact	532	61.5	9.5	401	2	Q50QJ0_ENTHI	Q50QJ0	entamoeba h
460	62	9.6	147	2	Q5UI18_HORVD	Q5UI18	hordeum vul	533	61.5	9.5	403	1	NR2F5_BRARE	NR2F5	brachydanio
461	62	9.6	157	2	Q61TX2_CABBR	Q61TX2	caenorhabdi	534	61.5	9.5	431	2	Q49155_MAIZE	Q49155	zea mays (m
462	62	9.6	192	2	Q7PL04_ANOGA	Q7PL04	anopheles g	535	61.5	9.5	432	2	Q49154_MAIZE	Q49154	zea mays (m
463	62	9.6	210	2	Q61I77_DROME	Q61I77	drosophila	536	61.5	9.5	441	2	Q5MQC6_9COCO	Q5MQC6	human coron
464	62	9.6	211	2	Q6V277_9BACT	Q6V277	symbiont ba	537	61.5	9.5	464	2	Q8GR22_ORYSA	Q8GR22	oryza sativ
465	62	9.6	217	1	GP111_CANGA	Q6F2D7	candida gla	538	61.5	9.5	537	2	Q4J5M5_AZOVI	Q4J5M5	azotobacter
466	62	9.6	226	2	Q5BXH7_SCHJA	Q5BXH7	schistosoma	539	61.5	9.5	545	1	ZNF77_HUMAN	ZNF77	homo sapien
467	62	9.6	235	2	Q22621_CAEEL	Q22621	caenorhabdi	540	61.5	9.5	581	2	Q5V7Y6_HALMA	Q5V7Y6	haloarcula
468	62	9.6	284	2	Q2ULB0_ASPOR	Q2ULB0	aspergillus	541	61.5	9.5	605	2	Q4HW21_GIBZE	Q4HW21	gibberella
469	62	9.6	293	2	Q73709_BRARE	Q73709	brachydanio	542	61.5	9.5	623	1	VEIN_DROME	VEIN	drosophila

543	61.5	9.5	623	2	Q59E20_DROME	Q59e20 drosophila	616	61	9.5	392	2	Q4PB11_USTMA	Q4pb11 ustilago ma
544	61.5	9.5	690	2	Q3WSA6_9RHIZ	Q3wsa6 mesorhizobi	617	61	9.5	398	2	Q7AB12_ECO57	Q7ab12 escherichia
545	61.5	9.5	696	2	Q3UVG7_MOUSE	Q3uv7 mus musculus	618	61	9.5	402	2	Q5QZP3_IDILO	Q5qzp3 idiomarina
546	61.5	9.5	774	2	Q3PEE8_PARDE	Q3pee8 paracoccus	619	61	9.5	416	2	Q4IQV6_GIBZE	Q4iqv6 gibberella
547	61.5	9.5	789	2	Q5NNC3_ZYMO	Q5nnc3 zymononas m	620	61	9.5	429	2	Q14401_SCLSC	Q14401 sclerotinia
548	61.5	9.5	808	2	Q3JHW2_BURP1	Q3jhw2 burkholderi	621	61	9.5	432	2	Q4S157_MAZE	Q4s157 zea mays m
549	61.5	9.5	809	2	Q8CA82_MOUSE	Q8ca82 mus musculus	622	61	9.5	457	2	Q2JHA8_9CYAN	Q2jha8 cyanobacter
550	61.5	9.5	864	1	ADA15_MOUSE	Q8ca82 mus musculus	623	61	9.5	458	1	Q2N275_HUMAN	Q9fr44 arabidopsis
551	61.5	9.5	864	2	Q3UE21_MOUSE	Q3ue21 m bone marr	624	61	9.5	491	1	PEAM1_ARATH	Q73np5 treponema d
552	61.5	9.5	864	2	Q3UE21_MOUSE	Q3ue21 mus musculus	625	61	9.5	495	2	Q73NP5_TREDE	Q4QX22 leishmania
553	61.5	9.5	866	2	Q6F352_ORYSA	Q6f352 oryza sativ	626	61	9.5	520	2	Q4QX22_LEIMA	Q4qxc6 caenorhabdi
554	61.5	9.5	874	2	Q6DC11_XENLA	Q6dc11 xenopus lae	627	61	9.5	536	2	Q9XTC6_CAEEL	Q3nms shewanella
555	61.5	9.5	900	2	Q4IXJ0_AZOVI	Q4ixj0 azotobacter	628	61	9.5	542	2	Q3NNU8_SHEFR	Q8ekj5 shewanella
556	61.5	9.5	983	1	NBRI_RAT	Q501r9 rattus norv	629	61	9.5	556	1	HUTU_SHEON	Q361w0 shewanella
557	61.5	9.5	1118	2	Q7Y006_ORYSA	Q7y006 oryza sativ	630	61	9.5	556	2	Q4JUV5_TETNG	Q4rjv5 tetraodon n
558	61.5	9.5	2035	2	Q4DZF1_TRYCR	Q4dzf1 trypanosoma	631	61	9.5	577	2	Q2ZAI8_9GAMM	Q2za18 shewanella
559	61	9.5	95	2	Q6YZ56_ORYSA	Q6yz56 oryza sativ	632	61	9.5	584	2	Q2ZAI8_9GAMM	Q2za18 shewanella
560	61	9.5	119	2	Q3Q442_9GAMM	Q3q442 shewanella	633	61	9.5	593	2	Q8INE2_DROME	Q8ine2 drosophila
561	61	9.5	134	2	Q4WYK2_ASPFU	Q4wyk2 aspergillus	634	61	9.5	621	2	Q5JQV7_ORYSA	Q5jqv7 oryza sativ
562	61	9.5	137	2	Q6VT91_ORYSA	Q6vt91 oryza sativ	635	61	9.5	629	2	Q8IN39_DROME	Q8in39 drosophila
563	61	9.5	153	2	Q9LI15_ARATH	Q9li15 arabidopsis	636	61	9.5	684	2	Q8S2Z8_DROME	Q8s2z8 drosophila
564	61	9.5	158	2	Q3B7G7_BRARE	Q3b7g7 brachydanio	637	61	9.5	746	2	Q8TG17_TALEM	Q8tg17 talaromyces
565	61	9.5	171	2	Q8ERN0_SHEON	Q8ern0 shewanella	638	61	9.5	776	2	Q33AE0_ORYSA	Q33ae0 oryza sativ
566	61	9.5	172	2	Q4IYB4_AZOVI	Q4iyb4 azotobacter	639	61	9.5	784	2	Q7SFE3_NEUCR	Q7sfe3 neurospora
567	61	9.5	181	1	SPL5_ARATH	Q9s758 arabidopsis	640	61	9.5	795	1	DEGY_CAEEL	Q01635 caenorhabdi
568	61	9.5	183	1	GSPH_ABRHY	P31735 aeromonas h	641	61	9.5	820	2	Q4QDA1_LEIMA	Q4qda1 leishmania
569	61	9.5	184	2	Q9VK16_DROME	Q9vk16 drosophila	642	61	9.5	846	2	Q9SUS1_LOCMI	Q9sus1 locusta mig
570	61	9.5	222	2	Q8H4Q5_ORYSA	Q8h4q5 oryza sativ	643	61	9.5	893	2	Q8GCM9_CHRVO	Q8gcm9 chromobacte
571	61	9.5	227	2	Q6YMWZ_ORYSA	Q6ywmz oryza sativ	644	61	9.5	901	2	Q6NZS3_BRARE	Q6nzs3 brachydanio
572	61	9.5	245	2	Q54125_DICDI	Q54125 dictyosteli	645	61	9.5	901	2	Q7ZVY7_BRARE	Q7zvy7 brachydanio
573	61	9.5	255	2	Q9N6L7_DROSI	Q9n6l7 drosophila	646	61	9.5	912	2	Q4SL99_TETNG	Q4sl99 tetraodon n
574	61	9.5	255	2	Q9N6N5_DROSI	Q9n6n5 drosophila	647	61	9.5	961	1	MEI9_DROME	Q24087 drosophila
575	61	9.5	255	2	Q9NGS5_DROSI	Q9ngs5 drosophila	648	61	9.5	1000	2	Q96V19_PNECA	Q96v19 pneumocysti
576	61	9.5	257	2	Q2LL45_BORAV	Q2ll45 bordetella	649	61	9.5	1014	2	Q74673_PNECJ	Q74673 pneumocysti
577	61	9.5	288	2	Q59HE1_HUMAN	Q59hei homo sapien	650	61	9.5	1028	2	Q7Y1N2_ORYSA	Q7y1n2 oryza sativ
578	61	9.5	286	2	Q5JNG1_ORYSA	Q5jng1 oryza sativ	651	61	9.5	1064	1	JMU2A_HUMAN	Q75164 homo sapien
579	61	9.5	301	2	Q7W1H8_BORPA	Q7w1h8 bordetella	652	61	9.5	1068	2	Q5STG3_DROME	Q5stg3 drosophila
580	61	9.5	302	2	Q7WP88_BORBR	Q7wp88 bordetella	653	61	9.5	1092	2	Q4WEI8_ASPFU	Q4wei8 aspergillus
581	61	9.5	308	2	Q5C3G7_SCHJA	Q5c3g7 schistosoma	654	61	9.5	1095	2	Q7RSJ8_PLAVO	Q7rsj8 plasmodium
582	61	9.5	309	2	P79352_HORSE	P79352 equus caball	655	61	9.5	1246	2	Q4RKK1_TETNG	Q4rkk1 tetraodon n
583	61	9.5	325	2	Q98NW3_RHILO	Q98nw3 rhizobium l	656	61	9.5	1259	2	Q5RAJ0_PONPY	Q5raj0 pongo pygma
584	61	9.5	327	1	FKBP6_MOUSE	Q91xw8 mus musculus	657	61	9.5	1264	2	Q3U2X9_MOUSE	Q3u2x9 mus musculus
585	61	9.5	327	2	Q8C1Y1_MOUSE	Q8c1y1 mus musculus	658	61	9.5	1340	2	Q9WQO1_DROME	Q9wqo1 drosophila
586	61	9.5	327	2	Q91VB7_MOUSE	Q91vb7 mus musculus	659	61	9.5	1375	2	Q3USI2_MOUSE	Q3usi2 mus musculus
587	61	9.5	322	2	Q6K1D2_9GALL	Q6k1d2 crax globul	660	61	9.5	1545	2	Q30DN6_CANFA	Q30dn6 canis famil
588	61	9.5	332	2	Q8SEE4_CRABL	Q8see4 crax blumen	661	61	9.5	1556	2	Q38JA7_CANFA	Q38ja7 canis famil
589	61	9.5	333	2	Q2PTB0_PSEAB	Q2ptb0 pseudomonas	662	61	9.5	1557	2	Q5JUX3_HUMAN	Q5jux3 homo sapien
590	61	9.5	333	2	Q8GL60_9BACT	Q8gl60 uncultured	663	61	9.5	1560	1	JADIC_HUMAN	Q41229 homo sapien
591	61	9.5	340	2	Q8M809_9COLU	Q8m809 streptopeli	664	61	9.5	1560	2	Q5JUX5_HUMAN	Q5jux5 homo sapien
592	61	9.5	346	2	Q79393_RHEAM	Q79393 rhea ameri	665	61	9.5	1619	2	Q9UJU7_ANOGA	Q9ujj9 anopheles g
593	61	9.5	346	2	Q3B9F1_9EMBE	Q3b9f1 myioborus m	666	61	9.5	1623	2	Q9UJU7_ANOGA	Q9ujj9 anopheles g
594	61	9.5	346	2	Q4VD77_NECMO	Q4vd77 necrosyrtes	667	61	9.5	1799	2	Q8ROY0_MOUSE	Q8roy0 mus musculus
595	61	9.5	346	2	Q7IN06_9EMBE	Q7in06 parula supe	668	61	9.5	2068	2	Q87WF0_ORYSA	Q87wf0 oryza sativ
596	61	9.5	346	2	Q85UK3_COTCH	Q85uk3 coturnix ch	669	61	9.5	3063	2	Q81284_PLAP7	Q81284 plasmodium
597	61	9.5	346	2	Q8M458_9EMBE	Q8m458 microligea	670	60.5	9.4	98	2	Q3GNL0_9GAMM	Q3gml0 psychobact
598	61	9.5	346	2	Q9G8M1_9EMBE	Q9g8m1 spiza ameri	671	60.5	9.4	106	1	GASA4_ARATH	Q46630 arabidopsis
599	61	9.5	346	2	Q9MAV8_PARGU	Q9maj8 parula gutt	672	60.5	9.4	118	2	Q3NU02_SHEFR	Q3nu02 shewanella
600	61	9.5	346	2	Q9TCR8_9ICTE	Q9tcr8 icterus mes	673	60.5	9.4	133	2	Q4SXT9_TETNG	Q4sxt9 tetraodon n
601	61	9.5	346	2	Q9TCM7_9ICTE	Q9tcm7 icterus mes	674	60.5	9.4	162	1	HSPB6_RAT	Q97541 rattus norv
602	61	9.5	346	2	Q9TCW8_9ICTE	Q9tcw8 icterus mes	675	60.5	9.4	210	2	Q40919_HHV8	Q40919 human herpe
603	61	9.5	346	2	Q9TCW3_RHEAM	Q9tcw3 rhea ameri	676	60.5	9.4	210	2	P90486_HHV8	P90486 human herpe
604	61	9.5	346	2	Q5J683_9EMBE	Q5j683 basileuteru	677	60.5	9.4	217	2	Q9HA66_HUMAN	Q9ha66 homo sapien
605	61	9.5	346	2	Q6VSL5_9PASE	Q6vsl5 prunella at	678	60.5	9.4	220	2	Q4TGF7_TETNG	Q4tgf7 tetraodon n
606	61	9.5	346	2	Q6WR11_9AVES	Q6wr11 crotophaga	679	60.5	9.4	244	2	Q6DFT8_XENLA	Q6dff8 xenopus lae
607	61	9.5	346	2	Q8M459_9EMBE	Q8m459 hemispingus	680	60.5	9.4	256	2	Q9HY17_PSEAE	Q9hy17 pseudomonas
608	61	9.5	346	2	Q8SIP8_9CORV	Q8sip8 eurocephalu	681	60.5	9.4	272	1	SIX3_ORYLA	Q36242 arabidopsis
609	61	9.5	346	2	Q9MDH2_PARGU	Q9mdh2 parula gutt	682	60.5	9.4	290	2	Q3EB42_ARATH	Q3eb42 arabidopsis
610	61	9.5	348	2	Q4VD74_9FALC	Q4vd74 gyps fulvus	683	60.5	9.4	316	2	Q9N1Y1_PIG	Q9n1y1 sus scrofa
611	61	9.5	362	2	Q8C2F8_MOUSE	Q8c2f8 mus musculus	684	60.5	9.4	322	2	Q9HNV6_HALSA	Q9hmv6 halobacteri
612	61	9.5	364	1	YBOK2_HUMAN	Q9y2t7 homo sapien	685	60.5	9.4	326	2	Q5M800_HUMAN	Q5m800 homo sapien
613	61	9.5	364	2	Q3GW96_9ACTO	Q3gw96 nocardioid	686	60.5	9.4	326	2	Q9BVC4_HUMAN	Q9bvc4 homo sapien
614	61	9.5	383	2	Q2JVZ0_9CYAN	Q2jvz0 cyanobacter	687	60.5	9.4	326	2	Q4SGI3_TETNG	Q4sg43 tetraodon n
615	61	9.5	383	2	Q4SEK7_TETNG	Q4sek7 tetraodon n	688	60.5	9.4	327	2	Q8WUI5_HUMAN	Q8wu15 homo sapien

689	60.5	9.4	328	2	Q2UJF2	aspergillus	Q2UJF2	aspergillus	762	60	9.3	294	2	Q73708	BRARE	Q73708	brachydanio
690	60.5	9.4	343	2	Q7PZ66	anopheles 9	Q7PZ66	anopheles 9	763	60	9.3	294	2	Q6PCA5	BRARE	Q6PCA5	brachydanio
691	60.5	9.4	344	2	Q8VC87	mouse	Q8VC87	mouse	764	60	9.3	307	2	Q5DHU6	HUMAN	Q5DHU6	homo sapien
692	60.5	9.4	348	1	NR113	CALLORHINUS	P62044	callorhinus	765	60	9.3	308	2	Q5DHU6	SCHJA	Q5DHU6	schistosoma
693	60.5	9.4	348	2	Q2T9C7	BURTH	Q2T9C7	burholderi	766	60	9.3	319	2	Q93529	XENLA	Q93529	xenopus lae
694	60.5	9.4	353	2	Q66KP5	XENLA	Q66KP5	xenopus lae	767	60	9.3	326	2	Q510B4	XENTR	Q510B4	xenopus tro
695	60.5	9.4	362	1	CPRI	ARETH	Q91C77	arabidopsis	768	60	9.3	326	2	Q6PA72	XENLA	Q6PA72	xenopus lae
696	60.5	9.4	365	2	Q8KS88	ECOLI	Q8KS88	escherichia	769	60	9.3	327	2	Q983K7	RHILO	Q983K7	rhizobium 1
697	60.5	9.4	377	2	Q6LEV5	PLAF7	Q6LEV5	plasmodium	770	60	9.3	333	2	Q7YK9	9TRYP	Q7YK9	trypanosoma
698	60.5	9.4	382	2	Q3GH98	CHLVI	Q3GH98	prothecoch	771	60	9.3	337	2	Q7NR98	CHROV	Q7NR98	chromobace
699	60.5	9.4	388	2	Q7XHC8	ORYSA	Q7XHC8	oryza sativ	772	60	9.3	346	1	NU2M	COTJA	P24971	coturnix co
700	60.5	9.4	388	2	Q8S7Z9	ORYSA	Q8S7Z9	oryza sativ	773	60	9.3	346	2	Q8HJD2	NECTARINIA	Q8HJD2	nectarinia
701	60.5	9.4	395	2	Q7SHK2	NEUCR	Q7SHK2	neurospora	774	60	9.3	346	2	Q8M07	9COLU	Q8M07	streptopeli
702	60.5	9.4	396	2	Q9XW00	CAEEL	Q9XW00	caenorhabdi	775	60	9.3	346	2	Q9B6T3	EUEDEL	Q9B6T3	eudromia el
703	60.5	9.4	405	2	Q9VXS3	DROME	Q9VXS3	drosophila	776	60	9.3	346	2	Q63788	9AVES	Q63788	callonetta
704	60.5	9.4	410	2	Q9VXS4	DROME	Q9VXS4	drosophila	777	60	9.3	346	2	Q8M2V6	9PASE	Q8M2V6	nectarinia
705	60.5	9.4	412	2	Q4RRU8	TETNG	Q4RRU8	tetraodon n	778	60	9.3	346	2	Q8M05	9COLU	Q8M05	streptopeli
706	60.5	9.4	416	2	Q4S7R5	TETNG	Q4S7R5	tetraodon n	779	60	9.3	359	1	WNT8A	BRARE	P51028	brachydanio
707	60.5	9.4	420	1	BMP2	TETNG	Q80482	tetraodon n	780	60	9.3	361	2	Q848K8	9BACT	Q848K8	uncultured
708	60.5	9.4	425	2	Q4S0H1	TETNG	Q4S0H1	tetraodon n	781	60	9.3	363	1	PGLR	ASPPA	P49575	aspergillus
709	60.5	9.4	452	2	Q91C77	ARETH	Q91C77	arabidopsis	782	60	9.3	372	2	QSEPB2	NEIGO	QSEPB2	neisseria 9
710	60.5	9.4	494	2	Q852S7	9CARY	Q852S7	suaeda japo	783	60	9.3	378	1	PGLR	PENEN	O59925	penicillium
711	60.5	9.4	503	2	Q3BKV1	9HEPC	Q3BKV1	hepatitis c	784	60	9.3	379	2	Q9S4U3	SELRU	Q9S4U3	selenomonas
712	60.5	9.4	527	2	Q7TNK4	MOUSE	Q7TNK4	mouse	785	60	9.3	383	1	SNIP1	MOUSE	Q8B1Z6	mus musculus
713	60.5	9.4	553	2	Q4S5L1	HUMAN	Q4S5L1	homo sapien	786	60	9.3	383	2	Q3V106	MOUSE	Q3V106	m adult mal
714	60.5	9.4	553	2	Q4S5L2	HUMAN	Q4S5L2	homo sapien	787	60	9.3	395	2	Q7K742	CAEEL	Q7K742	caenorhabdi
715	60.5	9.4	584	2	Q4IA69	GIBBE	Q4IA69	gibberella	788	60	9.3	400	2	Q9U8B1	9TRYP	Q9U8B1	trypanosoma
716	60.5	9.4	622	2	Q9W3C4	DROME	Q9W3C4	drosophila	789	60	9.3	407	2	Q9NKK2	HUMAN	Q9NKK2	homo sapien
717	60.5	9.4	627	2	P74489	SYNY3	P74489	synecocyst	790	60	9.3	418	1	PPA6	MOUSE	Q8BP40	mus musculus
718	60.5	9.4	640	1	SPT10	YEAST	P35208	saccharomyc	791	60	9.3	418	2	Q3TNE2	MOUSE	Q3TNE2	m 6 days ne
719	60.5	9.4	655	2	Q705H8	HPV43	Q705H8	human papil	792	60	9.3	424	2	Q86UV1	HUMAN	Q86UV1	homo sapien
720	60.5	9.4	659	2	Q9S0U8	DROME	Q9S0U8	drosophila	793	60	9.3	435	2	Q5LKK1	SILPO	Q5LKK1	ellicibacte
721	60.5	9.4	664	2	Q5N000	CRINE	Q5N000	cryptococcu	794	60	9.3	445	2	Q38Y05	LACSS	Q38Y05	lactobacill
722	60.5	9.4	664	2	Q5KBC9	CRINE	Q5KBC9	cryptococcu	795	60	9.3	450	2	Q4UF91	THEAN	Q4UF91	theileria a
723	60.5	9.4	746	2	Q4ORX8	DESAC	Q4ORX8	desulfuromo	796	60	9.3	462	2	Q4V791	XENTR	Q4V791	xenopus tro
724	60.5	9.4	751	1	Q3HKG4	RHOS4	Q3HKG4	rhodobacter	797	60	9.3	464	2	Q9JUR1	MOUSE	Q9JUR1	mus musculus
725	60.5	9.4	807	1	YNPF	ECOLI	P77783	escherichia	798	60	9.3	467	2	Q60Q96	CAEBR	Q60Q96	caenorhabdi
726	60.5	9.4	808	2	Q6EMW7	ECOLI	Q6EMW7	escherichia	799	60	9.3	494	2	Q2ULV3	ASPOR	Q2ULV3	aspergillus
727	60.5	9.4	808	2	Q7ADN3	ECO57	Q7ADN3	escherichia	800	60	9.3	495	2	Q2UUP9	ASPOR	Q2UUP9	aspergillus
728	60.5	9.4	808	2	Q8CW17	ECOL6	Q8CW17	escherichia	801	60	9.3	530	2	Q5D5K3	ALV	Q5D5K3	avian leuko
729	60.5	9.4	817	2	Q8DCT9	VIBVU	Q8DCT9	vibrio vuln	802	60	9.3	533	2	Q5D5K1	ALV	Q5D5K1	avian leuko
730	60.5	9.4	819	2	Q7MH12	VIBVU	Q7MH12	vibrio vuln	803	60	9.3	533	2	Q5D5K2	ALV	Q5D5K2	avian leuko
731	60.5	9.4	879	2	Q8IM68	PLAF7	Q8IM68	plasmodium	804	60	9.3	548	2	Q7U124	MYCBO	Q7U124	mycobacteri
732	60.5	9.4	914	2	Q8S5Q2	ORYSA	Q8S5Q2	oryza sativ	805	60	9.3	555	2	Q2X5W6	9GAMM	Q2X5W6	shewanella
733	60.5	9.4	1006	2	Q2X8S2	PSEPU	Q2X8S2	pseudomonas	806	60	9.3	555	2	Q2ZSX0	SHEPU	Q2ZSX0	shewanella
734	60.5	9.4	1019	1	LFC	CARRO	Q26422	c limulus c	807	60	9.3	555	2	Q3Q9M1	9GAMM	Q3Q9M1	shewanella
735	60.5	9.4	1055	2	Q8OS37	RHILO	Q8OS37	rhizobium 1	808	60	9.3	559	1	Y876	MYCTU	Y876	mycobacteri
736	60.5	9.4	1265	2	Q8S7Z9	ORYSA	Q8S7Z9	oryza sativ	809	60	9.3	565	2	Q4SHE1	TETNG	Q4SHE1	tetraodon n
737	60.5	9.4	1362	2	Q2JTG4	9CYAN	Q2JTG4	cyanobacter	810	60	9.3	610	2	Q5ZLS5	CHICK	Q5ZLS5	gallus gall
738	60.5	9.4	1710	2	Q6Q114	RAT	Q6Q114	rattus norv	811	60	9.3	614	1	Y268	CHLMU	Y268	chlamydia m
739	60.5	9.4	1974	2	Q7RBL5	PLAYO	Q7RBL5	plasmodium	812	60	9.3	636	2	Q4WCS1	ASPFU	Q4WCS1	aspergillus
740	60.5	9.4	2104	2	Q21281	CAEEL	Q21281	caenorhabdi	813	60	9.3	644	2	Q6NUU9	HUMAN	Q6NUU9	homo sapien
741	60.5	9.4	2104	2	Q964N4	CAEEL	Q964N4	caenorhabdi	814	60	9.3	647	2	Q4RES8	TETNG	Q4RES8	tetraodon n
742	60.5	9.4	2239	2	Q8IBW8	PLAF7	Q8IBW8	plasmodium	815	60	9.3	656	2	Q4H332	CIOIN	Q4H332	clona intes
743	60.5	9.4	2353	2	Q7M560	BRARE	Q7M560	brachydanio	816	60	9.3	683	2	Q3JV89	BURP1	Q3JV89	burkholderi
744	60.5	9.4	4006	2	Q4S7X0	TETNG	Q4S7X0	tetraodon n	817	60	9.3	725	2	Q6MBT5	PARUM	Q6MBT5	parachlamyd
745	60.5	9.4	5138	2	Q9ZW94	ARETH	Q9ZW94	arabidopsis	818	60	9.3	734	2	Q3TYU8	MOUSE	Q3TYU8	mus musculus
746	60	9.3	53	2	Q3BS46	XANC5	Q3BS46	xanthomonas	819	60	9.3	746	2	Q4Q1E3	LEIMA	Q4Q1E3	leishmania
747	60	9.3	67	1	YHFD	BACSU	Q07602	bacillus su	820	60	9.3	795	2	Q2QPR8	ORYSA	Q2QPR8	oryza sativ
748	60	9.3	74	2	Q7UY67	RHOBA	Q7UY67	rhodopirell	821	60	9.3	812	2	Q4SKQ4	TETNG	Q4SKQ4	tetraodon n
749	60	9.3	89	2	Q6UMG9	HUMAN	Q6UMG9	homo sapien	822	60	9.3	825	1	SE5	RAT	SE5	rattus norv
750	60	9.3	139	2	Q6DFZ6	BRARE	Q6DFZ6	brachydanio	823	60	9.3	843	2	Q7XQC6	ORYSA	Q7XQC6	oryza sativ
751	60	9.3	166	2	Q66TW3	9DIPT	Q66TW3	culicoides	824	60	9.3	896	2	Q6FEG8	BRARE	Q6FEG8	brachydanio
752	60	9.3	197	2	Q4SNJ2	TETNG	Q4SNJ2	tetraodon n	825	60	9.3	903	2	Q6P9F4	HUMAN	Q6P9F4	homo sapien
753	60	9.3	209	2	Q6S9J2	HYDMA	Q6S9J2	hydra magni	826	60	9.3	903	2	Q8TDY4	HUMAN	Q8TDY4	homo sapien
754	60	9.3	230	2	Q4SNN1	TETNG	Q4SNN1	tetraodon n	827	60	9.3	903	2	Q6P949	BRARE	Q6P949	brachydanio
755	60	9.3	231	2	Q82547	CITSI	Q82547	citrus sine	828	60	9.3	979	2	Q3GSA1	9GAMM	Q3GSA1	psychrobact
756	60	9.3	241	2	Q69RG1	ORYSA	Q69RG1	oryza sativ	829	60	9.3	1020	2	Q3C0D4	HUMAN	Q3C0D4	homo sapien
757	60	9.3	254	2	Q3SQ78	9BRAD	Q3SQ78	bradyrhizob	830	60	9.3	1069	2	Q67WC7	ORYSA	Q67WC7	oryza sativ
758	60	9.3	263	2	Q8CGG4	MOUSE	Q8CGG4	mus musculus	831	60	9.3	1193	2	Q4QGS0	LEIMA	Q4QGS0	leishmania
759	60	9.3	284	2	Q8WNS2	BOVIN	Q8WNS2	bos taurus	832	60	9.3	1254	2	Q6K517	ORYSA	Q6K517	oryza sativ
760	60	9.3	293	2	Q2TTT1	ECOLI	Q2TTT1	escherichia	833	60	9.3	1337	2	Q4RKW0	TETNG	Q4RKW0	tetraodon n
761	60	9.3	294	2	Q4WRZ3	ASPFU	Q4WRZ3	aspergillus	834	60	9.3	1455	2	Q4SBV5	TETNG	Q4SBV5	tetraodon n

835	60	9.3	1551	2	Q3UIX6_MOUSE	Q3UIX6 mus musculus	908	59.5	9.2	698	2	Q3BEC0_9TRYP	Q3BEC0 trypanosoma
836	60	9.3	1554	1	JADIC_MOUSE	F41230 mus musculus	909	59.5	9.2	768	2	Q1SD3_CAEBR	Q1SD3 caenorhabdi
837	60	9.3	1869	2	Q93809_MAGGR	F91309 magnaporthie	910	59.5	9.2	772	2	Q4WKQ8_ASFPU	Q4WKQ8 aspergillus
838	60	9.3	2157	2	Q4SDX1_TETNG	Q4sdx1 tetraodon n	911	59.5	9.2	779	1	S2KJC7_BOVIN	Q2kjc7 bos taurus
839	60	9.3	3038	1	LKNS_ASPE	Q98a5 aspergillus	912	59.5	9.2	866	1	SREC2_HUMAN	Q9696 homo sapien
840	60	9.3	3161	2	Q54511_YEREN	Q54511 yerbinia en	913	59.5	9.2	866	2	Q58A83_HUMAN	Q58a83 homo sapien
841	60	9.3	4823	2	Q93321_FUGRU	Q93321 fugu rubrip	914	59.5	9.2	870	1	SULP1_MOUSE	Q8K07 mus musculus
842	59.5	9.2	94	2	Q75150_ORYSA	Q75150 oryza sativ	915	59.5	9.2	946	2	Q3ED56_ARATH	Q3ED56 arabidopsis
843	59.5	9.2	104	1	RK25_PEA	P11892 pisum sativ	916	59.5	9.2	952	2	Q8NIT8_NEUCR	Q8nit8 neuropeptora
844	59.5	9.2	107	2	Q57ND5_SALCH	O57nd5 salmonella	917	59.5	9.2	977	2	Q4P2N9_USTWA	Q4p2n9 ustilago ma
845	59.5	9.2	110	2	Q562P5_ARATH	O562p5 arabidopsis	918	59.5	9.2	983	1	GLNE_PFOAC	Q6a924 propionibac
846	59.5	9.2	111	2	Q25104_HIRNI	Q25104 hirudo nipp	919	59.5	9.2	1006	2	Q7BJU5_PSEPU	Q7bj59 pseudomonas
847	59.5	9.2	120	2	Q6XHY7_DROYA	Q6xhy7 drosophila	920	59.5	9.2	1006	2	Q8BEH0_PSEPK	Q8BEH0 pseudomonas
848	59.5	9.2	120	2	Q9VMB9_DROME	Q9vmb9 drosophila	921	59.5	9.2	1019	2	Q8T9S1_TACTR	Q8t9s1 tachypleus
849	59.5	9.2	140	2	Q84J66_ORYSA	Q84j66 oryza sativ	922	59.5	9.2	1020	1	ACAI_ARATH	Q37145 arabidopsis
850	59.5	9.2	154	1	RNAS8_MIOTA	O8ep27 miopithecus	923	59.5	9.2	1079	2	Q6ZPZ0_MOUSE	Q6zpz0 mus musculus
851	59.5	9.2	154	2	Q86NN8_DROME	Q86nn8 drosophila	924	59.5	9.2	1243	2	Q7Z8F3_TRIRS	Q7z8f3 trichoderma
852	59.5	9.2	155	2	Q9JKN8_MUSPA	Q9jkn8 mus pahari	925	59.5	9.2	1313	2	Q8XRR8_RALSO	Q8xrr8 ralsconia s
853	59.5	9.2	158	2	Q647G8_ARAHY	Q647g8 arachis hyp	926	59.5	9.2	1449	2	Q9U112_DROME	Q9u112 drosophila
854	59.5	9.2	158	2	Q3VOS5_MOUSE	Q3vos5 mus musculus	927	59.5	9.2	1462	2	Q9U113_DROME	Q9u113 drosophila
855	59.5	9.2	160	1	HSPB6_HUMAN	O14558 homo sapien	928	59.5	9.2	1671	2	Q571L9_MOUSE	Q571l9 mus musculus
856	59.5	9.2	160	2	Q6NV13_HUMAN	O6nv13 homo sapien	929	59.5	9.2	1869	2	Q59FG1_HUMAN	Q59fg1 homo sapien
857	59.5	9.2	183	1	RM32_YEAST	P25348 saccharomyc	930	59.5	9.2	2114	1	MYO9B_MOUSE	Q9qy96 mus musculus
858	59.5	9.2	210	1	BAR2_CHITE	P02851 chironomus	931	59.5	9.2	2222	1	CAC1B_RAT	Q07652 rattus norv
859	59.5	9.2	220	2	Q5XYR8_BORGA	O5xyr8 borrelia ga	932	59.5	9.2	2224	2	Q9NYZ6_HUMAN	Q9nyz6 homo sapien
860	59.5	9.2	226	2	Q21128_CAEEL	Q21128 caenorhabdi	933	59.5	9.2	2251	2	Q5VZB6_HUMAN	Q5vzb6 homo sapien
861	59.5	9.2	239	2	Q2X1F0_9GAMM	Q2x1f0 shewanella	934	59.5	9.2	2259	1	CAC1E_EBIT	Q02343 cryocolagus
862	59.5	9.2	239	2	Q2ZU35_SHEPU	Q2zu35 shewanella	935	59.5	9.2	2270	2	Q5VZB8_HUMAN	Q5vzb8 homo sapien
863	59.5	9.2	240	2	Q855Y4_9CAUD	Q855y4 mycobacteri	936	59.5	9.2	2272	1	CAC1E_MOUSE	Q61290 mus musculus
864	59.5	9.2	248	2	Q41IQ5_GIBZE	Q41iq5 gibberella	937	59.5	9.2	2295	2	Q923K6_RAT	Q923k6 rattus norv
865	59.5	9.2	252	2	Q7YTD2_SACKO	Q7ytd2 saccolossu	938	59.5	9.2	2312	1	CAC1E_HUMAN	Q15878 homo sapien
866	59.5	9.2	258	2	Q94GT3_ORYSA	Q94gt3 oryza sativ	939	59.5	9.2	2313	2	Q5VZB7_HUMAN	Q5vzb7 homo sapien
867	59.5	9.2	258	2	Q7XCM7_ORYSA	Q7xcm7 oryza sativ	940	59.5	9.2	2382	2	Q9B119_DROME	Q9b119 drosophila
868	59.5	9.2	259	2	Q2QNF4_ORYSA	Q2qnf4 oryza sativ	941	59.5	9.2	2409	2	Q960G6_DROME	Q960g6 drosophila
869	59.5	9.2	260	2	Q86Y18_HUMAN	Q86y18 homo sapien	942	59.5	9.2	3034	1	CELK1_MOUSE	Q35161 mus musculus
870	59.5	9.2	265	2	Q5M8K0_XENTR	O5m8k0 xenopus tro	943	59.5	9.2	3312	1	CELK3_HUMAN	Q9ny97 homo sapien
871	59.5	9.2	293	2	Q6FQ16_CANGA	Q6fq16 candida gla	944	59.5	9.2	3689	2	Q7PPF9_ANOGA	Q7ppf9 anopheles g
872	59.5	9.2	343	1	Q5937_YEAST	O59377 saccharomyc	945	59.5	9.2	4186	2	Q5Y190_HUMAN	Q5y190 homo sapien
873	59.5	9.2	359	1	FIX2_RHILE	P07748 rhizobium l	946	59	9.2	65	2	Q6BZL3_DEBHA	Q6bzl3 debaryomyce
874	59.5	9.2	366	2	Q6ATF0_ORYSA	Q6atf0 oryza sativ	947	59	9.2	82	2	Q2NP17_NPVHC	Q2np17 hyphantria
875	59.5	9.2	368	1	CAAL_PSEPK	Q88nv0 pseudomonas	948	59	9.2	102	2	Q9SNM2_PENMO	Q9snm2 penaeus mon
876	59.5	9.2	381	2	Q98A22_RHILO	Q98a22 rhizobium l	949	59	9.2	109	2	Q6IG96_DROME	Q6ig96 drosophila
877	59.5	9.2	388	2	Q54G98_DICDI	O54g98 dictyosteli	950	59	9.2	115	2	Q3HNA5_9GEMI	Q3hna5 tobacco lea
878	59.5	9.2	409	2	Q94CL7_ARATH	Q94cl7 arabidopsis	951	59	9.2	155	2	Q9JUG8_MUSCR	Q9jkg8 mus caroli
879	59.5	9.2	420	2	Q98NE5_RHILO	Q98nb5 rhizobium l	952	59	9.2	157	2	Q9XTV5_CABEL	Q9xtv5 caenorhabdi
880	59.5	9.2	422	2	Q9M0H0_ARATH	Q9m0h0 arabidopsis	953	59	9.2	158	2	Q43M16_SOLUS	Q43m16 solibacter
881	59.5	9.2	436	2	Q4SBN4_TETNG	Q4sbn4 tetraodon n	954	59	9.2	158	2	Q9CTX4_MOUSE	Q9ctx4 mus musculus
882	59.5	9.2	437	1	CREA_ASFNG	O05620 aspergillus	955	59	9.2	160	1	ECF_HUMAN	P12724 homo sapien
883	59.5	9.2	428	2	Q4VB70_BRARE	Q4vb70 brachydanio	956	59	9.2	160	1	ECF_PONPY	P47781 pongo pygma
884	59.5	9.2	446	2	Q96E41_HUMAN	Q96e41 homo sapien	957	59	9.2	160	2	Q4VBC1_HUMAN	Q4vbc1 homo sapien
885	59.5	9.2	447	1	TBL2_HUMAN	Q9y4p3 homo sapien	958	59	9.2	171	2	Q22Q2_9GAMM	Q22q2 shewanella
886	59.5	9.2	447	2	Q5RDY0_PONPY	Q5rdy0 pongo pygma	959	59	9.2	171	2	Q364U9_9GAMM	Q364u9 shewanella
887	59.5	9.2	493	2	Q84SA4_ASSTR	Q84sa4 aster tripo	960	59	9.2	175	2	Q2NTQ1_SODGL	Q2ntq1 sodalis glo
888	59.5	9.2	503	2	Q3BKW0_9HEPC	Q3bkw0 heparitis c	961	59	9.2	178	2	Q6AVC1_ORYSA	Q6avc1 oryza sativ
889	59.5	9.2	510	2	Q4AE31_FUGRU	Q4ae31 fugu rubrip	962	59	9.2	193	1	PERP_HUMAN	Q96fx8 homo sapien
890	59.5	9.2	510	2	Q90WM4_FUGRU	Q90wm4 fugu rubrip	963	59	9.2	199	2	Q3Z51_9GAMM	Q3z51 alkalilimni
891	59.5	9.2	514	2	Q7PBJ7_ANOGA	Q7ppj7 anopheles g	964	59	9.2	227	2	Q7KPY6_LUCCU	Q7kpy6 lucilia cup
892	59.5	9.2	514	2	Q65BE4_ORYSA	Q65be4 oryza sativ	965	59	9.2	230	2	Q2ZLQ3_SHEPU	Q2zlq3 shewanella
893	59.5	9.2	533	2	Q6EBC1_LUPAL	Q6ebc1 lupinus alb	966	59	9.2	238	2	Q46G98_METBA	Q46g98 methanosarc
894	59.5	9.2	543	2	Q754G6_ASHGO	Q754g6 ashbya goss	967	59	9.2	245	2	Q7XV53_ORYSA	Q7xv53 oryza sativ
895	59.5	9.2	561	2	Q3F2A4_9BURK	Q3f2a4 burkholderi	968	59	9.2	259	2	Q5CPE3_CRYPV	Q5cpe3 cryptospori
896	59.5	9.2	572	2	Q80XH4_MOUSE	Q80xh4 mus musculus	969	59	9.2	272	2	Q2QWC6_ORYSA	Q2qwc6 oryza sativ
897	59.5	9.2	575	2	Q4D215_TRYCR	Q4d215 trypanosoma	970	59	9.2	280	2	Q448M1_SOLUS	Q448m1 solibacter
898	59.5	9.2	592	1	TLLI2_HUMAN	Q9bw77 homo sapien	971	59	9.2	284	2	Q801F0_XENLA	Q801f0 xenopus lae
899	59.5	9.2	594	2	Q9P4A3_EMENI	Q9p4a3 emeritella	972	59	9.2	296	2	Q66KB7_XENLA	Q66ke7 xenopus lae
900	59.5	9.2	594	2	Q5B7V8_EMENI	O5b7v8 aspergillus	973	59	9.2	307	2	Q4ZM71_PSEU2	Q4zm71 pseudomonas
901	59.5	9.2	605	2	Q5DU24_MOUSE	Q5du24 mus musculus	974	59	9.2	314	2	Q8S835_ORYSA	Q8s835 oryza sativ
902	59.5	9.2	622	2	Q7ZWK0_XENLA	Q7zwk0 xenopus lae	975	59	9.2	319	2	Q3O4R7_9GAMM	Q3o4r7 shewanella
903	59.5	9.2	633	1	MUTL_PSEAE	Q9hul8 pseudomonas	976	59	9.2	321	2	Q2QYP4_ORYSA	Q2qyp4 oryza sativ
904	59.5	9.2	659	2	Q341H5_RHOPA	Q341h5 rhodopseudo	977	59	9.2	328	2	Q68DU4_HUMAN	Q68du4 homo sapien
905	59.5	9.2	666	2	Q9SP14_MACIN	Q9sp14 macadamia i	978	59	9.2	332	2	Q85EE8_9GALL	Q85ee8 penelopina
906	59.5	9.2	698	2	Q9UV14_EMENI	Q9uv14 emeritella	979	59	9.2	346	2	Q7HXQ7_PSADE	Q7hxq7 psarocolius
907	59.5	9.2	698	2	Q5B961_EMENI	O5b961 aspergillus	980	59	9.2	346	2	Q8HJ63_9PASS	Q8hj63 apalis flav

981	59	9.2	346	2	Q8HN67	acryllium v	Q8hn67	1054	59	9.2	716	2	Q7M1Q5	ORYSA	Q7m1q5	oryza sativ
982	59	9.2	346	2	Q8LWV0	geothlypis	Q8lwv0	1055	59	9.2	730	1	IF2	BACHD	Q9ka77	bacillus ha
983	59	9.2	346	2	Q8M801	streptopeli	Q8m801	1056	59	9.2	745	2	Q4S190	TETNG	Q4s190	tetraodon n
984	59	9.2	346	2	Q8M810	streptopeli	Q8m810	1057	59	9.2	802	1	NAB3	YEAST	P38996	saccharomyc
985	59	9.2	346	2	Q8SEF0	psarocolius	Q8sef0	1058	59	9.2	832	2	Q7Z9H9	SCHPO	P38996	schizosacch
986	59	9.2	346	2	Q8SIR3	carduelis p	Q8sir3	1059	59	9.2	837	1	PHLD	MOUSE	O70362	mus musculus
987	59	9.2	346	2	Q8W7C4	dendragapus	Q8w7c4	1060	59	9.2	842	2	Q7TNZ4	MOUSE	O70362	mus musculus
988	59	9.2	346	2	Q957Y6	anomalopter	Q957y6	1061	59	9.2	842	2	Q8R4J2	MOUSE	O8a432	mus musculus
989	59	9.2	346	2	Q958B7	pteronemia	Q958b7	1062	59	9.2	842	2	Q8VCU2	MOUSE	Q8vcu2	mus musculus
990	59	9.2	346	2	Q9G8K1	geothlypis	Q9g8k1	1063	59	9.2	842	2	Q2LDBH3	MOUSE	Q9dbh3	mus musculus
991	59	9.2	346	2	Q9G8M6	carduelis p	Q9g8m6	1064	59	9.2	846	2	Q2LAB0	LOCOMI	Q2lab0	locusta mig
992	59	9.2	346	2	Q9G8N1	eremophila	Q9g8n1	1065	59	9.2	857	2	Q3GVH5	ACTO	Q3gvh5	nocardioid
993	59	9.2	346	2	Q9H160	numida mele	Q9h160	1066	59	9.2	860	2	Q8S6M6	ORYSA	Q8s6m6	oryza sativ
994	59	9.2	346	2	Q9ML67	numida mele	Q9ml67	1067	59	9.2	871	1	SULF1	HUMAN	Q81wu6	homo sapien
995	59	9.2	346	2	Q9ML72	centrocercu	Q9ml72	1068	59	9.2	871	2	Q7Z2M2	HUMAN	Q7z2m2	homo sapien
996	59	9.2	346	2	Q9ML729	streptopeli	Q9ml729	1069	59	9.2	874	2	Q4SDF0	TETNG	Q4sdf0	tetraodon n
997	59	9.2	346	2	Q8M808	streptopeli	Q8m808	1070	59	9.2	895	2	Q802U7	BRARE	Q802u7	brachydania
998	59	9.2	346	2	Q8SK79	psarocolius	Q8sk79	1071	59	9.2	895	2	Q8W2U4	ORYSA	Q8w2u4	oryza sativ
999	59	9.2	346	2	Q9ML71	corurnix au	Q9ml71	1072	59	9.2	895	2	Q8DW99	RCVMV	Q8dw99	rat cytohes
1000	59	9.2	348	2	Q3T078	bos taurus	Q3t078	1073	59	9.2	1009	2	Q4STN5	TETNG	Q4stn5	tetraodon n
1001	59	9.2	357	2	Q2PEX9	trifolium p	Q2pex9	1074	59	9.2	1018	2	Q7SFB6	ASHGO	Q7sfb6	ashbya gos
1002	59	9.2	359	2	Q9GRG4	toxoplasma	Q9grg4	1075	59	9.2	1046	2	Q7XE41	TRYCR	Q7xe41	oryza sativ
1003	59	9.2	369	2	Q4TGD6	tetraodon n	Q4tgd6	1076	59	9.2	1059	2	Q7XE41	ORYSA	Q7xe41	oryza sativ
1004	59	9.2	372	2	Q5JIV7	pyrococcus	Q5jiv7	1077	59	9.2	1064	1	JMJ2A	MOUSE	Q8bw72	mus musculus
1005	59	9.2	381	2	Q2R2Q3	oryza sativ	Q2r2q3	1078	59	9.2	1082	2	Q4CNR9	TRYCR	Q4cnr9	trypanosoma
1006	59	9.2	399	2	Q3WUF6	mesorhizobi	Q3wuf6	1079	59	9.2	1130	2	Q4SVS4	TETNG	Q4svs4	tetraodon n
1007	59	9.2	401	2	Q67XK9	arabidopsis	Q67xk9	1080	59	9.2	1149	2	Q8S2V5	TETNG	Q8s2v5	tetraodon n
1008	59	9.2	402	2	Q99037	trichoderma	Q99037	1081	59	9.2	1185	1	STB5L	MOUSE	Q5dqr4	mus musculus
1009	59	9.2	402	2	Q99032	trichoderma	Q99032	1082	59	9.2	1423	1	SSH2	MOUSE	Q5dqr4	mus musculus
1010	59	9.2	402	2	Q99038	trichoderma	Q99038	1083	59	9.2	1551	2	Q4S523	TETNG	Q4s523	tetraodon n
1011	59	9.2	404	2	Q2LAG2	ctenopharyn	Q2lag2	1084	59	9.2	1724	2	Q4RMC8	TETNG	Q4rnc8	tetraodon n
1012	59	9.2	409	2	Q6AWY1	oryza sativ	Q6awy1	1085	59	9.2	1942	2	Q4DY12	TRYCR	Q4dy12	trypanosoma
1013	59	9.2	412	2	Q93811	arabidopsis	Q93811	1086	59	9.2	2135	2	O61077	PLAFA	Q61077	plasmodium
1014	59	9.2	427	2	Q5XGD5	xenopus tro	Q5xgd5	1087	59	9.2	2162	2	Q9NYZ5	HUMAN	Q9nyz5	homo sapien
1015	59	9.2	429	2	Q4RYT6	tetraodon n	Q4ryt6	1088	59	9.2	2559	2	Q4RG76	TETNG	Q4rg76	tetraodon n
1016	59	9.2	429	2	Q9W6U3	fugu rubrip	Q9w6u3	1089	59	9.2	2633	1	PDZK3	HUMAN	O15018	homo sapien
1017	59	9.2	433	2	Q413E3	gibberella	Q413e3	1090	59	9.2	2839	2	Q9VAD3	DROME	Q9vad3	drosophila
1018	59	9.2	437	2	Q44555	caenorhabdi	Q44555	1091	59	9.2	3609	2	Q9VAD3	DROME	Q9vad3	drosophila
1019	59	9.2	439	2	Q5P447	azocarcus sp	Q5p447	1092	59	9.2	3657	2	Q7KRV0	DROME	Q7krv0	mus musculus
1020	59	9.2	441	2	Q3E9Z2	arabidopsis	Q3e9z2	1093	59	9.2	5374	2	Q99ND0	MOUSE	Q99nd0	mus musculus
1021	59	9.2	453	2	Q94LRS	oryza sativ	Q94lrs	1094	58.5	9.1	66	2	Q5FIW8	LACAC	Q5fiw8	lactobacill
1022	59	9.2	465	2	Q2KXN6	bordeletia	Q2kxn6	1095	58.5	9.1	88	2	Q74CU7	GEOSL	Q74cu7	geobacter s
1023	59	9.2	468	2	Q31VL0	RHOS4	Q31vl0	1096	58.5	9.1	114	2	Q3W400	ACTO	Q3w400	frankia sp.
1024	59	9.2	473	2	Q4SAMS	TETNG	Q4sam5	1097	58.5	9.1	114	2	Q6N3A0	RHOPD	Q6n3a0	rhodopseudo
1025	59	9.2	479	2	Q6ZSG2	HUMAN	Q6zsg2	1098	58.5	9.1	115	2	Q6N3A0	RHOPD	Q6n3a0	rhodopseudo
1026	59	9.2	491	1	ZN655	HUMAN	Q4f9r6	1099	58.5	9.1	147	2	Q19441	CABEL	Q19441	caenorhabdi
1027	59	9.2	500	2	Q4P9R6	9HIV1	Q4p9r6	1100	58.5	9.1	149	2	Q5IU48	HORVD	Q5iu48	hordeum vul
1028	59	9.2	509	1	TSSP	MOUSE	Q9qxe5	1101	58.5	9.1	151	2	Q8TEC6	HUMAN	Q8tec6	homo sapien
1029	59	9.2	509	2	Q5SZ30	MOUSE	Q5sz30	1102	58.5	9.1	162	2	Q9Y9C2	APERPE	Q9y9c2	aeropyrum p
1030	59	9.2	518	2	Q9LIH4	STRCO	Q9lih4	1103	58.5	9.1	169	2	Q5L8A0	BACFN	Q5l8a0	bacteroides
1031	59	9.2	530	2	Q7RC79	PLAYO	Q7rc79	1104	58.5	9.1	171	2	Q4NK0	BACFR	Q4nk0	bacteroides
1032	59	9.2	549	2	Q33UJ9	9GAMM	Q33uj9	1105	58.5	9.1	183	2	Q6YV86	ORYSA	Q6yv86	oryza sativ
1033	59	9.2	551	2	Q4BBL9	BURVI	Q4bb19	1106	58.5	9.1	225	2	Q96U87	NEUCR	Q96u87	neurospora
1034	59	9.2	553	2	Q3P2V7	9GAMM	Q3p2v7	1107	58.5	9.1	214	2	Q82E90	STRAW	Q82e90	streptomyce
1035	59	9.2	574	2	Q87N55	VBPA	Q87n55	1108	58.5	9.1	225	2	Q95JZ5	MACFA	Q95jz5	macaca fasc
1036	59	9.2	576	2	Q9VD52	DROME	Q9vd52	1109	58.5	9.1	230	2	Q9UJV6	HUMAN	Q9ujv6	homo sapien
1037	59	9.2	579	2	Q8C393	MOUSE	Q8c393	1110	58.5	9.1	232	2	Q3MAL3	ANAVT	Q3mal3	anabaena va
1038	59	9.2	579	2	Q9WV10	MOUSE	Q9wv10	1111	58.5	9.1	237	2	Q612S9	CABBR	Q612s9	caenorhabdi
1039	59	9.2	603	2	Q02302	PSESP	Q02302	1112	58.5	9.1	255	2	Q3KPM5	XENLA	Q3kpm5	xenopus lae
1040	59	9.2	605	2	Q5PTV1	MOUSE	Q5ptv1	1113	58.5	9.1	263	2	Q3KFJ3	PSEPF	Q3kfj3	pseudomonas
1041	59	9.2	614	2	Q4VPTC	MYXXA	Q4vptc	1114	58.5	9.1	267	2	Q84SX4	ORYSA	Q84sx4	oryza sativ
1042	59	9.2	633	2	Q3H5A9	9ACTO	Q3h5a9	1115	58.5	9.1	267	2	Q4SUL6	TETNG	Q4sul6	tetraodon n
1043	59	9.2	637	2	Q6PA32	XENLA	Q6pa32	1116	58.5	9.1	280	2	Q37050	SIVCZ	Q37050	chimpanzee
1044	59	9.2	644	2	Q44DN7	CHRLS	Q44dn7	1117	58.5	9.1	285	2	Q7JDC8	XENLA	Q7jdc8	xenopus lae
1045	59	9.2	646	2	Q30TT1	THIDN	Q30tt1	1118	58.5	9.1	302	2	Q7YT99	CABEL	Q7yt99	caenorhabdi
1046	59	9.2	651	2	Q2VTB8	9PAPI	Q2vtb8	1119	58.5	9.1	303	2	Q3H6M6	9ACTO	Q3h6m6	nocardioid
1047	59	9.2	660	1	CXCC1	MOUSE	Q9cww7	1120	58.5	9.1	310	2	Q4WY17	ASPFU	Q4wy17	aspergillus
1048	59	9.2	660	2	Q3UIZ4	MOUSE	Q3uiz4	1121	58.5	9.1	311	2	Q4RGB2	TETNG	Q4rgb2	tetraodon n
1049	59	9.2	660	2	Q541B1	MOUSE	Q541b1	1122	58.5	9.1	324	2	Q3FN61	9BURK	Q3fn61	rhodofera
1050	59	9.2	666	2	Q9SP15	MACIN	Q9sp15	1123	58.5	9.1	329	2	Q2LAB5	MOUSE	Q2lab5	mus musculus
1051	59	9.2	676	2	Q46A10	METBA	Q46a10	1124	58.5	9.1	340	2	Q4EON7	TRYCR	Q4eon7	trypanosoma
1052	59	9.2	693	2	Q4RAX0	TETNG	Q4rax0	1125	58.5	9.1	368	2	Q95WF7	ACRMI	Q95wf7	acropora ml
1053	59	9.2	714	2	Q3V0C1	m adult mal	Q3v0c1	1126	58.5	9.1	368	2	Q68FU6	RAT	Q68fu6	rattus norv

1127	58.5	9.1	371	2	Q389J9_9TRYP	Q389j9	trypanosoma	1200	58.5	9.1	3454	2	Q7Y1G0_ORYSA	Q7Y1g0	oryza sativ
1128	58.5	9.1	406	2	Q72ZY9_PETMA	Q72zy9	petromyzon	1201	58.5	9.1	3767	1	MUA3_CABEL	P34576	caenorhabdi
1129	58.5	9.1	414	2	Q8UZY19_PAPAI	Q8uzy19	phocoena sp	1202	58.5	9.1	5146	2	Q8SPM4_BOVIN	P34576	bos taurus
1130	58.5	9.1	416	2	Q4H3S1_CIOIN	Q4h3e1	ciona intes	1203	58	9.0	46	2	Q86B29_9CAEN	Q86b29	reishia cla
1131	58.5	9.1	416	2	Q80731_ARATH	Q80731	arabidopsis	1204	58	9.0	73	2	Q5Y4U8_AGEOR	Q5y4u8	agelena ori
1132	58.5	9.1	419	2	Q2NRG2_SODGL	Q2nrg2	sodalis gio	1205	58	9.0	92	2	Q8SKY9_DROME	Q8sky9	drosophila
1133	58.5	9.1	420	2	Q804S3_FUGRU	Q804s3	fugu rubrip	1206	58	9.0	96	2	Q61JUT6_DROME	Q61jtc6	drosophila
1134	58.5	9.1	422	2	Q75N54_PAROL	Q75n54	paralichthy	1207	58	9.0	105	2	Q6K2T3_ORYSA	Q6k2t3	oryza sativ
1135	58.5	9.1	439	2	Q3SEH3_PARTE	Q3seh3	paramemius	1208	58	9.0	114	2	P74050_SYNY3	P74050	synecocyst
1136	58.5	9.1	439	2	Q417L1_KINRA	Q417l1	kineococcus	1209	58	9.0	122	2	Q2K382_RH1ET	Q2k382	rhizobium e
1137	58.5	9.1	447	2	Q95RA7_DROME	Q95ra7	drosophila	1210	58	9.0	123	2	Q2RLJ3_MOOTH	Q2rlj3	moorella th
1138	58.5	9.1	456	2	Q9RAH1_HUMAN	Q9rahl1	homo sapien	1211	58	9.0	123	2	Q6D9N6_ERWCT	Q6d9n6	erwinia car
1139	58.5	9.1	461	2	Q6GQK7_XENLA	Q6gqk7	xenopus lae	1212	58	9.0	126	2	Q61JHS_DROME	Q61jhs	drosophila
1140	58.5	9.1	462	2	Q2R0J2_ORYSA	Q2r0j2	oryza sativ	1213	58	9.0	128	2	Q50E33_9MURI	Q50e33	arvicanthis
1141	58.5	9.1	475	2	Q6ETN5_ORYSA	Q6etn5	oryza sativ	1214	58	9.0	128	2	Q50E34_9MURI	Q50e34	arvicanthis
1142	58.5	9.1	476	2	Q4Q1J2_LEIMA	Q4q1j2	leishmania	1215	58	9.0	128	2	Q6V8J7_RAT	Q6v8j7	rattus norv
1143	58.5	9.1	478	2	Q4Q0Y3_SOLUS	Q4q0y3	solibacter	1216	58	9.0	136	2	Q7RUI5_NEUCR	Q7ruis5	neurospora
1144	58.5	9.1	486	2	Q2RP04_RHOKU	Q2rpu4	rhodospirill	1217	58	9.0	136	2	Q61JHS_DROME	Q61jhs	drosophila
1145	58.5	9.1	496	2	Q7S6G4_NEUCR	Q7s6g4	neurospora	1218	58	9.0	141	2	Q8QLK9_9NUCL	Q8qlk9	mamestra co
1146	58.5	9.1	509	2	Q8PKL3_XANAC	Q8pk13	xanthomonas	1219	58	9.0	143	2	Q9YCH7_AERPE	Q9ych7	aeropyrum p
1147	58.5	9.1	556	2	Q54WV4_DICDI	Q54wv4	dictyosteli	1220	58	9.0	145	1	RLJ5_MYCH7	Q4a819	mycoplasma
1148	58.5	9.1	561	2	Q9X9P8_STRTE	Q9x9p8	streptomyce	1221	58	9.0	145	1	RLJ5_MYCH7	Q4a819	mycoplasma
1149	58.5	9.1	569	2	Q6A2B2_9RETR	Q6a2b2	avian endog	1222	58	9.0	150	2	Q6ZVM6_HUMAN	Q6zvm6	homo sapien
1150	58.5	9.1	582	2	Q7UX40_RHOBA	Q7ux40	rhodopirell	1223	58	9.0	150	2	Q63831_MEUGE	Q63831	melospiza g
1151	58.5	9.1	630	2	Q7Q460_ANOGA	Q7q460	anophelies g	1224	58	9.0	153	2	Q6VVG3_ANOGA	Q6vvg3	anophelies g
1152	58.5	9.1	637	2	Q7UL95_RHOBA	Q7ul95	rhodopirell	1225	58	9.0	153	2	Q6VVG4_ANOGA	Q6vvg4	anophelies g
1153	58.5	9.1	642	2	Q4HZG6_GIBZE	Q4h2g6	gibberella	1226	58	9.0	154	2	Q9NEH6_DROME	Q9neh6	drosophila
1154	58.5	9.1	642	2	Q3SVX4_BOVIN	Q3svx4	bos taurus	1227	58	9.0	154	2	Q4SA33_TETNG	Q4sa33	tetradon n
1155	58.5	9.1	645	2	Q52KS4_XENLA	Q52ks4	xenopus lae	1228	58	9.0	155	2	Q2S577_9CNID	Q2s577	nematostell
1156	58.5	9.1	658	2	Q2N8M5_9SPHN	Q2n8m5	erythrobaet	1229	58	9.0	155	2	Q5GAM2_RAT	Q5gam2	rattus norv
1157	58.5	9.1	659	2	Q371D1_RHOPA	Q371d1	rhodopseudo	1230	58	9.0	155	2	Q9R125_MOUSE	Q9r125	mus musculus
1158	58.5	9.1	659	2	Q52128_XENLA	Q52128	xenopus lae	1231	58	9.0	155	2	Q9R127_RAT	Q9r127	rattus norv
1159	58.5	9.1	699	2	Q5KFX2_CRYNE	Q5kfx2	cryptococcu	1232	58	9.0	159	2	Q9FPB0_ORYSA	Q9fpb0	oryza sativ
1160	58.5	9.1	720	1	Q4CK9_RAT	Q4ck93	rattus norv	1233	58	9.0	169	2	Q60EA7_ORYSA	Q60ea7	oryza sativ
1161	58.5	9.1	720	2	Q4RSX3_TETNG	Q4rsx3	tetradon n	1234	58	9.0	170	2	Q3Q0D7_9GAMM	Q3q0d7	shewanella
1162	58.5	9.1	742	2	Q4P890_USTMA	Q4p890	ustilago ma	1235	58	9.0	171	2	Q3STC5_9GAMM	Q3stc5	shewanella
1163	58.5	9.1	761	2	Q951Q2_MACFA	Q951q2	macaca fasc	1236	58	9.0	171	2	Q5S8S1_9PSED	Q5s8s1	pseudomonas
1164	58.5	9.1	792	2	Q3JIK9_BURP1	Q3jik9	burkholderi	1237	58	9.0	172	2	Q5TV92_ANOGA	Q5tv92	anophelies g
1165	58.5	9.1	820	2	Q55W58_CRYNE	Q55w58	cryptococcu	1238	58	9.0	172	2	Q7XY01_CHLS6	Q7xyv1	chlorarachn
1166	58.5	9.1	820	2	Q5KK36_CRYNE	Q5kk36	cryptococcu	1239	58	9.0	175	2	Q2SNC3_9GAMM	Q2snc3	habella che
1167	58.5	9.1	825	2	Q216K7_9DELT	Q216k7	uncultured	1240	58	9.0	180	2	Q7XEP3_ORYSA	Q7xep3	oryza sativ
1168	58.5	9.1	870	1	SULF1_RAT	Q8v160	rattus norv	1241	58	9.0	186	2	Q9YF87_COWPX	Q9yfp87	cowpox viru
1169	58.5	9.1	874	1	EGFL4_RAT	Q9qyp0	rattus norv	1242	58	9.0	192	2	Q36EC1_9GAMM	Q36ec1	shewanella
1170	58.5	9.1	911	2	Q4XIS9_ASPFU	Q4x1e9	aspergillus	1243	58	9.0	193	2	Q351L7_9GAMM	Q351l7	alkalimni
1171	58.5	9.1	922	2	Q8BPR4_MOUSE	Q8bpr4	mus musculus	1244	58	9.0	200	2	Q2TE04_9HYME	Q2te04	spathius sp
1172	58.5	9.1	922	2	Q8K2D7_MOUSE	Q8k2d7	mus musculus	1245	58	9.0	203	2	Q3FCQ3_9BURK	Q3fcq3	rhodofera
1173	58.5	9.1	924	2	Q8BNE1_MOUSE	Q8bne1	m 12 days e	1246	58	9.0	205	2	Q4Y4M6_PLACH	Q4y4m6	plasmodium
1174	58.5	9.1	927	2	Q6A001_ANOGA	Q6a001	anophelies g	1247	58	9.0	218	2	Q3USA2_MOUSE	Q3usa2	mus musculus
1175	58.5	9.1	952	2	Q6A005_MOUSE	Q6a005	mus musculus	1248	58	9.0	219	2	Q2R312_ORYSA	Q2r312	oryza sativ
1176	58.5	9.1	960	2	Q4S187_TETNG	Q4s187	tetradon n	1249	58	9.0	222	2	Q61GT3_CABBR	Q61gt3	caenorhabdi
1177	58.5	9.1	971	2	Q751Y2_ORYSA	Q751y2	oryza sativ	1250	58	9.0	230	2	Q7R8X0_PLAYO	Q7r8x0	plasmodium
1178	58.5	9.1	996	2	Q6BME4_DEBHA	Q6bme4	debaryomyce	1251	58	9.0	233	2	Q8NJJ6_PONPY	Q8njh6	pongo pygma
1179	58.5	9.1	1002	2	Q6AVJ4_ORYSA	Q6avj4	oryza sativ	1252	58	9.0	233	2	Q8MJH7_PONPY	Q8mj10	pongo pygma
1180	58.5	9.1	1002	2	Q7Q052_RHOBA	Q7uq52	rhodopirell	1253	58	9.0	233	2	Q8MJ10_PONPY	Q8mj10	pongo pygma
1181	58.5	9.1	1019	1	LFC_TACTR	P28175	tachypleus	1254	58	9.0	245	2	Q4RM34_TETNG	Q4rm34	tetradon n
1182	58.5	9.1	1060	2	Q5B600_EMENI	Q5b600	aspergillus	1255	58	9.0	248	2	Q9SL34_ARATH	Q9sl34	arabidopsis
1183	58.5	9.1	1100	2	Q2SUL9_BURTH	Q2sul9	burkholderi	1256	58	9.0	259	2	Q8MKQ6_DROME	Q8mkq6	drosophila
1184	58.5	9.1	1107	2	Q4TB26_TETNG	Q4tb26	tetradon n	1257	58	9.0	268	2	Q96N84_HUMAN	Q96n84	homo sapien
1185	58.5	9.1	1238	2	Q74808_SCHPO	Q74808	schizosacch	1258	58	9.0	283	2	Q37051_SIVCZ	Q37051	chimpazee
1186	58.5	9.1	1363	2	Q2UUR2_ASPOR	Q2uur2	tetradon n	1259	58	9.0	284	2	Q4S4X5_TETNG	Q4s4x5	tetradon n
1187	58.5	9.1	1426	2	Q4Q868_LEIMA	Q4q868	leishmania	1260	58	9.0	285	2	Q5PPS7_XENLA	Q5pps7	xenopus lae
1188	58.5	9.1	1467	2	Q4T699_TETNG	Q4t699	tetradon n	1261	58	9.0	289	2	Q75D76_ASHGO	Q75d76	ashbya goss
1189	58.5	9.1	1474	2	Q3SGQ4_BURP1	Q3sgq4	burkholderi	1262	58	9.0	295	2	Q34V57_9GAMM	Q34v57	alkalimni
1190	58.5	9.1	1610	2	Q4S5Z3_TETNG	Q4s5z3	burkholderi	1263	58	9.0	298	2	Q6UVV4_PSEAK	Q6uvv4	pseudococ
1191	58.5	9.1	1637	2	Q9XSU8_BOVIN	Q9xsu8	bos taurus	1264	58	9.0	309	2	Q4V9A2_BRARE	Q4v9a2	brachydanio
1192	58.5	9.1	1673	2	Q5B6R4_EMENI	Q5b6r4	aspergillus	1265	58	9.0	330	2	Q8DLU4_SYNEL	Q8dlu4	synecococc
1193	58.5	9.1	1724	2	Q751X6_ORYSA	Q751x6	oryza sativ	1266	58	9.0	332	2	Q6K1C8_9GALL	Q6k1c8	mitu toment
1194	58.5	9.1	1726	2	Q5B8E1_EMENI	Q5b8e1	aspergillus	1267	58	9.0	332	2	Q6K1C9_9GALL	Q6k1c9	salvin
1195	58.5	9.1	1761	2	Q86XN2_HUMAN	Q86xn2	homo sapien	1268	58	9.0	332	2	Q8SEEE_PAUPA	Q8seee	pauzi pauxi
1196	58.5	9.1	2282	1	ZAN_RABIT	P57999	oryctolagus	1269	58	9.0	332	2	Q8SEEE_OREPHASIE	Q8seee	oreophasia
1197	58.5	9.1	2330	1	EGFL4_MOUSE	P60882	mus musculus	1270	58	9.0	335	2	Q8HCJ6_MOTFL	Q8hcj6	motacilla f
1198	58.5	9.1	2386	1	EGFL4_HUMAN	Q7z7m0	homo sapien	1271	58	9.0	341	2	Q674B4_9CORV	Q674b4	lanioturdus
1199	58.5	9.1	2783	2	Q4Q1Z9_LEIMA	Q4q1z9	leishmania	1272	58	9.0	343	2	Q7Y6Z6_PASIL	Q7y6z6	passerella

1273	58	9.0	343	2	Q7H869_PASIL	Q7H869 passerella	1346	58	9.0	346	2	Q8LXD1_9ICTE	Q8Lxd1 pearocolius
1274	58	9.0	343	2	Q7Y113_9EMBE	Q7Y113 pipilo chlo	1347	58	9.0	346	2	Q8M2V5_9EMBE	Q8m2v5 paroaria co
1275	58	9.0	343	2	Q7Y114_PASIL	Q7Y114 passerella	1348	58	9.0	346	2	Q8M2W2_1CTVI	Q8m2w2 icteria vir
1276	58	9.0	343	2	Q7Y115_PASIL	Q7Y115 passerella	1349	58	9.0	346	2	Q8M2W9_9EMBE	Q8m2w9 emberiza sp
1277	58	9.0	343	2	Q7Y116_PASIL	Q7Y116 passerella	1350	58	9.0	346	2	Q8M2X4_9EMBE	Q8m2x4 chlorospiza
1278	58	9.0	343	2	Q7Y117_PASIL	Q7Y117 passerella	1351	58	9.0	346	2	Q8M2X9_9EMBE	Q8m2x9 callamospiza
1279	58	9.0	343	2	Q7Y118_PASIL	Q7Y118 passerella	1352	58	9.0	346	2	Q8M2Y2_9EMBE	Q8m2y2 atlappetes s
1280	58	9.0	343	2	Q7Y119_PASIL	Q7Y119 passerella	1353	58	9.0	346	2	Q8M2Y3_9EMBE	Q8m2y3 atmophila c
1281	58	9.0	343	2	Q7Y120_9EMBE	Q7Y120 zontichia	1354	58	9.0	346	2	Q8M456_9EMBE	Q8m456 zontichia
1282	58	9.0	343	2	Q7Y121_SPIAR	Q7Y121 spizella ar	1355	58	9.0	346	2	Q8M726_9COLU	Q8m726 streptopeli
1283	58	9.0	343	2	Q7Y122_PASIL	Q7Y122 passerella	1356	58	9.0	346	2	Q8SE19_9ICTE	Q8se19 pearocolius
1284	58	9.0	343	2	Q7Y123_PASIL	Q7Y123 passerella	1357	58	9.0	346	2	Q8SEU3_9ICTE	Q8seu3 pearocolius
1285	58	9.0	343	2	Q7Y124_PASIL	Q7Y124 passerella	1358	58	9.0	346	2	Q8SIRS_9PASE	Q8sirs petronia de
1286	58	9.0	345	2	Q8CMH5_SYNEL	Q8cmh5 synechococc	1359	58	9.0	346	2	Q8SIS4_9PASE	Q8sis4 quelea quel
1287	58	9.0	345	2	Q8CMIB_SYNEL	Q8cmib synechococc	1360	58	9.0	346	2	Q8SK74_9ICTE	Q8sk74 gymnostinop
1288	58	9.0	345	2	Q8DKD0_SYNEL	Q8dkd0 synechococc	1361	58	9.0	346	2	Q8SK75_9ICTE	Q8sk75 gymnostinop
1289	58	9.0	345	2	Q8DMA6_SYNEL	Q8dma6 synechococc	1362	58	9.0	346	2	Q8SK77_9ICTE	Q8sk77 gymnostinop
1290	58	9.0	345	2	Q8G8L2_9EMBE	Q8g8l2 haplospiza	1363	58	9.0	346	2	Q8SK78_PSADE	Q8sk78 pearocolius
1291	58	9.0	346	1	NUZM_ANAAC	Q63767 anas acuta	1364	58	9.0	346	2	Q8SK80_PSADE	Q8sk80 pearocolius
1292	58	9.0	346	1	NUZM_ANAAM	Q63794 anas americ	1365	58	9.0	346	2	Q8SK81_PSADE	Q8sk81 pearocolius
1293	58	9.0	346	1	NUZM_ANACA	Q63796 anas capens	1366	58	9.0	346	2	Q8SK82_9ICTE	Q8sk82 pearocolius
1294	58	9.0	346	1	NUZM_ANAFA	Q63797 anas falcata	1367	58	9.0	346	2	Q8SK83_9ICTE	Q8sk83 pearocolius
1295	58	9.0	346	1	NUZM_ANAFO	Q63775 anas formos	1368	58	9.0	346	2	Q950A9_9CORV	Q950a9 viroleolanius
1296	58	9.0	346	1	NUZM_ANAPE	Q63798 anas penelo	1369	58	9.0	346	2	Q9G8K3_9ICTE	Q9g8k3 pearocolius
1297	58	9.0	346	1	NUZM_STRCA	Q21398 struthio ca	1370	58	9.0	346	2	Q9G8K6_9AMSA	Q9g8k6 ammodramus
1298	58	9.0	346	2	Q674V2_PODCA	Q674v2 podocoryne	1371	58	9.0	346	2	Q9G8K8_9EMBE	Q9g8k8 pipilo fusc
1299	58	9.0	346	2	Q8DKX8_SYNEL	Q8dkx8 synechococc	1372	58	9.0	346	2	Q9G8L0_MELMO	Q9g8l0 melospiza m
1300	58	9.0	346	2	Q63768_ANAAU	Q63768 anas auckla	1373	58	9.0	346	2	Q9G8L0_SPIBR	Q9g8l0 spizella br
1301	58	9.0	346	2	Q63769_ANAAU	Q63769 anas auckla	1374	58	9.0	346	2	Q9G8M9_9FRIN	Q9g8m9 peucedramus
1302	58	9.0	346	2	Q63771_ANACH	Q63771 anas chlora	1375	58	9.0	346	2	Q9TCL5_9ICTE	Q9tcl5 gymnostinop
1303	58	9.0	346	2	Q63772_9AVES	Q63772 anas caroli	1376	58	9.0	346	2	Q9TCM3_9ICTE	Q9tcm3 icterus par
1304	58	9.0	346	2	Q63773_ANACN	Q63773 anas cyanop	1377	58	9.0	346	2	Q63776_ANABR	Q63766 amazonetta
1305	58	9.0	346	2	Q63774_ANAER	Q63774 anas erythr	1378	58	9.0	346	2	Q63776_ANAGE	Q63776 anas georgi
1306	58	9.0	346	2	Q63777_ANAHO	Q63777 anas hotten	1379	58	9.0	346	2	Q63787_AYATM	Q63787 aythya amer
1307	58	9.0	346	2	Q63779_ANAPA	Q63779 anas platat	1380	58	9.0	346	2	Q63791_CHEJU	Q63791 chenonetta
1308	58	9.0	346	2	Q63780_ANAPN	Q63780 anas puna (1381	58	9.0	346	2	Q63792_CVACY	Q63792 cyanochen c
1309	58	9.0	346	2	Q63781_ANAQU	Q63781 anas querqu	1382	58	9.0	346	2	Q63799_ANASI	Q63799 anas sibia
1310	58	9.0	346	2	Q63782_ANASM	Q63782 anas smithi	1383	58	9.0	346	2	Q63800_ANAST	Q63800 anas strepe
1311	58	9.0	346	2	Q63783_9AVES	Q63783 specularias	1384	58	9.0	346	2	Q2TRB9_DENTO	Q2tre9 dendroica t
1312	58	9.0	346	2	Q63784_9ANASA	Q63784 anas sparsa	1385	58	9.0	346	2	Q2TRP9_9EMBE	Q2trp9 dendroica g
1313	58	9.0	346	2	Q63785_9ANASE	Q63785 anas superc	1386	58	9.0	346	2	Q2TRT9_9EMBE	Q2trt9 dendroica n
1314	58	9.0	346	2	Q63790_9AVES	Q63790 aescornia	1387	58	9.0	346	2	Q2TRU4_DENVR	Q2tr4 dendroica v
1315	58	9.0	346	2	Q63792_LOPSP	Q63792 lophonetta	1388	58	9.0	346	2	Q2SEYK6_9EMBE	Q2seyk6 ammodramus
1316	58	9.0	346	2	Q63802_SARME	Q63802 sarkidiorni	1389	58	9.0	346	2	Q2SEYK7_9EMBE	Q2seyk7 passerulus
1317	58	9.0	346	2	Q63804_9AVES	Q63804 tadorna tad	1390	58	9.0	346	2	Q2SEYT2_PASSN	Q2seyt2 passerulus
1318	58	9.0	346	2	Q63955_9AVES	Q63955 anas zonorh	1391	58	9.0	346	2	Q2SEYT3_PASSN	Q2seyt3 passerulus
1319	58	9.0	346	2	Q63967_9ANABA	Q63967 anas bahame	1392	58	9.0	346	2	Q6VSN7_BOMGA	Q6vsn7 bombycilla
1320	58	9.0	346	2	Q63970_9ANAFV	Q63970 anas flavir	1393	58	9.0	346	2	Q8M2U4_9EMBE	Q8m2u4 tiaris oliv
1321	58	9.0	346	2	Q63975_9ANAGI	Q63975 anas gibber	1394	58	9.0	346	2	Q8M451_1CTVI	Q8m451 icteria vir
1322	58	9.0	346	2	Q63978_ANACL	Q63978 anas clypea	1395	58	9.0	346	2	Q8M728_9COLU	Q8m728 streptopeli
1323	58	9.0	346	2	Q63983_9ANALZ	Q63983 anas luzoni	1396	58	9.0	346	2	Q8SK76_9ICTE	Q8sk76 gymnostinop
1324	58	9.0	346	2	Q58VF3_9PASS	Q58vf3 cecropis da	1397	58	9.0	346	2	Q8SK85_9ICTE	Q8sk85 pearocolius
1325	58	9.0	346	2	Q58VF5_9PASS	Q58vf5 cecropis ab	1398	58	9.0	346	2	Q955U9_MELGA	Q955u9 meleagris g
1326	58	9.0	346	2	Q58VP8_PASSN	Q58vp8 passerulus	1399	58	9.0	346	2	Q9G8K5_1CTVI	Q9g8k5 icteria vir
1327	58	9.0	346	2	Q7H6D3_9ICTE	Q7h6d3 pearocolius	1400	58	9.0	347	2	Q4RC25_TETNG	Q4rc25 tetraodon n
1328	58	9.0	346	2	Q7HXQ8_9ICTE	Q7hxq8 pearocolius	1401	58	9.0	350	2	Q8DH23_SYNEL	Q8dh23 synechococc
1329	58	9.0	346	2	Q7HXQ9_9ICTE	Q7hxq9 pearocolius	1402	58	9.0	367	2	Q2UHL4_ASPOR	Q2uhl4 aspergillus
1330	58	9.0	346	2	Q734X3_ANAUN	Q734x3 anas undula	1403	58	9.0	369	2	Q8DJ75_SYNEL	Q8dj75 synechococc
1331	58	9.0	346	2	Q734X4_ANAUN	Q734x4 anas rubrip	1404	58	9.0	378	2	Q4H2J6_CIOIN	Q4h2j6 ciona intes
1332	58	9.0	346	2	Q734X5_9ANARH	Q734x5 anas rhynch	1405	58	9.0	394	1	ZN193_HUMAN	Q15535 homo sapien
1333	58	9.0	346	2	Q7J4X6_9ANAPL	Q7j4x6 anas poeclt	1406	58	9.0	394	2	Q2TTR1_HUMAN	Q2ttr1 homo sapien
1334	58	9.0	346	2	Q7J4X8_9ANAPL	Q7j4x8 anas platyr	1407	58	9.0	394	2	Q58400_PRRHO	Q58400 pyrococtus
1335	58	9.0	346	2	Q7J4X9_9ANALA	Q7j4x9 anas layean	1408	58	9.0	413	2	Q6PH97_MOUSE	Q6ph97 mus musculus
1336	58	9.0	346	2	Q7J4Y0_9ANALA	Q7j4y0 anas fulvig	1409	58	9.0	414	2	Q4H293_GIBZE	Q4h293 gibberella
1337	58	9.0	346	2	Q7J4Y1_9ANAFV	Q7j4y1 anas flavir	1410	58	9.0	416	2	Q86K46_DICDI	Q86k46 dictyosteli
1338	58	9.0	346	2	Q7J4Y2_9AVES	Q7j4y2 anas diaxi	1411	58	9.0	423	2	Q8X205_TALEM	Q8x205 talaromyces
1339	58	9.0	346	2	Q7J4Y3_9ANADI	Q7j4y3 anas discor	1412	58	9.0	435	2	Q3V3T7_MOUSE	Q3v3t7 mus musculu
1340	58	9.0	346	2	Q7J4Y4_9ANACN	Q7j4y4 anas cyanop	1413	58	9.0	451	2	Q4S027_TETNG	Q4s027 tetraodon n
1341	58	9.0	346	2	Q7J4Y5_9ANACS	Q7j4y5 anas castan	1414	58	9.0	454	2	Q55FQ0_DICDI	Q55fq0 dictyosteli
1342	58	9.0	346	2	Q7J4Y6_9ANACR	Q7j4y6 anas crecca	1415	58	9.0	459	2	Q55FQ0_DICDI	Q55fq0 dictyosteli
1343	58	9.0	346	2	Q7J4Y7_9ANABA	Q7j4y7 anas bahame	1416	58	9.0	460	2	Q7PR34_ANOGA	Q7pr34 anopheles g
1344	58	9.0	346	2	Q85IT3_MOTFL	Q85it3 motacilla f	1417	58	9.0	470	2	Q9P758_NEUCR	Q9p758 neuropora
1345	58	9.0	346	2	Q85IT5_MOTFL	Q85it5 motacilla f	1418	58	9.0	470	2	Q9XUY1_CABEL	Q9xuy1 caenorhabdi

1419	58	9.0	472	2	Q4RGH9_TETNG	Q4rgh9 tetraodon n	1492	58	9.0	1514	2	Q9VUN0_DROME	Q9vun0 drosophila
1420	58	9.0	479	2	Q8DIU5_SYNEL	Q8diu5 synecococc	1493	58	9.0	1639	1	LAMC1_DROME	rl5215 drosophila
1421	58	9.0	484	2	Q9AQK9_9BACT	Q9aak9 prevotella	1494	58	9.0	1639	2	Q5BI30_DROME	Q5bi30 drosophila
1422	58	9.0	487	1	CSN1_XENLA	Q6nts xenopus lae	1495	58	9.0	1739	2	Q4SRN8_TETNG	Q4arn8 tetraodon n
1423	58	9.0	489	2	Q3UQZ0_BURP1	Q3jqz0 burkholderi	1496	58	9.0	1965	2	Q6FRD9_CANGA	Q6frd9 candida gla
1424	58	9.0	492	2	Q5FPM1_GLUOX	Q5fpm1 gluconobact	1497	58	9.0	2101	2	Q61KX2_CABER	Q61kx2 caenorhabdi
1425	58	9.0	504	2	Q8BIF4_MOUSE	Q8bif4 mus musculus	1498	58	9.0	2396	2	Q2YV00_STAAB	Q2yv00 staphylococ
1426	58	9.0	521	2	Q7SXB6_BRARE	Q7sxb6 brachydanio	1499	58	9.0	3550	2	Q9JUN2_MOUSE	Q9jjn2 mus musculus
1427	58	9.0	536	2	Q9SRJ5_DICDI	Q9spj5 dictyosteli	1500	58	9.0	5376	1	ZAN_MOUSE	O88799 mus musculus
1428	58	9.0	543	2	Q67SV0_SYMTH	Q67sv0 symbiobacte							
1429	58	9.0	544	2	Q33OX7_9GAMM	Q33qx7 shewanella							
1430	58	9.0	545	2	Q2W9X9_MAGSA	Q2w9x9 magnetospir							
1431	58	9.0	552	2	Q8DHL8_SYNEL	Q8dhl8 synecococc							
1432	58	9.0	569	2	Q4QDG9_LEIMA	Q4qdg9 leishmania							
1433	58	9.0	572	1	MPIP3_XENLA	P3031 xenopus lae							
1434	58	9.0	585	2	Q9YHU3_FUGRU	Q9yhu3 fugu rubrip							
1435	58	9.0	588	2	Q4P2X7_USTWA	Q4px7 ustilago ma							
1436	58	9.0	588	2	Q55ZA9_CRYNE	Q55za9 cryptococcu							
1437	58	9.0	589	1	ZNI131_PONPY	Q5rauv pongo pygma							
1438	58	9.0	596	2	Q5RAL5_PONPY	Q5ral5 pongo pygma							
1439	58	9.0	602	2	Q3UZ32_MOUSE	Q3uz32 mus musculus							
1440	58	9.0	603	2	Q22787_ARATH	Q22787 arabidopsis							
1441	58	9.0	603	2	Q4RSD5_TETNG	Q4rsd5 tetraodon n							
1442	58	9.0	606	2	Q3TDM4_MOUSE	Q3tdw4 mus musculus							
1443	58	9.0	610	2	Q8CC52_MOUSE	Q8cc52 mus musculus							
1444	58	9.0	629	2	Q4QOQ4_LEIMA	Q4qoq4 leishmania							
1445	58	9.0	635	2	Q3NCR3_9PROT	Q3ncr3 nitrosomona							
1446	58	9.0	654	2	Q4H828_9DELO	Q4h828 deinococcus							
1447	58	9.0	673	2	Q6PLT6_CANGA	Q6plt6 candida gla							
1448	58	9.0	679	2	Q6NNW4_DROME	Q6nnw4 drosophila							
1449	58	9.0	694	2	Q8D4H0_VIEVU	Q8d4h0 vibrio vuln							
1450	58	9.0	706	2	Q39912_GONPO	Q39912 gonaulax p							
1451	58	9.0	707	2	Q4DPE5_TRYCR	Q4dpe5 trypanosoma							
1452	58	9.0	709	2	Q4TCA2_TETNG	Q4tca2 tetraodon n							
1453	58	9.0	727	2	Q9SRV9_DROME	Q9srv9 drosophila							
1454	58	9.0	743	2	Q9VLD23_DROME	Q9vld23 drosophila							
1455	58	9.0	744	2	Q3FKL8_9BURK	Q3fkl8 rhodofera							
1456	58	9.0	764	2	Q3UAU1_MOUSE	Q3ua1 mus musculus							
1457	58	9.0	783	2	Q6A167_PEA	Q6a167 pisum sativ							
1458	58	9.0	786	2	Q9FGM0_ARATH	Q9fgm0 arabidopsis							
1459	58	9.0	806	2	Q6GUA3_MOUSE	Q6gua3 mus musculus							
1460	58	9.0	810	2	Q4QAE1_LEIMA	Q4qae1 leishmania							
1461	58	9.0	828	1	POSTN_MOUSE	Q62009 mus musculus							
1462	58	9.0	838	1	Q5RBR3_PONPY	Q5r8r3 pongo pygma							
1463	58	9.0	841	2	Q4MNV8_ASEPU	Q4mnv8 aspergillus							
1464	58	9.0	852	2	Q675V8_9UROC	Q675v8 oikopleura							
1465	58	9.0	908	2	Q4T520_TETNG	Q4t520 tetraodon n							
1466	58	9.0	909	2	Q7L665_HUMAN	Q7l665 homo sapien							
1467	58	9.0	919	2	Q75KM8_HUMAN	Q75km8 homo sapien							
1468	58	9.0	919	2	Q75KM8_HUMAN	Q75km8 homo sapien							
1469	58	9.0	921	2	Q9Y4C2_HUMAN	Q9y4c2 homo sapien							
1470	58	9.0	941	2	Q61ZN8_CABER	Q61zn8 caenorhabdi							
1471	58	9.0	962	2	Q8R381_MOUSE	Q8r381 mus musculus							
1472	58	9.0	994	2	Q8R381_MOUSE	Q8r381 mus musculus							
1473	58	9.0	998	1	EPHA7_HUMAN	Q15375 homo sapien							
1474	58	9.0	998	1	EPHA7_MOUSE	Q61772 mus musculus							
1475	58	9.0	998	1	EPHA7_RAT	P54759 rattus norv							
1476	58	9.0	998	2	Q8BSU8_MOUSE	Q8bsu8 mus musculus							
1477	58	9.0	1033	1	PHF8_MOUSE	Q80tj7 mus musculus							
1478	58	9.0	1037	1	Q3UG39_MOUSE	Q9qv01 mus musculus							
1479	58	9.0	1037	2	Q3UJ15_MOUSE	Q3ug39 mus musculus							
1480	58	9.0	1037	2	Q3UJ41_BURP1	Q3uj41 burkholderi							
1481	58	9.0	1060	2	Q5SUB4_MOUSE	Q5sub4 mus musculus							
1482	58	9.0	1118	2	Q4WZFO_ASEPU	Q4wzf0 aspergillus							
1483	58	9.0	1129	2	Q7RFW1_NEUCR	Q7rfw1 neurospora							
1484	58	9.0	1131	2	Q4WZFO_ASEPU	Q7rfw1 neurospora							
1485	58	9.0	1186	1	STB5L_HUMAN	Q9y2k9 homo sapien							
1486	58	9.0	1205	2	Q3JRH4_BURP1	Q3jrh4 burkholderi							
1487	58	9.0	1206	2	Q2XG17_PSEPU	Q2xg17 pseudomonas							
1488	58	9.0	1292	2	Q9NJAS_BABBO	Q9njas babesia bov							
1489	58	9.0	1423	1	SSH2_HUMAN	Q76176 homo sapien							
1490	58	9.0	1514	2	Q6NN49_DROME	Q6nn49 drosophila							
1491	58	9.0	1514	2	Q9NBK9_DROME	Q9nbk9 drosophila							

ALIGNMENTS

RESULT 1

Q6UXB2_HUMAN PRELIMINARY; PRT; 119 AA.

ID Q6UXB2_HUMAN PRELIMINARY; PRT; 119 AA.

AC Q6UXB2;

DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.

DT 05-JUL-2004, sequence version 1.

DT 21-FEB-2006, entry version 11.

DE DMC (VEGF co-regulated chemokine 1 precursor).

GN Name=VCC1; ORFNames=UNQ473;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;

OC Homo.

OX NCBI_TaxID=9606;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RX MEDLINE=22887236; PubMed=12975309; DOI=10.1101/gr.1293003;

RA Clark H.P., Gurney A.L., Abaya E., Baker K., Baldwin D.T., Brush J.,

RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,

RA Eaton D., Foster J.S., Grimaldi C., Gu Q., Hass P.E., Heldens S.,

RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,

RA Lewis L., Liao D., Mark M.R., Robbie E., Sanchez C., Schoenfeld J.,

RA Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,

RA Vandlen R.L., Watanabe C., Weand D., Woods K., Xie M.-H.,

RA Yansura D.G., Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A.D.,

RA Wood W.L., Godowski P.J., Gray A.M.;

RT "The secreted protein discovery initiative (SPDI), a large-scale

RT effort to identify novel human secreted and transmembrane proteins: a

RT bioinformatics assessment.";

RL Genome Res. 13:2265-2270(2003).

RN [2]

RP NUCLEOTIDE SEQUENCE.

RC TISSUE=Lung and heart;

RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko M., Marusina K., Farmer A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalón D.K., Muny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Whiting J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,

RA Whaley M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Butterfield Y.S., Krzywinski M.I., Skalska U., Smallos D.E.,

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

RT "Generation and initial analysis of more than 15,000 full-length human

RT and mouse cDNA sequences.";

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

RN [3]

RP NUCLEOTIDE SEQUENCE.

RC TISSUE=Lung and heart;

RG NIH MGC Project;

RL Submitted (JAN-2006) to the EMBL/GenBank/DBJ databases.

Dd 61 KRKATAVLGPPRKQPCDCHVKGREKK 86

RESULT 4
Q52VJ8 CIOIN PRELIMINARY; PRT; 170 AA.
ID Q52VJ8 CIOIN PRELIMINARY; PRT; 170 AA.
AC Q52VJ8;
DT 24-MAY-2005, integrated into UniProtKB/TrEMBL.
DT 24-MAY-2005, sequence version 1.
DT 07-FEB-2006, entry version 2.
DE Secreted protein (Fragment).
GN Name=S7;
OS Ciona intestinalis.
OC Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
OC Phlebobranchia; Clonidae; Ciona.
OX NCBI_TaxID=7719;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=14;
RA Khalurin K., Kuern U., Pinnow N., Bosch T.C.G.;
RT "Towards a molecular code for individuality in the absence of MHC:
RT screening for individually variable genes in the urochordate Ciona
RL intestinalis.";
RL Dev. Comp. Immunol. 0:0-0(2005).
CC -----
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CC -----
DR EMBL: AY895028; AAY19463.1; -; mRNA.
CR 1
FT NON TER 1
FT NON TER 170
SQ SEQUENCE 170 AA; 19396 MW; 57776EDA75E2FFE CRC64;

Query Match 12.6%; Score 81; DB 2; Length 170;
Best Local Similarity 27.9%; Pred. No. 3.7; Indels 28; Gaps 5;
Matches 31; Conservative 15; Mismatches 37;

Qy 1 MKVLI-----SSLLLLPLMLMSVSSSLNPGVGARGHRRDGRQAARRWLQEGQQE 49
|||:|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 MRILLILQLVSTASQLSLLPALLLPRLPS-----RSSCSRGCSNAHCRVG--V 51

Qy 50 CECKDWFLR-----APPRKMTVSGLPKKQCPCDHFK--GNVKTRHQRH 92
|||:|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 52 CECNRYYTRGLYGCVAADRSVFSGTGLTVRSPDCGVKYKCIGKARCEPERH 102

RESULT 5
Q52VK0 CIOIN PRELIMINARY; PRT; 170 AA.
ID Q52VK0 CIOIN PRELIMINARY; PRT; 170 AA.
AC Q52VK0;
DT 24-MAY-2005, integrated into UniProtKB/TrEMBL.
DT 24-MAY-2005, sequence version 1.
DT 07-FEB-2006, entry version 2.
DE Secreted protein (Fragment).
GN Name=S7;
OS Ciona intestinalis.
OC Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
OC Phlebobranchia; Clonidae; Ciona.
OX NCBI_TaxID=7719;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=13;
RA Khalurin K., Kuern U., Pinnow N., Bosch T.C.G.;
RT "Towards a molecular code for individuality in the absence of MHC:
RT screening for individually variable genes in the urochordate Ciona
RL intestinalis.";
RL Dev. Comp. Immunol. 0:0-0(2005).
CC -----
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CC -----
DR EMBL: AY895026; AAY19461.1; -; mRNA.
CR 1
FT NON TER 1


```

QY    99 HSRACQQ-----FLKQCQLRSFA 116  
      :|||:|:||  
Db    79 GTRPVQAGTAVFVKELQAERSFA 100  
  
RESULT 11  
Q4BU62_BURVI PRELIMINARY; PRT; 844 AA.  
ID Q4BU62;  
AC AC  
DT 13-SEP-2005, integrated into UniProtKB/TREMBL.  
DT 13-SEP-2005, sequence version 1.  
DT 07-FEB-2006, entry version 2.  
DE Aldehyde dehydrogenase.  
GN ORFNAMES=Bcep1808DRAFT_7356;  
GC Burkholderia vietnamiensis G4.  
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;  
OC Burkholderiaceae; Burkholderia; Burkholderia cepacia complex.  
OX NCBI_Taxid=269482;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=G4;  
RG US DOE Joint Genome Institute (JGI-PGF);  
RA Copeland A., Lucas S., Lapidus A., Barry K., Detter C., Glavina T.,  
RA Hammon N., Israni S., Piluck S., Richardson P.;  
RT "Sequencing of the draft genome and assembly of Burkholderia  
RT vietnamiensis G4.";  
RL Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases.  
[2]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=G4;  
RG US DOE Joint Genome Institute (JGI-ORNL);  
RA Larimer F., Land M.;  
RT Annotation of the draft genome assembly of Burkholderia vietnamiensis  
RT G4.";  
RL Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases.  
[3]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=G4;  
RG US DOE Joint Genome Institute (JGI-PGF);  
RA Copeland A., Lucas S., Lapidus A., Barry K., Detter C., Glavina T.,  
RA Hammon N., Israni S., Piluck S., Richardson P.;  
RT "Sequencing of the draft genome and assembly of Burkholderia  
RT vietnamiensis G4.";  
RL Submitted (JUN-2005) to the EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is  
CC preliminary data.  
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CC EMBL; AEAEH02000001; EM33087.1; -; Genomic DNA.  
DR GO; GO:0016491; F:oxygenated compound catabolic process; IEA.  
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DT 01-MAR-2003, sequence version 3.
DT 07-FEB-2006, entry version 22.
DE Hypothetical protein.
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RG The C. elegans sequencing consortium;
RT "Genome sequence of the nematode C. elegans: a platform for
investigating biology."
RL Science 282:2012-2018(1998).
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OM protein - protein search, using sw model

Run on: August 3, 2006, 09:54:47 ; Search time 26 Seconds
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400.621 Million cell updates/sec

Title: US-10-015-967-2

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Listing first 1500 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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158	61.5	9.5	691	2	US-09-313-942-18	Sequence 18, Appl	231	59	9.2	180	2	US-09-949-016-10723	Sequence 10723, A
159	61.5	9.5	694	2	US-09-313-942-22	Sequence 22, Appl	232	59	9.2	193	2	US-09-919-172-37	Sequence 37, Appl
160	61.5	9.5	694	2	US-10-282-162-18	Sequence 18, Appl	233	59	9.2	197	2	US-09-370-838-206	Sequence 206, App
161	61.5	9.5	694	2	US-10-282-162-22	Sequence 22, Appl	234	59	9.2	197	2	US-09-854-133-206	Sequence 206, App
162	61	9.5	71	2	US-09-894-882-125	Sequence 125, App	235	59	9.2	228	2	US-09-673-395A-514	Sequence 514, App
163	61	9.5	136	2	US-09-513-999C-7844	Sequence 7844, Ap	236	59	9.2	238	2	US-09-480-884A-174	Sequence 174, App
164	61	9.5	161	2	US-09-252-991A-30023	Sequence 30023, A	237	59	9.2	238	2	US-09-542-615A-174	Sequence 174, App
165	61	9.5	339	2	US-10-101-464A-899	Sequence 899, App	238	59	9.2	238	2	US-09-606-421B-174	Sequence 174, App
166	61	9.5	428	2	US-09-252-991A-25955	Sequence 25955, A	239	59	9.2	238	2	US-09-466-396A-174	Sequence 174, App
167	61	9.5	1014	2	US-09-762-724-2	Sequence 2, Appli	240	59	9.2	238	2	US-09-476-496A-174	Sequence 174, App
168	60.5	9.4	90	2	US-09-252-991A-28743	Sequence 28743, A	241	59	9.2	238	2	US-09-630-940B-174	Sequence 174, App
169	60.5	9.4	106	2	US-09-950-933A-78	Sequence 78, Appl	242	59	9.2	238	2	US-10-007-700-174	Sequence 174, App
170	60.5	9.4	115	2	US-09-270-767-33388	Sequence 33388, A	243	59	9.2	259	2	US-09-252-991A-28573	Sequence 28573, A
171	60.5	9.4	115	2	US-09-270-767-48605	Sequence 48605, A	244	59	9.2	305	2	US-09-270-767-56884	Sequence 56884, A
172	60.5	9.4	162	2	US-09-328-352-5594	Sequence 5594, Ap	245	59	9.2	305	2	US-09-270-767-56884	Sequence 56884, A

246	59	9.2	354	2	US-10-104-047-3587	Sequence 3587, Ap	319	58	9.0	994	3	US-10-073-064-12	Sequence 12, Appl
247	59	9.2	372	2	US-09-252-991A-32717	Sequence 32717, A	320	58	9.0	998	1	US-08-449-645A-17	Sequence 17, Appl
248	59	9.2	402	2	US-09-029-755C-5	Sequence 5, Appli	321	58	9.0	998	1	US-08-702-367A-17	Sequence 17, Appl
249	59	9.2	402	2	US-09-252-991A-24729	Sequence 24729, A	322	58	9.0	998	2	US-08-368-776A-2	Sequence 2, Appli
250	59	9.2	416	2	US-09-270-767-41646	Sequence 41646, A	323	58	9.0	998	2	US-09-949-016-6501	Sequence 6501, Ap
251	59	9.2	587	2	US-09-252-991A-18280	Sequence 18280, A	324	58	9.0	998	2	US-09-378-759-17	Sequence 17, Appl
252	59	9.2	780	2	US-09-252-991A-18846	Sequence 18846, A	325	58	9.0	998	5	US-10-073-064-2	Sequence 2, Appli
253	59	9.2	871	2	US-09-773-426A-3	Sequence 3, Appli	326	58	9.0	998	5	PCT-US95-04681-17	Sequence 17, Appl
254	59	9.2	871	2	US-10-314-881-3	Sequence 3, Appli	327	58	9.0	998	5	PCT-US96-00419-2	Sequence 2, Appli
255	59	9.2	871	2	US-09-495-823-3	Sequence 3, Appli	328	58	9.0	1005	2	US-09-949-016-9901	Sequence 9901, Ap
256	59	9.2	871	3	US-10-426-776-11	Sequence 11, Appl	329	58	9.0	1037	2	US-09-428-711A-21	Sequence 21, Appl
257	59	9.2	981	2	US-09-252-991A-16920	Sequence 16920, A	330	58	9.0	1039	2	US-09-252-991A-31121	Sequence 31121, A
258	59	9.2	1008	2	US-09-252-991A-27063	Sequence 27063, A	331	58	9.0	1439	2	US-09-543-681A-7560	Sequence 7560, Ap
259	59	9.2	1608	2	US-09-964-956-61	Sequence 61, Appl	332	58	9.0	2955	1	US-08-443-260-3	Sequence 3, Appli
260	59	9.2	1611	2	US-09-668-673B-16	Sequence 16, Appl	333	58	9.0	2955	2	US-08-442-805A-3	Sequence 3, Appli
261	59	9.2	1611	2	US-10-389-532-16	Sequence 16, Appl	334	58	9.0	2955	2	US-08-443-900A-3	Sequence 3, Appli
262	59	9.2	1788	2	US-09-964-956-60	Sequence 60, Appl	335	58	9.0	2955	2	US-08-444-818-124	Sequence 124, App
263	59	9.2	2641	2	US-09-964-956-63	Sequence 63, Appl	336	58	9.0	2955	2	US-08-249-843-3	Sequence 3, Appli
264	59	9.2	2811	2	US-09-964-956-27	Sequence 27, Appl	337	58	9.0	2995	1	US-08-444-818-138	Sequence 138, App
265	59	9.2	2814	2	US-09-964-956-25	Sequence 25, Appl	338	58	9.0	3011	1	US-08-833-678A-6	Sequence 6, Appli
266	58.5	9.1	81	2	US-09-621-976-6450	Sequence 6450, Ap	339	58	9.0	3011	2	US-08-444-818-177	Sequence 177, App
267	58.5	9.1	132	2	US-09-270-767-32010	Sequence 32010, A	340	58	9.0	3011	2	US-08-529-169A-6	Sequence 6, Appli
268	58.5	9.1	132	2	US-09-270-767-47227	Sequence 47227, A	341	58	9.0	3011	2	US-09-483-793-6	Sequence 6, Appli
269	58.5	9.1	138	2	US-09-252-991A-20349	Sequence 20349, A	342	58	9.0	3011	3	US-10-232-643-6	Sequence 6, Appli
270	58.5	9.1	170	2	US-09-252-991A-16827	Sequence 16827, A	343	57.5	8.9	128	2	US-09-252-991A-32567	Sequence 32567, A
271	58.5	9.1	184	2	US-09-270-767-31979	Sequence 31979, A	344	57.5	8.9	145	2	US-09-270-767-39242	Sequence 39242, A
272	58.5	9.1	184	2	US-09-270-767-47196	Sequence 47196, A	345	57.5	8.9	145	2	US-09-270-767-54459	Sequence 54459, A
273	58.5	9.1	185	2	US-09-252-991A-21225	Sequence 21225, A	346	57.5	8.9	217	2	US-09-602-543-5	Sequence 5, Appli
274	58.5	9.1	198	2	US-09-252-991A-22691	Sequence 22691, A	347	57.5	8.9	218	2	US-09-252-991A-19579	Sequence 19579, A
275	58.5	9.1	208	2	US-09-252-991A-23874	Sequence 23874, A	348	57.5	8.9	231	2	US-09-252-991A-27366	Sequence 27366, A
276	58.5	9.1	302	2	US-09-252-991A-24042	Sequence 24042, A	349	57.5	8.9	232	2	US-08-807-992B-4	Sequence 4, Appli
277	58.5	9.1	328	2	US-09-252-991A-26593	Sequence 26593, A	350	57.5	8.9	235	2	US-09-602-543-4	Sequence 18254, A
278	58.5	9.1	346	2	US-09-252-991A-26988	Sequence 26988, A	351	57.5	8.9	237	2	US-09-252-991A-18254	Sequence 18254, A
279	58.5	9.1	366	2	US-09-252-991A-22528	Sequence 22528, A	352	57.5	8.9	248	2	US-09-252-991A-30679	Sequence 30679, A
280	58.5	9.1	392	2	US-09-252-991A-27219	Sequence 27219, A	353	57.5	8.9	296	2	US-09-252-991A-17538	Sequence 17538, A
281	58.5	9.1	404	2	US-10-375-693-26	Sequence 26, Appl	354	57.5	8.9	377	2	US-09-252-991A-24649	Sequence 24649, A
282	58.5	9.1	428	2	US-09-270-767-45014	Sequence 45014, A	355	57.5	8.9	432	2	US-09-439-261-9	Sequence 9, Appli
283	58.5	9.1	430	2	US-09-252-991A-33661	Sequence 32661, A	356	57.5	8.9	432	2	US-09-227-613-9	Sequence 9, Appli
284	58.5	9.1	431	2	US-10-029-180-32	Sequence 32, Appl	357	57.5	8.9	432	2	US-10-191-513A-9	Sequence 9, Appli
285	58.5	9.1	431	2	US-09-270-767-45143	Sequence 45143, A	358	57.5	8.9	465	2	US-09-439-261-40	Sequence 40, Appl
286	58.5	9.1	480	2	US-09-252-991A-20125	Sequence 20125, A	359	57.5	8.9	465	2	US-09-227-613-38	Sequence 38, Appl
287	58.5	9.1	498	2	US-10-183-992-2	Sequence 2, Appli	360	57.5	8.9	465	2	US-10-191-513A-38	Sequence 38, Appl
288	58.5	9.1	618	2	US-09-252-991A-28358	Sequence 28358, A	361	57.5	8.9	475	2	US-09-252-991A-31078	Sequence 31078, A
289	58.5	9.1	977	2	US-09-252-991A-16655	Sequence 16655, A	362	57.5	8.9	564	2	US-09-252-991A-26890	Sequence 26890, A
290	58.5	9.1	1019	2	US-10-183-992-4	Sequence 4, Appli	363	57.5	8.9	709	2	US-08-937-067-12	Sequence 12, Appl
291	58.5	9.1	1101	2	US-09-561-709B-5	Sequence 5, Appli	364	57.5	8.9	890	3	US-09-958-359-34	Sequence 34, Appl
292	58.5	9.1	1761	2	US-09-561-709B-1	Sequence 1, Appli	365	57.5	8.9	955	2	US-10-094-749-2652	Sequence 2652, Ap
293	58	9.0	160	2	US-08-444-818-18	Sequence 18, Appl	366	57.5	8.9	1083	1	US-08-296-014A-2	Sequence 2, Appli
294	58	9.0	186	1	US-08-089-458B-6	Sequence 6, Appli	367	57.5	8.9	1083	1	US-08-596-405-2	Sequence 2, Appli
295	58	9.0	202	2	US-10-104-047-3917	Sequence 3917, Ap	368	57.5	8.9	1083	1	US-08-877-620-2	Sequence 2, Appli
296	58	9.0	211	2	US-09-252-991A-32460	Sequence 32460, A	369	57.5	8.9	1083	2	US-09-287-368-2	Sequence 2, Appli
297	58	9.0	255	2	US-09-252-991A-31670	Sequence 31670, A	370	57.5	8.9	1083	2	US-09-626-795-2	Sequence 2, Appli
298	58	9.0	268	2	US-10-094-749-3060	Sequence 3060, Ap	371	57.5	8.9	1083	2	US-10-183-992-6	Sequence 6, Appli
299	58	9.0	276	2	US-09-252-991A-18128	Sequence 18128, A	372	57.5	8.9	2120	2	US-09-949-016-9768	Sequence 9768, Ap
300	58	9.0	394	2	US-09-949-016-6716	Sequence 6716, Ap	373	57	8.9	119	2	US-09-950-933A-63	Sequence 63, Appl
301	58	9.0	410	2	US-09-252-991A-30570	Sequence 30570, A	374	57	8.9	144	2	US-09-180-100-21	Sequence 21, Appl
302	58	9.0	427	2	US-09-949-016-9842	Sequence 9842, Ap	375	57	8.9	144	2	US-09-252-991A-21500	Sequence 21500, A
303	58	9.0	485	2	US-09-252-991A-17797	Sequence 17797, A	376	57	8.9	144	2	US-09-949-713-21	Sequence 21, Appl
304	58	9.0	508	2	US-09-252-991A-32651	Sequence 32651, A	377	57	8.9	150	2	US-09-732-210-626	Sequence 626, App
305	58	9.0	530	2	US-09-252-991A-28311	Sequence 28311, A	378	57	8.9	156	2	US-10-031-607-9	Sequence 9, Appli
306	58	9.0	610	2	US-08-368-776A-3	Sequence 3, Appli	379	57	8.9	159	2	US-09-180-100-23	Sequence 23, Appl
307	58	9.0	610	3	US-10-073-064-3	Sequence 3, Appli	380	57	8.9	159	2	US-09-949-713-23	Sequence 23, Appl
308	58	9.0	610	5	PCT-US96-00419-3	Sequence 3, Appli	381	57	8.9	185	2	US-09-252-991A-17220	Sequence 17220, A
309	58	9.0	626	2	US-08-368-776A-5	Sequence 5, Appli	382	57	8.9	195	2	US-10-031-607-11	Sequence 11, Appl
310	58	9.0	626	5	US-10-073-064-5	Sequence 5, Appli	383	57	8.9	197	2	US-08-974-022-49	Sequence 49, Appl
311	58	9.0	626	5	PCT-US96-00419-5	Sequence 5, Appli	384	57	8.9	197	2	US-08-795-445A-49	Sequence 49, Appl
312	58	9.0	739	2	US-08-444-818-148	Sequence 148, App	385	57	8.9	197	2	US-08-795-447A-49	Sequence 49, Appl
313	58	9.0	794	2	US-09-949-016-9883	Sequence 9883, Ap	386	57	8.9	197	2	US-08-974-185-49	Sequence 49, Appl
314	58	9.0	811	1	US-08-426-627-2	Sequence 2, Appli	387	57	8.9	197	2	US-08-795-446B-49	Sequence 49, Appl
315	58	9.0	811	1	US-08-426-627-22	Sequence 22, Appl	388	57	8.9	197	2	US-08-706-945D-435	Sequence 135, App
316	58	9.0	993	2	US-08-368-776A-11	Sequence 11, Appl	389	57	8.9	197	2	US-08-577-788C-49	Sequence 49, Appl
317	58	9.0	993	3	US-10-073-064-11	Sequence 11, Appl	390	57	8.9	197	3	US-09-613-591F-132	Sequence 132, App
318	58	9.0	994	2	US-08-368-776A-12	Sequence 12, Appl	391	57	8.9	203	2	US-10-031-607-10	Sequence 10, Appl

392	57	8.9	213	2	US-10-375-693-3	Sequence 3, Appli	455	56	8.7	160	2	US-09-270-767-52886	Sequence 52886, A
393	57	8.9	217	2	US-09-252-991A-28385	Sequence 28385, A	456	56	8.7	165	1	US-08-350-884-82	Sequence 82, Appl
394	57	8.9	218	2	US-09-252-991A-26852	Sequence 26852, A	467	56	8.7	165	1	US-08-709-173-82	Sequence 82, Appl
395	57	8.9	232	2	US-09-533-310B-4	Sequence 4, Appli	468	56	8.7	165	1	US-08-709-177-82	Sequence 82, Appl
396	57	8.9	235	2	US-09-489-039A-7180	Sequence 7180, Ap	469	56	8.7	174	2	US-09-854-133-426	Sequence 426, App
397	57	8.9	239	2	US-09-252-991A-32603	Sequence 32603, A	470	56	8.7	221	2	US-09-252-991A-31566	Sequence 31566, A
398	57	8.9	284	2	US-09-252-991A-17772	Sequence 17772, A	471	56	8.7	224	2	US-09-252-991A-20377	Sequence 20377, A
399	57	8.9	289	2	US-09-042-785A-11	Sequence 11, Appl	472	56	8.7	297	2	US-09-252-991A-21551	Sequence 21551, A
400	57	8.9	298	2	US-09-252-991A-31845	Sequence 31845, A	473	56	8.7	313	1	US-08-483-695-7	Sequence 7, Appli
401	57	8.9	300	2	US-09-107-532A-6782	Sequence 6782, Ap	474	56	8.7	313	1	US-08-483-695-45	Sequence 45, Appl
402	57	8.9	301	2	US-09-252-991A-27597	Sequence 27597, A	475	56	8.7	313	1	US-07-965-285-7	Sequence 7, Appli
403	57	8.9	306	2	US-09-107-532A-5464	Sequence 5464, Ap	476	56	8.7	313	1	US-07-965-285-45	Sequence 45, Appl
404	57	8.9	376	2	US-09-180-100-22	Sequence 22, Appl	477	56	8.7	313	1	US-08-487-231-7	Sequence 7, Appli
405	57	8.9	376	2	US-09-949-713-22	Sequence 22, Appl	478	56	8.7	313	1	US-08-487-231-45	Sequence 45, Appl
406	57	8.9	405	2	US-10-375-693-34	Sequence 34, Appl	479	56	8.7	313	2	US-09-201-912-7	Sequence 7, Appli
407	57	8.9	416	2	US-09-487-558B-80	Sequence 80, Appl	480	56	8.7	313	2	US-09-201-912-45	Sequence 45, Appl
408	57	8.9	448	2	US-09-252-991A-27497	Sequence 27497, A	481	56	8.7	338	2	US-09-252-991A-31201	Sequence 31201, A
409	57	8.9	479	2	US-09-252-991A-32884	Sequence 32884, A	482	56	8.7	342	2	US-10-104-047-2985	Sequence 2985, Ap
410	57	8.9	496	2	US-09-252-991A-21949	Sequence 21949, A	483	56	8.7	352	2	US-09-252-991A-24482	Sequence 24482, A
411	57	8.9	508	2	US-09-949-016-9414	Sequence 9414, Ap	484	56	8.7	416	2	US-09-949-016-11669	Sequence 11669, A
412	57	8.9	564	2	US-09-442-100-15	Sequence 15, Appl	485	56	8.7	417	2	US-08-867-611-20	Sequence 20, Appl
413	57	8.9	564	2	US-08-939-106-15	Sequence 15, Appl	486	56	8.7	417	2	US-09-690-359-20	Sequence 20, Appl
414	57	8.9	564	2	US-09-442-102-15	Sequence 15, Appl	487	56	8.7	417	5	PCT-US92-06965A-25	Sequence 25, Appl
415	57	8.9	579	2	US-08-743-168B-36	Sequence 36, Appl	488	56	8.7	421	2	US-09-600-588-1	Sequence 1, Appli
416	57	8.9	592	2	US-10-438-339-8	Sequence 3, Appli	489	56	8.7	422	2	US-10-104-047-2882	Sequence 2882, Ap
417	57	8.9	786	2	US-09-103-429A-3	Sequence 3, Appli	490	56	8.7	428	2	US-03-489-039A-14169	Sequence 14169, A
418	57	8.9	788	2	US-09-294-663-3	Sequence 3, Appli	491	56	8.7	428	2	US-09-907-794A-142	Sequence 142, App
419	57	8.9	790	2	US-09-252-991A-23247	Sequence 23247, A	492	56	8.7	428	2	US-09-905-125A-142	Sequence 142, App
420	57	8.9	812	2	US-09-252-991A-18528	Sequence 18528, A	493	56	8.7	428	2	US-09-902-775A-142	Sequence 142, App
421	57	8.9	878	2	US-10-104-047-2027	Sequence 2027, Ap	494	56	8.7	428	2	US-09-906-700-142	Sequence 142, App
422	57	8.9	976	1	US-08-449-645A-18	Sequence 18, Appl	495	56	8.7	428	2	US-03-903-603A-142	Sequence 142, App
423	57	8.9	976	1	US-08-702-367A-18	Sequence 18, Appl	496	56	8.7	428	2	US-09-904-920A-142	Sequence 142, App
424	57	8.9	976	1	US-09-949-016-6499	Sequence 6499, Ap	497	56	8.7	428	2	US-09-905-381A-142	Sequence 142, App
425	57	8.9	976	2	US-09-378-759-18	Sequence 18, Appl	498	56	8.7	428	2	US-09-906-618-142	Sequence 142, App
426	57	8.9	976	5	PCT-US95-04681-18	Sequence 18, Appl	499	56	8.7	428	2	US-09-906-646-142	Sequence 142, App
427	57	8.9	976	1	US-08-673-789-8	Sequence 8, Appli	500	56	8.7	428	2	US-09-904-652-142	Sequence 142, App
428	57	8.9	1013	2	US-09-949-016-7991	Sequence 7991, Ap	501	56	8.7	428	2	US-09-902-736A-142	Sequence 142, App
429	57	8.9	1225	2	US-09-252-991A-25018	Sequence 25018, A	502	56	8.7	428	2	US-09-906-722A-142	Sequence 142, App
430	57	8.9	1264	2	US-10-375-693-30	Sequence 30, Appl	503	56	8.7	428	2	US-09-905-449-142	Sequence 142, App
431	57	8.9	3080	7	5233423-4	Patent No. 5233423	504	56	8.7	428	2	US-09-903-562B-142	Sequence 142, App
432	57	8.9	3287	1	US-08-477-451-7	Sequence 7, Appli	505	56	8.7	428	2	US-09-906-679A-142	Sequence 142, App
433	57	8.9	140	2	US-09-252-991A-25137	Sequence 25137, A	506	56	8.7	428	3	US-09-907-841-142	Sequence 142, App
434	56.5	8.8	161	5	PCT-US95-05741-11	Sequence 11, Appl	507	56	8.7	428	3	US-09-252-991A-21838	Sequence 21838, A
435	56.5	8.8	173	2	US-09-270-767-31671	Sequence 31671, A	508	56	8.7	435	2	US-09-270-767-41457	Sequence 41457, A
436	56.5	8.8	173	2	US-09-270-767-46888	Sequence 46888, A	509	56	8.7	462	2	US-10-104-047-3571	Sequence 3571, Ap
437	56.5	8.8	181	2	US-09-252-991A-30203	Sequence 30203, A	510	56	8.7	462	1	US-08-833-678A-2	Sequence 2, Appli
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443	56.5	8.8	326	2	US-09-252-991A-18751	Sequence 18751, A	516	56	8.7	521	2	US-09-370-368-4	Sequence 40, Appli
444	56.5	8.8	340	2	US-09-940-244-365	Sequence 365, App	517	56	8.7	521	2	US-09-252-991A-26010	Sequence 26010, A
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446	56.5	8.8	347	2	US-09-489-039A-9485	Sequence 9485, Ap	519	56	8.7	585	2	US-09-270-767-56754	Sequence 56754, A
447	56.5	8.8	409	2	US-09-489-039A-8655	Sequence 8655, Ap	520	56	8.7	589	2	US-10-094-749-3079	Sequence 3079, Ap
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449	56.5	8.8	418	2	US-09-355-700-13	Sequence 13, Appl	522	56	8.7	595	2	US-09-370-838-187	Sequence 187, App
450	56.5	8.8	418	2	US-09-534-376A-13	Sequence 13, Appl	523	56	8.7	595	2	US-09-252-991A-18995	Sequence 18995, A
451	56.5	8.8	447	2	US-09-482-273-128	Sequence 128, App	524	56	8.7	595	2	US-09-854-133-187	Sequence 187, App
452	56.5	8.8	451	2	US-09-949-016-9567	Sequence 9567, Ap	525	56	8.7	610	2	US-09-949-016-6945	Sequence 6945, Ap
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462	56	8.7	156	2	US-09-252-991A-32450	Sequence 32450, A	535	56	8.7	678	2	US-09-583-110-3422	Sequence 3422, Ap
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581	56	8.7	915	2	US-09-903-603A-34	Sequence 34, Appli	654	55.5	8.6	206	1	US-08-468-847B-20	Sequence 20, Appli
582	56	8.7	915	2	US-09-904-920A-34	Sequence 34, Appli	655	55.5	8.6	206	2	US-09-188-930-159	Sequence 159, App
583	56	8.7	915	2	US-09-909-064-34	Sequence 34, Appli	656	55.5	8.6	206	2	US-09-188-930-286	Sequence 286, App
584	56	8.7	915	2	US-09-905-381A-34	Sequence 34, Appli	657	55.5	8.6	206	2	US-09-312-283C-159	Sequence 159, App
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687	55.5	8.6	2237	1	US-08-455-543A-48	Sequence 48, Appl	760	54.5	8.5	138	2	US-09-252-991A-26969	Sequence 26969, A
688	55.5	8.6	2237	1	US-08-223-305C-48	Sequence 48, Appl	761	54.5	8.5	149	2	US-09-270-767-38212	Sequence 38212, A
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693	55.5	8.6	2339	1	US-08-455-543A-47	Sequence 47, Appl	766	54.5	8.5	164	2	US-09-252-991A-21892	Sequence 21892, A
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701	55	8.5	72	2	US-09-894-882-338	Sequence 338, App	774	54.5	8.5	232	2	US-09-042-105-7	Sequence 7, Appli
702	55	8.5	80	2	US-09-461-697-464	Sequence 464, App	775	54.5	8.5	232	2	US-09-574-708A-10	Sequence 10, Appl
703	55	8.5	93	2	US-09-489-847-240	Sequence 240, App	776	54.5	8.5	232	2	US-10-084-488-7	Sequence 7, Appli
704	55	8.5	93	2	US-09-489-847-362	Sequence 362, App	777	54.5	8.5	232	2	US-09-214-982-33	Sequence 33, Appl
705	55	8.5	177	2	US-09-492-709A-369	Sequence 369, App	778	54.5	8.5	232	2	US-10-268-447-10	Sequence 10, Appl
706	55	8.5	181	2	US-09-780-717-23	Sequence 23, Appl	779	54.5	8.5	232	2	US-09-795-006A-147	Sequence 147, App
707	55	8.5	260	2	US-09-252-991A-26958	Sequence 26958, A	780	54.5	8.5	232	2	US-09-499-468-7	Sequence 7, Appli
708	55	8.5	267	2	US-09-252-991A-18758	Sequence 18758, A	781	54.5	8.5	232	2	US-09-219-442-7	Sequence 7, Appli
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712	55	8.5	347	2	US-09-543-681A-6173	Sequence 6173, Ap	785	54.5	8.5	305	2	US-08-558-135-6	Sequence 6, Appli
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716	55	8.5	411	2	US-09-799-978-10	Sequence 10, Appl	789	54.5	8.5	353	2	US-09-270-767-47841	Sequence 47841, A
717	55	8.5	411	2	US-09-881-401-8	Sequence 8, Appli	790	54.5	8.5	354	2	US-09-252-991A-17512	Sequence 17512, A
718	55	8.5	411	2	US-09-631-603-12	Sequence 12, Appl	791	54.5	8.5	361	2	US-09-252-991A-28125	Sequence 28125, A
719	55	8.5	411	2	US-09-949-016-10763	Sequence 10763, A	792	54.5	8.5	366	2	US-09-252-991A-24338	Sequence 24338, A
720	55	8.5	411	2	US-09-949-016-10764	Sequence 10764, A	793	54.5	8.5	368	2	US-09-252-991A-20452	Sequence 20452, A
721	55	8.5	411	3	US-10-821-502-8	Sequence 8, Appli	794	54.5	8.5	371	2	US-09-252-991A-19098	Sequence 19098, A
722	55	8.5	412	2	US-09-252-991A-21701	Sequence 21701, A	795	54.5	8.5	375	2	US-08-867-611-50	Sequence 50, Appl
723	55	8.5	415	1	US-08-176-620A-4	Sequence 4, Appli	796	54.5	8.5	375	2	US-09-690-359-50	Sequence 50, Appl
724	55	8.5	415	1	US-08-463-862-4	Sequence 4, Appli	797	54.5	8.5	414	2	US-09-252-991A-16649	Sequence 16649, A
725	55	8.5	415	1	US-08-463-985-4	Sequence 4, Appli	798	54.5	8.5	460	2	US-08-444-818-20	Sequence 20, Appl
726	55	8.5	415	1	US-08-458-887-4	Sequence 4, Appli	799	54.5	8.5	465	2	US-09-252-991A-23099	Sequence 23099, A
727	55	8.5	415	2	US-08-932-787B-4	Sequence 4, Appli	800	54.5	8.5	493	2	US-09-252-991A-16925	Sequence 16925, A
728	55	8.5	415	2	US-08-932-012C-4	Sequence 4, Appli	801	54.5	8.5	493	2	US-09-252-991A-28992	Sequence 28992, A
729	55	8.5	415	2	US-08-888-818C-4	Sequence 4, Appli	802	54.5	8.5	494	2	US-09-525-885-2	Sequence 2, Appli
730	55	8.5	415	2	US-10-104-047-2624	Sequence 2624, Ap	803	54.5	8.5	496	2	US-09-252-991A-26668	Sequence 26668, A
731	55	8.5	434	2	US-09-964-899-45	Sequence 45, Appl	804	54.5	8.5	516	2	US-08-927-219-140	Sequence 140, App
732	55	8.5	438	2	US-09-799-978-12	Sequence 12, Appl	805	54.5	8.5	562	2	US-10-104-047-3214	Sequence 3214, Ap
733	55	8.5	441	2	US-09-252-991A-24012	Sequence 24012, A	806	54.5	8.5	564	2	US-09-252-991A-28765	Sequence 28765, A
734	55	8.5	495	2	US-09-252-991A-16768	Sequence 16768, A	807	54.5	8.5	567	2	US-09-927-219-131	Sequence 131, Appl
735	55	8.5	511	2	US-09-252-991A-19753	Sequence 19753, A	808	54.5	8.5	571	1	US-07-955-905A-25	Sequence 25, Appl
736	55	8.5	521	2	US-09-492-709A-368	Sequence 368, App	809	54.5	8.5	581	2	US-09-252-991A-20966	Sequence 20966, A
737	55	8.5	532	2	US-09-583-310-6	Sequence 6, Appli	810	54.5	8.5	587	2	US-09-252-991A-25368	Sequence 25368, A
738	55	8.5	614	2	US-09-252-991A-20210	Sequence 20210, A	811	54.5	8.5	592	2	US-09-252-991A-18124	Sequence 18124, A
739	55	8.5	666	2	US-09-252-991A-17462	Sequence 17462, A	812	54.5	8.5	598	2	US-08-949-016-6699	Sequence 6699, Ap
740	55	8.5	671	2	US-09-252-991A-19375	Sequence 19375, A	813	54.5	8.5	617	2	US-09-949-016-10338	Sequence 10338, A
741	55	8.5	686	1	US-08-350-884-70	Sequence 70, Appl	814	54.5	8.5	631	2	US-09-128-314-2	Sequence 2, Appli
742	55	8.5	686	1	US-08-709-173-70	Sequence 70, Appl	815	54.5	8.5	636	2	US-09-252-991A-32429	Sequence 32429, A
743	55	8.5	686	1	US-08-709-177-70	Sequence 70, Appl	816	54.5	8.5	654	2	US-09-252-991A-25801	Sequence 25801, A
744	55	8.5	797	2	US-09-949-016-6657	Sequence 6657, Ap	817	54.5	8.5	658	2	US-09-252-991A-18483	Sequence 18483, A
745	55	8.5	797	2	US-09-422-999B-8	Sequence 8, Appli	818	54.5	8.5	659	2	US-09-252-991A-17333	Sequence 17333, A
746	55	8.5	841	1	US-08-350-884-86	Sequence 86, Appl	819	54.5	8.5	687	1	US-08-188-281B-14	Sequence 14, Appl
747	55	8.5	841	1	US-08-709-173-86	Sequence 86, Appl	820	54.5	8.5	687	5	PCT-US94-07280-14	Sequence 14, Appl
748	55	8.5	841	1	US-08-709-177-86	Sequence 86, Appl	821	54.5	8.5	687	5	PCT-US95-01087-14	Sequence 14, Appl
749	55	8.5	1056	2	US-09-252-991A-24162	Sequence 24162, A	822	54.5	8.5	937	2	US-09-252-991A-19446	Sequence 19446, A
750	55	8.5	1147	1	US-08-144-121-3	Sequence 3, Appli	823	54.5	8.5	971	2	US-08-867-611-52	Sequence 52, Appl
751	55	8.5	1147	1	US-08-735-893-3	Sequence 3, Appli	824	54.5	8.5	971	2	US-09-690-359-52	Sequence 52, Appl
752	55	8.5	1147	2	US-10-841-139-3	Sequence 3, Appli	825	54.5	8.5	973	2	US-08-867-611-53	Sequence 53, Appl
753	55	8.5	1165	1	US-08-144-121-2	Sequence 2, Appli	826	54.5	8.5	973	2	US-09-690-359-53	Sequence 53, Appl
754	55	8.5	1165	1	US-08-735-893-2	Sequence 2, Appli	827	54.5	8.5	977	2	US-09-302-812-2	Sequence 2, Appli
755	55	8.5	1165	2	US-10-841-139-2	Sequence 2, Appli	828	54.5	8.5	977	2	US-09-511-477-2	Sequence 2, Appli
756	55	8.5	1366	2	US-09-004-838-22	Sequence 22, Appl	829	54.5	8.5	977	2	US-09-511-507-2	Sequence 2, Appli

830	54.5	8.5	977	2	US-09-973-451-2	Sequence 2, Appli	903	54	8.4	323	2	US-10-191-513A-17	Sequence 17, Appl
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832	54.5	8.5	992	2	US-09-690-359-54	Sequence 54, Appl	905	54	8.4	334	2	US-09-949-016-8516	Sequence 8516, Ap
833	54.5	8.5	1342	2	US-09-561-709B-13	Sequence 13, Appl	906	54	8.4	341	2	US-09-029-045-12	Sequence 12, Appl
834	54.5	8.5	1411	2	US-09-252-991A-28408	Sequence 28408, A	907	54	8.4	341	2	US-09-435-321-12	Sequence 12, Appl
835	54.5	8.5	1648	1	US-08-188-281B-12	Sequence 12, Appl	908	54	8.4	347	2	US-09-439-261-42	Sequence 42, Appl
836	54.5	8.5	1648	5	PCT-US94-07080-12	Sequence 12, Appl	909	54	8.4	347	2	US-09-227-613-40	Sequence 40, Appl
837	54.5	8.5	1648	5	PCT-US95-01080-12	Sequence 12, Appl	910	54	8.4	347	2	US-10-191-513A-40	Sequence 40, Appl
838	54.5	8.5	1995	2	US-09-495-714C-6	Sequence 6, Appli	911	54	8.4	351	2	US-09-252-991A-18551	Sequence 18551, A
839	54.5	8.5	2262	2	US-09-269-446D-44	Sequence 44, Appl	912	54	8.4	355	1	US-08-834-655-5	Sequence 5, Appli
840	54.5	8.5	2546	2	US-09-949-016-9500	Sequence 9500, Ap	913	54	8.4	355	2	US-08-834-033A-6	Sequence 6, Appli
841	54.5	8.5	2546	2	US-09-949-016-9501	Sequence 9501, Ap	914	54	8.4	355	2	US-09-363-574-5	Sequence 5, Appli
842	54.5	8.5	2636	2	US-09-252-991A-25753	Sequence 25753, A	915	54	8.4	355	2	US-09-363-526-5	Sequence 5, Appli
843	54.5	8.5	2894	1	US-08-466-975A-23	Sequence 23, Appl	916	54	8.4	359	1	US-08-976-074-5	Sequence 5, Appli
844	54.5	8.5	2894	1	US-08-391-671A-23	Sequence 23, Appl	917	54	8.4	359	1	US-08-083-741-5	Sequence 5, Appli
845	54.5	8.5	2894	2	US-08-467-902B-23	Sequence 23, Appl	918	54	8.4	359	2	US-08-976-166A-5	Sequence 5, Appli
846	54.5	8.5	2894	2	US-09-275-265-23	Sequence 23, Appl	919	54	8.4	360	2	US-09-252-991A-17551	Sequence 17551, A
847	54.5	8.5	2894	2	US-09-941-611-23	Sequence 23, Appl	920	54	8.4	371	2	US-09-252-991A-23955	Sequence 23955, A
848	54.5	8.5	2894	2	US-10-044-995-23	Sequence 23, Appl	921	54	8.4	390	2	US-09-252-991A-27049	Sequence 27049, A
849	54.5	8.5	3011	1	US-08-188-281B-1	Sequence 1, Appli	922	54	8.4	395	2	US-09-248-796A-16028	Sequence 16028, A
850	54.5	8.5	3011	1	US-08-453-552-1	Sequence 1, Appli	923	54	8.4	399	2	US-09-252-991A-21997	Sequence 21997, A
851	54.5	8.5	3011	1	US-08-710-637-1	Sequence 1, Appli	924	54	8.4	403	2	US-09-252-991A-23081	Sequence 23081, A
852	54.5	8.5	3011	2	US-09-014-416-1	Sequence 1, Appli	925	54	8.4	418	2	US-09-252-991A-32095	Sequence 32095, A
853	54.5	8.5	3011	2	US-09-014-416-5	Sequence 5, Appli	926	54	8.4	419	2	US-10-237-551-198	Sequence 198, App
854	54.5	8.5	3011	2	US-09-952-572-9	Sequence 9, Appli	927	54	8.4	437	2	US-09-489-039A-8958	Sequence 8958, Ap
855	54.5	8.5	3011	2	US-10-259-275-20	Sequence 20, Appl	928	54	8.4	451	2	US-09-357-251-35	Sequence 35, Appl
856	54.5	8.5	3011	3	US-10-184-150-3	Sequence 3, Appli	929	54	8.4	457	1	US-08-834-655-2	Sequence 2, Appli
857	54.5	8.5	3011	5	PCT-US93-00907-1	Sequence 1, Appli	930	54	8.4	457	1	US-08-833-610-4	Sequence 4, Appli
858	54.5	8.5	3011	5	PCT-US94-07080-1	Sequence 1, Appli	931	54	8.4	457	2	US-08-834-033A-2	Sequence 2, Appli
859	54.5	8.5	3011	5	PCT-US95-01080-1	Sequence 1, Appli	932	54	8.4	457	2	US-08-834-033A-14	Sequence 14, Appl
860	54.5	8.5	3012	2	US-08-811-566-2	Sequence 2, Appli	933	54	8.4	457	2	US-09-363-574-2	Sequence 2, Appli
861	54.5	8.5	3012	2	US-09-034-756-2	Sequence 2, Appli	934	54	8.4	457	2	US-09-363-526-2	Sequence 2, Appli
862	54	8.4	94	2	US-09-252-991A-28217	Sequence 28217, A	935	54	8.4	457	2	US-09-330-235-18	Sequence 18, Appl
863	54	8.4	106	2	US-09-732-210-1286	Sequence 1286, Ap	936	54	8.4	457	2	US-09-377-452-4	Sequence 4, Appli
864	54	8.4	106	2	US-09-950-933A-70	Sequence 70, Appl	937	54	8.4	458	2	US-09-439-261-10	Sequence 10, Appl
865	54	8.4	120	2	US-10-104-047-2417	Sequence 2417, Ap	938	54	8.4	458	2	US-09-439-261-44	Sequence 44, Appl
866	54	8.4	140	2	US-10-104-074-1769	Sequence 1769, Ap	939	54	8.4	458	2	US-09-227-613-11	Sequence 11, Appl
867	54	8.4	177	2	US-09-252-991A-22998	Sequence 22998, A	940	54	8.4	458	2	US-09-227-613-41	Sequence 41, Appl
868	54	8.4	179	2	US-09-252-991A-27201	Sequence 27201, A	941	54	8.4	458	2	US-10-191-513A-11	Sequence 11, Appl
869	54	8.4	180	2	US-10-094-749-1783	Sequence 1783, Ap	942	54	8.4	458	2	US-10-191-513A-41	Sequence 41, Appl
870	54	8.4	181	2	US-09-893-737-252	Sequence 252, App	943	54	8.4	466	2	US-09-302-540-11407	Sequence 11407, A
871	54	8.4	184	1	US-08-484-905-83	Sequence 83, Appl	944	54	8.4	481	2	US-09-252-991A-23317	Sequence 23317, A
872	54	8.4	184	2	US-08-481-985B-83	Sequence 83, Appl	945	54	8.4	481	2	US-09-252-991A-31018	Sequence 31018, A
873	54	8.4	184	2	US-08-370-476-83	Sequence 83, Appl	946	54	8.4	484	2	US-09-252-991A-24249	Sequence 24249, A
874	54	8.4	192	2	US-09-252-991A-31607	Sequence 31607, A	947	54	8.4	521	2	US-10-094-749-2483	Sequence 2483, Ap
875	54	8.4	206	2	US-09-252-991A-31591	Sequence 31591, A	948	54	8.4	524	1	US-08-447-500-24	Sequence 24, Appl
876	54	8.4	226	2	US-09-252-991A-30602	Sequence 30602, A	949	54	8.4	524	1	US-08-454-097-24	Sequence 24, Appl
877	54	8.4	250	2	US-09-502-540-13813	Sequence 13813, A	950	54	8.4	524	1	US-08-453-866-24	Sequence 24, Appl
878	54	8.4	260	2	US-09-070-526-2	Sequence 2, Appli	951	54	8.4	524	1	US-08-185-359-24	Sequence 24, Appl
879	54	8.4	260	2	US-09-008-271A-7	Sequence 7, Appli	952	54	8.4	588	2	US-09-252-991A-18578	Sequence 18578, A
880	54	8.4	260	2	US-09-618-259-7	Sequence 7, Appli	953	54	8.4	614	2	US-09-017-706-9	Sequence 9, Appli
881	54	8.4	260	2	US-09-368-415-7	Sequence 7, Appli	954	54	8.4	614	2	US-09-017-706-10	Sequence 10, Appl
882	54	8.4	260	2	US-09-999-833A-395	Sequence 395, App	955	54	8.4	614	2	US-09-017-706-11	Sequence 11, Appl
883	54	8.4	260	2	US-10-020-445A-395	Sequence 395, App	956	54	8.4	614	2	US-09-017-706-12	Sequence 12, Appl
884	54	8.4	260	2	US-09-978-189-395	Sequence 395, App	957	54	8.4	614	2	US-09-017-706-13	Sequence 13, Appl
885	54	8.4	260	2	US-10-017-085A-395	Sequence 395, App	958	54	8.4	614	2	US-09-017-706-14	Sequence 14, Appl
886	54	8.4	260	3	US-08-915-659A-7	Sequence 7, Appli	959	54	8.4	625	2	US-09-252-991A-33087	Sequence 33087, A
887	54	8.4	260	3	US-10-145-129A-395	Sequence 395, App	960	54	8.4	644	2	US-09-252-991A-27860	Sequence 27860, A
888	54	8.4	260	3	US-10-013-929A-395	Sequence 395, App	961	54	8.4	658	2	US-09-252-991A-23861	Sequence 23861, A
889	54	8.4	260	3	US-09-936-271C-83	Sequence 83, Appl	962	54	8.4	669	2	US-09-013-895A-3	Sequence 3, Appli
890	54	8.4	260	3	US-10-013-917A-395	Sequence 395, App	963	54	8.4	669	2	US-09-448-868-3	Sequence 3, Appli
891	54	8.4	262	2	US-09-252-991A-21401	Sequence 21401, A	964	54	8.4	669	2	US-10-226-296-3	Sequence 3, Appli
892	54	8.4	292	2	US-09-328-352-5522	Sequence 5522, Ap	965	54	8.4	694	2	US-09-252-991A-13096	Sequence 13096, A
893	54	8.4	272	1	US-08-887-997B-2	Sequence 2, Appli	966	54	8.4	760	2	US-09-252-991A-19869	Sequence 19869, A
894	54	8.4	275	3	US-09-936-271C-72	Sequence 72, Appl	967	54	8.4	779	1	US-08-426-627-4	Sequence 4, Appli
895	54	8.4	287	2	US-09-252-991A-27503	Sequence 27503, A	968	54	8.4	779	1	US-08-426-627-24	Sequence 24, Appl
896	54	8.4	287	2	US-09-252-991A-29475	Sequence 29475, A	969	54	8.4	779	2	US-09-461-912A-39	Sequence 39, Appl
897	54	8.4	288	2	US-09-386-642-13	Sequence 13, Appl	970	54	8.4	817	2	US-09-508-377-68	Sequence 68, Appl
898	54	8.4	311	1	US-08-484-905-69	Sequence 69, Appl	971	54	8.4	831	2	US-09-252-991A-24901	Sequence 24901, A
899	54	8.4	311	2	US-08-481-985B-69	Sequence 69, Appl	972	54	8.4	836	1	US-08-426-627-6	Sequence 6, Appli
900	54	8.4	311	2	US-08-370-476-69	Sequence 69, Appl	973	54	8.4	837	1	US-08-426-627-23	Sequence 23, Appl
901	54	8.4	323	2	US-09-439-261-17	Sequence 17, Appl	974	54	8.4	915	2	US-10-029-180-74	Sequence 74, Appl
902	54	8.4	323	2	US-09-227-613-17	Sequence 17, Appl	975	54	8.4	1046	2	US-09-252-991A-27508	Sequence 27508, A

976	54	8.4	1191	2	US-09-949-016-6356	Sequence 6356, App	1049	53.5	8.3	607	2	US-09-252-991A-30814	Sequence 30814, A
977	54	8.4	1427	2	US-09-252-991A-20577	Sequence 20577, A	1050	53.5	8.3	613	2	US-10-104-966-6	Sequence 6, Appl
978	53.5	8.3	67	2	US-09-910-009A-86	Sequence 86, Appl	1051	53.5	8.3	613	2	US-09-929-955-6	Sequence 6, Appl
979	53.5	8.3	73	2	US-09-894-882-176	Sequence 176, App	1052	53.5	8.3	619	2	US-09-762-767B-4	Sequence 4, Appl
980	53.5	8.3	95	2	US-09-313-283C-378	Sequence 378, App	1053	53.5	8.3	631	2	US-09-417-197-39	Sequence 39, Appl
981	53.5	8.3	127	2	US-09-621-976-5373	Sequence 5373, Ap	1054	53.5	8.3	638	2	US-09-288-391-25	Sequence 25, Appl
982	53.5	8.3	129	1	US-08-360-914B-15	Sequence 15, Appl	1055	53.5	8.3	642	2	US-10-094-749-2092	Sequence 2092, Ap
983	53.5	8.3	129	1	US-08-741-589A-13	Sequence 13, Appl	1056	53.5	8.3	645	2	US-09-949-016-9562	Sequence 9562, Ap
984	53.5	8.3	129	1	US-09-921-397-90	Sequence 90, Appl	1057	53.5	8.3	649	2	US-09-252-991A-20954	Sequence 20954, A
985	53.5	8.3	145	1	US-08-732-228-4	Sequence 4, Appl	1058	53.5	8.3	681	2	US-09-252-991A-18889	Sequence 18889, A
986	53.5	8.3	145	1	US-09-185-245-3	Sequence 3, Appl	1059	53.5	8.3	700	2	US-07-757-342D-3	Sequence 3, Appl
987	53.5	8.3	145	2	US-09-919-497-68	Sequence 68, Appl	1060	53.5	8.3	700	2	US-09-461-657B-3	Sequence 3, Appl
988	53.5	8.3	157	2	US-07-757-022B-102	Sequence 102, App	1061	53.5	8.3	706	1	US-08-987-289-2	Sequence 2, Appl
989	53.5	8.3	157	2	US-07-757-022B-114	Sequence 114, App	1062	53.5	8.3	708	2	US-09-252-991A-27035	Sequence 27035, A
990	53.5	8.3	157	3	US-10-124-557-102	Sequence 102, App	1063	53.5	8.3	721	2	US-09-949-016-11031	Sequence 11031, A
991	53.5	8.3	157	3	US-10-124-557-114	Sequence 114, App	1064	53.5	8.3	725	2	US-09-252-991A-22300	Sequence 22300, A
992	53.5	8.3	178	2	US-09-253-991A-18672	Sequence 18672, A	1065	53.5	8.3	785	2	US-09-569-611C-43	Sequence 43, Appl
993	53.5	8.3	179	2	US-10-000-489-36	Sequence 36, Appl	1066	53.5	8.3	895	3	US-09-555-275A-13	Sequence 13, Appl
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1007	53.5	8.3	268	2	US-09-610-651-22	Sequence 22, Appl	1080	53.5	8.3	1719	2	US-10-024-450-4	Sequence 4, Appl
1008	53.5	8.3	268	2	US-09-345-373-22	Sequence 22, Appl	1081	53.5	8.3	1719	2	US-10-142-650-1	Sequence 1, Appl
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1158	52.5	8.2	94	2	US-09-043-861-2	Sequence 2, Appl	1231	52.5	8.2	666	2	US-08-532-384-17	Sequence 17, Appl
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1160	52.5	8.2	94	3	US-09-509-165A-43	Sequence 43, Appl	1233	52.5	8.2	667	2	US-09-252-991A-22794	Sequence 22794, A
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ALIGNMENTS

RESULT 1

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6	PRIOR FILING DATE: 1998-06-02
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Best Local Similarity 100.0%; Pred. No. 8e-69;
Matches 119; Conservative 0; Mismatches 0; Indels

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; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
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; APPLICANT: Pao, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumaas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
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Query Match 100.0%; Score 644; DB 2; Length 119;
Best Local Similarity 100.0%; Pred. No. 8e-69;

Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 6

US-09-989-726-165
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; Patent No. 7018811
; GENERAL INFORMATION:
; APPLICANT: Aekhenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Baton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kijavini, Ivar J.
; APPLICANT: Napier, Mary A.
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; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730PIC60
; CURRENT FILING DATE: 2001-11-19
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; Sequence 165, Application US/09997514
; Patent No. 7019116
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C46
; CURRENT APPLICATION NUMBER: US/09/997,514
; CURRENT FILING DATE: 2001-11-15
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55 PRIOR FILING DATE: 1998-07-07
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57 PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 644; DB 3; Length 119;
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RESULT 8
US-09-989-728-165

Sequence 165, Application US/09989728
Patent No. 7029873
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
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APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
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APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730P1C72
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;; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 644; DB 3; Length 119;

Best Local Similarity 100.0%; Pred. No. 8e-69;

Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MKVLISLLLLPLMLMSVSSSLNPGVARGHRDRGQASRRWLQEGGQCECKDFLRAP 60

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RESULT 10

US-09-997-653-165

; Sequence 165, Application US/09997653

; Patent No. 7034122

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi J.

; APPLICANT: Baker, Kevin P.

; APPLICANT: Botstein, David

APPLICANT: Deenoyers, Luc
APPLICANT: Baton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
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APPLICANT: Stewart, Timothy A.
APPLICANT: Tunas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730P1C38
CURRENT APPLICATION NUMBER: US/09/997,653
CURRENT FILING DATE: 2001-11-15
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;; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 644; DB 3; Length 119;

Best Local Similarity 100.0%; Pred. No. 9e-69;

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RESULT 11

US-09-989-293A-165
; Sequence 165, Application US/09989293A

; Patent No. 7034136

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi J.

; APPLICANT: Baker, Kevin P.

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan L.

; APPLICANT: Ferrara, Napoleone

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Query Match 100.0%; Score 644; DB 3; Length 119;
Best Local Similarity 100.0%; Pred. No. 8e-69;
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 12
US-09-621-976-3926
; Sequence 3926, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm


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US-09-621-976-3926

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RESULT 13
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; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 17301
; LENGTH: 620
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-17301

Query Match
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Matches 27; Conservative 11; Mismatches 23; Indels 27; Gaps 4;

QY 29 ARGHRDRGQA-----SRRWLQGGGCECKQWFLRAPRRKFTVSGLPKKQCPCHDFKGN 83
DB 538 ARSHRDGQQRDHNRRRPHREGROQRE--DQYRREPHR-----GR 576
QY 84 VKKTRHORHRRKPNKHSRACQQLKQCOL 111
DB 577 RQQRDHQ-HRRRPHREGROQRDQHRQC 603

RESULT 14
US-09-248-796A-19808
; Sequence 19808, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstein et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
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; SEQ ID NO 19808
; LENGTH: 456
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-19808

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Matches 23; Conservative 7; Mismatches 17; Indels 20; Gaps 6;

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QY 112 LRSFALP 118
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RESULT 15
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; Sequence 23977, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstein et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 23977
; LENGTH: 131
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; ORGANISM: Candida albicans
US-09-248-796A-23977

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DB 79 QQVHQQTQLRTFSQP 93

Search completed: August 3, 2006, 09:56:24
Job time : 43 secs
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OM protein - protein search, using sw model

Run on: August 3, 2006, 10:12:44 ; Search time 184 Seconds
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Title: US-10-015-967-2

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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744	644	100.0	119	5	US-10-972-317-26
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769	386	59.9	97	4	US-10-412-548-6
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862	69	10.7	234	5	US-10-450-763-59683	Sequence 59683, A	935	65	10.1	628	5	US-10-473-127-373	Sequence 373, App
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906	65.5	10.2	174	4	US-10-437-963-107985	Sequence 107985,	979	63.5	9.9	261	4	US-10-425-114-63205	Sequence 63205, A
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910	65.5	10.2	428	4	US-10-437-963-134092	Sequence 134092,	983	63.5	9.9	435	5	US-10-450-763-58077	Sequence 58077, A
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917	65.5	10.2	706	4	US-10-295-027-1332	Sequence 1332, Ap	990	63.5	9.9	815	4	US-10-437-963-112487	Sequence 112487,
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994	63.5	9.9	1598	4	US-10-437-963-112315	Sequence 112315,	1187	62	9.6	1270	6	US-11-169-232-44	Sequence 44, Appl
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996	63.5	9.9	2406	4	US-10-408-763A-1504	Sequence 1504, App	1189	62	9.6	1630	4	US-10-425-115-187278	Sequence 187278,
997	63.5	9.9	2406	5	US-10-701-401-2	Sequence 2, Appl	1190	62	9.6	1642	4	US-10-786-720-39	Sequence 39, Appl
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1005	63	9.8	343	5	US-10-450-763-54326	Sequence 54326, A	1198	61.5	9.5	232	4	US-10-060-523-9	Sequence 9, Appl
1006	63	9.8	464	4	US-10-437-963-146979	Sequence 146979,	1199	61.5	9.5	232	4	US-10-853-232-9	Sequence 9, Appl
1007	63	9.8	671	4	US-10-437-963-185751	Sequence 185751,	1200	61.5	9.5	232	6	US-11-211-724-5	Sequence 5, Appl
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1012	62.5	9.7	156	3	US-09-796-753-118	Sequence 118, App	1205	61.5	9.5	357	5	US-10-511-722-20	Sequence 20, Appl
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1056	62.5	9.7	156	4	US-10-223-088-342	Sequence 342, App	1210	61.5	9.5	369	5	US-10-473-127-266	Sequence 266, App
1057	62.5	9.7	156	4	US-10-223-090-342	Sequence 342, App	1211	61.5	9.5	369	5	US-10-473-127-267	Sequence 267, App
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1114	62.5	9.7	156	4	US-10-223-081-342	Sequence 342, App	1215	61.5	9.5	369	5	US-10-473-127-278	Sequence 278, App
1128	62.5	9.7	156	4	US-10-223-082-342	Sequence 342, App	1216	61.5	9.5	369	5	US-10-473-127-279	Sequence 279, App
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1158	62	9.6	116	4	US-10-124-557-120	Sequence 120, App	1231	61.5	9.5	482	3	US-10-473-127-274	Sequence 274, App
1159	62	9.6	116	4	US-10-124-557-138	Sequence 138, App	1232	61.5	9.5	545	4	US-10-112-944-480	Sequence 480, App
1160	62	9.6	116	6	US-11-169-232-98	Sequence 98, Appl	1233	61.5	9.5	629	4	US-10-182-243-51	Sequence 51, Appl
1161	62	9.6	116	6	US-11-169-232-110	Sequence 110, App	1234	61.5	9.5	688	4	US-10-437-963-152448	Sequence 152448,
1162	62	9.6	116	6	US-11-169-232-120	Sequence 120, App	1235	61.5	9.5	691	3	US-09-313-942-20	Sequence 20, Appl
1163	62	9.6	116	6	US-11-169-232-138	Sequence 138, App	1236	61.5	9.5	691	3	US-09-313-942-20	Sequence 20, Appl
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1167	62	9.6	182	4	US-10-425-115-230707	Sequence 230707,	1240	61.5	9.5	691	6	US-11-134-114-20	Sequence 20, Appl
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1170	62	9.6	233	4	US-10-425-115-186741	Sequence 186741,	1243	61.5	9.5	694	3	US-09-313-942-22	Sequence 22, Appl
1171	62	9.6	303	3	US-09-764-846-142	Sequence 142, App	1244	61.5	9.5	694	3	US-09-313-942-22	Sequence 22, Appl
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1176	62	9.6	412	4	US-10-029-386-32440	Sequence 32440, A	1249	61.5	9.5	694	5	US-10-473-127-277	Sequence 277, App
1177	62	9.6	577	3	US-09-853-386-42	Sequence 42, Appl	1250	61.5	9.5	694	5	US-10-473-127-277	Sequence 277, App
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1291	61	9.5	339	5	US-10-864-252-899	Sequence 899, App							
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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6	527	81.8	118	6	US-10-553-436-174
7	521	80.9	94	6	US-10-553-436-173
8	521	80.9	100	6	US-10-553-436-175
9	415	64.4	84	6	US-10-553-436-177
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22	69	10.7	293	7	US-11-056-355B-74703
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24	69	10.7	293	7	US-11-056-355B-42510
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26	69	10.7	299	7	US-11-056-355B-84548

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29	69	10.7	400	7	US-11-056-355B-42509	Sequence 42509, A
30	69	10.7	400	7	US-11-056-355B-106420	Sequence 106420,
31	69	10.7	400	7	US-11-056-355B-117659	Sequence 117659,
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33	69	10.7	418	7	US-11-056-355B-106419	Sequence 106419,
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36	68.5	10.6	427	7	US-11-283-329-52	Sequence 52, Appl
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38	67	10.4	287	6	US-10-953-349-21008	Sequence 21008, A
39	67	10.4	325	6	US-10-953-349-21007	Sequence 21007, A
40	67	10.4	345	6	US-10-953-349-21006	Sequence 21006, A
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43	67	10.4	376	7	US-11-056-355B-103004	Sequence 103004,
44	67	10.4	376	7	US-11-056-355B-114243	Sequence 114243,
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47	67	10.4	385	7	US-11-056-355B-103003	Sequence 103003,
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56	64	9.9	176	7	US-11-056-355B-61026	Sequence 61026, A
57	64	9.9	181	7	US-11-056-355B-61039	Sequence 61039, A
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59	64	9.9	321	6	US-10-449-902-35935	Sequence 35935, A
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65	63	9.8	307	6	US-10-449-902-29497	Sequence 29497, A
66	63	9.8	464	6	US-10-449-902-53294	Sequence 53294, A
67	63	9.8	674	7	US-11-056-355B-79153	Sequence 79153, A
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71	63	9.8	2343	6	US-10-540-898-904	Sequence 904, App
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78	62	9.6	1161	6	US-10-449-902-36756	Sequence 36756, A
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83	61	9.5	175	7	US-11-056-355B-8053	Sequence 8053, Ap
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86	61	9.5	181	7	US-11-056-355B-40737	Sequence 40737, A
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135	59	9.2	203	7	US-11-354-653-28	Sequence 28, Appl	208	57	8.9	136	6	US-10-449-902-42497	Sequence 42497, A
136	59	9.2	199	6	US-10-449-902-53547	Sequence 53547, A	209	57	8.9	152	7	US-11-334-081-26	Sequence 26, Appl
137	59	9.2	245	6	US-10-449-902-47213	Sequence 47213, A	210	57	8.9	153	6	US-10-953-349-30101	Sequence 30101, A
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167	58	9.0	626	7	US-11-303-935-5	Sequence 5, Appl1	240	57	8.9	463	7	US-11-056-355B-37078	Sequence 37078, A
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169	58	9.0	663	7	US-11-056-355B-21133	Sequence 21133, A	242	57	8.9	463	7	US-11-056-355B-50701	Sequence 50701, A
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171	58	9.0	663	7	US-11-056-355B-110822	Sequence 110822,	244	57	8.9	486	7	US-11-056-355B-8192	Sequence 8192, Ap
172	58	9.0	806	6	US-10-953-349-8640	Sequence 8640, Ap	245	57	8.9	527	6	US-10-449-902-47155	Sequence 47155, A
173	58	9.0	806	7	US-11-056-355B-21132	Sequence 21132, A	246	57	8.9	578	7	US-11-056-355B-37077	Sequence 37077, A
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249	57	8.9	578	7	US-11-330-403-7904	Sequence 7904, Ap	322	55.5	8.6	312	7	US-11-174-307B-202	Sequence 202, App
250	57	8.9	578	7	US-11-330-403-13173	Sequence 13173, A	323	55.5	8.6	377	6	US-10-953-349-30064	Sequence 30064, A
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457 54.5 8.5 5738 6 US-10-505-928-150 Sequence 150, App 530 54 458 7 US-11-264-784-5 Sequence 5, Appl
458 54 8.4 79 7 US-11-056-355B-393 Sequence 393, App 531 54 458 7 US-11-264-784-5 Sequence 5, Appl
459 54 8.4 98 6 US-10-540-898-12 Sequence 12, Appl 532 54 458 7 US-11-265-761-5 Sequence 5, Appl
460 54 8.4 98 6 US-10-540-898-14 Sequence 14, Appl 533 54 461 7 US-11-056-355B-6754 Sequence 6754, Ap
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466 54 8.4 152 7 US-11-056-355B-113740 Sequence 113740, A 539 54 606 7 US-11-330-403-4136 Sequence 4136, Ap
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546	54	8.4	779	7	US-11-226-554-123	Sequence 123, App	619	53	8.2	515	7	US-11-056-355B-93623	Sequence 93623, A
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551	54	8.4	809	7	US-11-248-718-120	Sequence 120, App	624	53	8.2	562	7	US-11-056-355B-93622	Sequence 93622, A
552	54	8.4	836	7	US-11-105-233-154	Sequence 154, App	625	53	8.2	622	7	US-11-056-355B-89865	Sequence 89865, A
553	54	8.4	836	7	US-11-226-554-119	Sequence 119, App	626	53	8.2	622	7	US-11-056-355B-93621	Sequence 93621, A
554	54	8.4	836	7	US-11-248-718-119	Sequence 119, App	627	53	8.2	653	6	US-10-449-902-41022	Sequence 41022, A
555	54	8.4	954	6	US-10-449-902-41286	Sequence 41286, A	628	53	8.2	727	7	US-11-293-697-3060	Sequence 3060, Ap
556	54	8.4	1014	6	US-10-953-349-16525	Sequence 16525, A	629	53	8.2	738	6	US-10-539-228-571	Sequence 571, App
557	53.5	8.3	133	6	US-10-449-902-37351	Sequence 37351, A	630	53	8.2	789	7	US-11-056-355B-79149	Sequence 79149, A
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561	53.5	8.3	236	7	US-11-293-697-4829	Sequence 4829, Ap	634	53	8.2	832	6	US-10-449-902-45254	Sequence 45254, A
562	53.5	8.3	243	7	US-11-356-373-21	Sequence 21, Appl	635	53	8.2	853	7	US-11-056-355B-20589	Sequence 20589, A
563	53.5	8.3	263	7	US-11-356-373-18	Sequence 18, Appl	636	53	8.2	864	7	US-11-056-355B-20588	Sequence 20588, A
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578	53.5	8.3	398	7	US-11-056-355B-93668	Sequence 93668, A	651	52.5	8.2	190	6	US-10-953-349-29909	Sequence 29909, A
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588	53.5	8.3	502	7	US-11-056-355B-1175	Sequence 1175, Ap	661	52.5	8.2	303	6	US-10-953-349-39198	Sequence 39198, A
589	53.5	8.3	534	6	US-10-449-902-48245	Sequence 48245, A	662	52.5	8.2	303	7	US-11-056-355B-1253	Sequence 1253, Ap
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694	52.5	8.2	769	7	US-11-246-999-67	Sequence 67, Appl	767	52	8.1	910	7	US-11-301-924-46	Sequence 16, Appl
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697	52.5	8.2	1009	6	US-10-539-228-696	Sequence 696, App	771	52	8.1	1428	7	US-11-299-791-22	Sequence 22, Appl
698	52.5	8.2	1503	7	US-11-312-958-48	Sequence 48, Appl	772	52	8.1	1850	7	US-11-056-355B-40081	Sequence 40081, A
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705	52	8.1	134	7	US-11-284-236-132	Sequence 192, App	779	51.5	8.0	72	6	US-10-449-902-44043	Sequence 44043, A
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711	52	8.1	173	7	US-11-056-355B-117507	Sequence 117507, A	785	51.5	8.0	122	6	US-10-953-349-9037	Sequence 9037, Ap
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715	52	8.1	187	7	US-11-056-355B-8417	Sequence 8417, Ap	789	51.5	8.0	126	7	US-11-056-355B-37126	Sequence 37126, A
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724	52	8.1	271	6	US-10-991-309B-164	Sequence 164, App	798	51.5	8.0	198	7	US-11-051-725-87	Sequence 87, Appl
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736	52	8.1	331	6	US-10-449-902-46038	Sequence 46038, A	810	51.5	8.0	245	7	US-11-056-355B-3881	Sequence 3881, Ap
737	52	8.1	337	6	US-10-953-349-7389	Sequence 7389, Ap	811	51.5	8.0	267	6	US-10-953-349-23517	Sequence 23517, A
738	52	8.1	337	7	US-11-056-355B-25024	Sequence 25024, A	812	51.5	8.0	269	6	US-10-953-349-23516	Sequence 23516, A
739	52	8.1	337	7	US-11-056-355B-103005	Sequence 103005, A	813	51.5	8.0	279	6	US-10-449-902-29997	Sequence 29997, A
740	52	8.1	337	7	US-11-056-355B-114244	Sequence 114244, A	814	51.5	8.0	279	6	US-10-449-902-30297	Sequence 30297, A
741	52	8.1	345	6	US-10-449-902-49942	Sequence 49942, A	815	51.5	8.0	279	6	US-10-449-902-45407	Sequence 45407, A
742	52	8.1	349	6	US-10-449-902-49942	Sequence 49942, A	816	51.5	8.0	280	6	US-10-953-349-12686	Sequence 12686, A
743	52	8.1	349	6	US-10-449-902-50970	Sequence 50970, A	817	51.5	8.0	284	6	US-10-953-349-14864	Sequence 14864, A
744	52	8.1	354	6	US-10-449-902-52922	Sequence 52922, A	818	51.5	8.0	284	7	US-11-056-355B-52109	Sequence 52109, A
745	52	8.1	358	6	US-10-953-349-37125	Sequence 37125, A	819	51.5	8.0	301	6	US-10-953-349-14863	Sequence 14863, A
746	52	8.1	371	7	US-11-330-403-10198	Sequence 10198, A	820	51.5	8.0	301	7	US-11-056-355B-52108	Sequence 52108, A
747	52	8.1	401	6	US-10-953-349-3688	Sequence 3688, Ap	821	51.5	8.0	307	6	US-10-953-349-14862	Sequence 14862, A
748	52	8.1	438	7	US-11-174-307B-2968	Sequence 2968, Ap	822	51.5	8.0	307	7	US-11-056-355B-52107	Sequence 52107, A
749	52	8.1	439	7	US-11-342-731-4	Sequence 4, Appl	823	51.5	8.0	309	6	US-10-449-902-40558	Sequence 40558, A
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751	52	8.1	523	7	US-11-330-403-5559	Sequence 5559, Ap	825	51.5	8.0	316	6	US-10-953-349-23515	Sequence 23515, A
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753	52	8.1	550	6	US-10-449-902-48072	Sequence 48072, A	827	51.5	8.0	330	6	US-10-953-349-12685	Sequence 12685, A
754	52	8.1	578	7	US-11-330-403-13171	Sequence 13171, A	828	51.5	8.0	339	6	US-10-449-902-34829	Sequence 34829, A
755	52	8.1	581	6	US-10-374-780A-2556	Sequence 2556, Ap	829	51.5	8.0	347	7	US-11-056-355B-807	Sequence 807, App
756	52	8.1	603	6	US-10-449-902-53745	Sequence 53745, A	830	51.5	8.0	361	6	US-10-953-349-12684	Sequence 12684, A
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758	52	8.1	612	6	US-10-449-902-55786	Sequence 55786, A	832	51.5	8.0	390	7	US-11-056-355B-72592	Sequence 72592, A
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841	51.5	8.0	448	7	US-11-056-355B-53654	Sequence 52654, A	916	7.9	351	7	US-11-056-355B-65495	Sequence 65495, A
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843	51.5	8.0	466	7	US-11-355-324-2	Sequence 2, Appl	918	7.9	385	6	US-10-953-349-7747	Sequence 7747, Ap
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845	51.5	8.0	473	7	US-11-355-324-18	Sequence 18, Appl	920	7.9	388	7	US-11-056-355B-110889	Sequence 110889, A
846	51.5	8.0	496	7	US-11-056-355B-72595	Sequence 72595, A	921	7.9	408	6	US-10-713-648A-60	Sequence 60, Appl
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849	51.5	8.0	504	6	US-11-330-403-8684	Sequence 8684, Ap	924	7.9	438	7	US-11-330-403-1788	Sequence 1788, Ap
850	51.5	8.0	556	7	US-11-330-403-16027	Sequence 16027, A	925	7.9	442	7	US-11-234-173-56	Sequence 56, Appl
851	51.5	8.0	557	7	US-11-293-697-3317	Sequence 3317, Ap	926	7.9	442	7	US-11-264-784-9	Sequence 9, Appl
852	51.5	8.0	558	6	US-10-449-902-37712	Sequence 37712, A	927	7.9	442	7	US-11-264-737-9	Sequence 9, Appl
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855	51.5	8.0	663	7	US-11-293-697-3986	Sequence 3986, Ap	930	7.9	467	7	US-11-056-355B-68552	Sequence 68552, A
856	51.5	8.0	717	7	US-11-175-714-9	Sequence 9, Appl	931	7.9	468	6	US-10-953-349-7746	Sequence 7746, Ap
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858	51.5	8.0	756	7	US-11-289-102-324	Sequence 324, App	933	7.9	476	7	US-11-056-355B-99649	Sequence 99649, A
859	51.5	8.0	764	7	US-11-223-738-6	Sequence 6, Appl	934	7.9	476	7	US-11-056-355B-110888	Sequence 110888, A
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862	51.5	8.0	842	7	US-11-293-697-4134	Sequence 4134, Ap	937	7.9	496	7	US-11-056-355B-110887	Sequence 110887, A
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866	51.5	8.0	938	7	US-11-056-355B-49198	Sequence 49198, A	941	7.9	529	7	US-11-106-014-44	Sequence 44, Appl
867	51.5	8.0	948	7	US-11-056-355B-74244	Sequence 74244, A	942	7.9	535	7	US-11-293-697-3884	Sequence 3884, Ap
868	51.5	8.0	949	7	US-11-293-697-3033	Sequence 3033, Ap	943	7.9	555	6	US-10-449-902-36526	Sequence 36526, A
869	51.5	8.0	971	7	US-11-056-355B-74243	Sequence 74243, A	944	7.9	585	6	US-11-330-403-5825	Sequence 5825, Ap
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872	51	7.9	115	7	US-11-056-355B-52366	Sequence 6268, Ap	947	7.9	735	7	US-11-056-355B-75493	Sequence 75493, A
873	51	7.9	117	7	US-11-330-403-6268	Sequence 15139, A	948	7.9	735	7	US-11-056-355B-45530	Sequence 45530, A
874	51	7.9	133	7	US-11-056-355B-15139	Sequence 15139, A	949	7.9	753	7	US-11-056-355B-45529	Sequence 45529, A
875	51	7.9	153	7	US-11-293-697-3623	Sequence 3623, Ap	950	7.9	757	7	US-11-056-355B-48657	Sequence 48657, A
876	51	7.9	156	6	US-10-449-902-40285	Sequence 40285, A	951	7.9	774	7	US-11-056-355B-48656	Sequence 48656, A
877	51	7.9	157	6	US-10-540-898-473	Sequence 473, App	952	7.9	778	7	US-11-056-355B-48655	Sequence 48655, A
878	51	7.9	157	6	US-11-056-355B-57064	Sequence 57064, A	953	7.9	782	7	US-11-056-355B-48655	Sequence 48655, A
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892	51	7.9	220	7	US-11-056-355B-2528	Sequence 2528, Ap	967	7.8	96	6	US-10-449-902-37750	Sequence 28693, A
893	51	7.9	223	6	US-10-953-349-12454	Sequence 12454, A	968	7.8	112	6	US-10-953-349-28693	Sequence 68365, A
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895	51	7.9	229	6	US-10-449-902-55034	Sequence 55034, A	970	7.8	114	6	US-10-953-349-35200	Sequence 35200, A
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897	51	7.9	235	7	US-11-056-355B-4715	Sequence 4715, Ap	972	7.8	130	7	US-11-056-355B-580	Sequence 580, App
898	51	7.9	244	7	US-11-056-355B-57063	Sequence 57063, A	973	7.8	133	6	US-10-449-902-35994	Sequence 35994, A
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900	51	7.9	247	7	US-11-056-355B-67863	Sequence 67863, A	975	7.8	147	7	US-11-056-355B-60989	Sequence 60989, A
901	51	7.9	248	7	US-11-330-403-379	Sequence 379, App	976	7.8	157	7	US-11-056-355B-74469	Sequence 74469, A
902	51	7.9	262	6	US-11-056-355B-9087	Sequence 9087, Ap	977	7.8	158	7	US-11-056-355B-948	Sequence 948, Ap
903	51	7.9	263	6	US-10-449-902-37027	Sequence 37027, A	978	7.8	163	7	US-11-056-355B-948	Sequence 948, Ap
904	51	7.9	263	6	US-10-449-902-37323	Sequence 37323, A	979	7.8	168	6	US-10-953-349-35399	Sequence 35399, A
905	51	7.9	268	7	US-11-056-355B-9086	Sequence 9086, Ap	980	7.8	169	6	US-10-953-349-29043	Sequence 29043, A
906	51	7.9	268	7	US-11-056-355B-46567	Sequence 46567, A	981	7.8	174	7	US-11-056-355B-51604	Sequence 51604, A
907	51	7.9	282	6	US-10-471-571A-2348	Sequence 2348, Ap	982	7.8	175	7	US-11-056-355B-66858	Sequence 66858, A

981	50.5	7.8	181	7	US-11-056-355B-9498	Sequence 9498, Ap	1057	50.5	7.8	1181	7	US-11-241-596-255	Sequence 255, App
982	50.5	7.8	201	7	US-11-056-355B-21385	Sequence 21385, A	1058	50.5	7.8	1181	7	US-11-241-596-256	Sequence 256, App
983	50.5	7.8	204	6	US-10-953-349-37463	Sequence 37463, A	1059	50.5	7.8	1181	7	US-11-241-596-257	Sequence 257, App
984	50.5	7.8	216	6	US-10-449-902-35401	Sequence 35401, A	1060	50.5	7.8	1181	7	US-11-241-596-258	Sequence 258, App
985	50.5	7.8	216	6	US-10-449-902-35401	Sequence 35401, A	1061	50.5	7.8	1384	6	US-10-529-931-18	Sequence 18, Appl
986	50.5	7.8	251	6	US-10-953-349-38140	Sequence 38140, A	1062	50.5	7.8	1384	6	US-10-529-931-20	Sequence 20, Appl
987	50.5	7.8	260	7	US-11-056-355B-8517	Sequence 8517, Ap	1063	50.5	7.8	1384	6	US-10-529-931-22	Sequence 22, Appl
988	50.5	7.8	264	7	US-11-056-355B-10540	Sequence 10540, A	1064	50.5	7.8	2440	6	US-11-283-329-196	Sequence 196, App
989	50.5	7.8	268	7	US-11-056-355B-51603	Sequence 51603, A	1065	50.5	7.8	3010	6	US-10-534-774-24	Sequence 24, Appl
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991	50.5	7.8	289	7	US-11-056-355B-8516	Sequence 8516, Ap	1067	50.5	7.8	3010	7	US-11-140-487A-770	Sequence 770, App
992	50.5	7.8	295	6	US-10-504-973-34	Sequence 34, Appl	1068	50.5	7.8	3697	6	US-11-063-439-288	Sequence 288, App
993	50.5	7.8	304	7	US-11-056-355B-8515	Sequence 8515, Ap	1069	50	7.8	88	6	US-10-449-902-40412	Sequence 40412, A
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995	50.5	7.8	327	7	US-11-056-355B-84860	Sequence 84860, A	1071	50	7.8	109	7	US-11-330-403-2710	Sequence 2710, Ap
996	50.5	7.8	331	7	US-11-293-697-2499	Sequence 2499, Ap	1072	50	7.8	112	6	US-10-449-902-33801	Sequence 33801, A
997	50.5	7.8	332	6	US-10-953-349-27867	Sequence 27867, A	1073	50	7.8	132	7	US-11-056-355B-55088	Sequence 55088, A
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1005	50.5	7.8	343	7	US-11-056-355B-111195	Sequence 111195, A	1081	50	7.8	215	7	US-11-056-355B-70364	Sequence 70364, A
1006	50.5	7.8	358	7	US-11-293-697-3662	Sequence 3662, Ap	1082	50	7.8	229	6	US-10-449-902-30195	Sequence 30195, A
1007	50.5	7.8	360	7	US-11-242-111-19	Sequence 19, Appl	1083	50	7.8	266	6	US-10-449-902-48321	Sequence 48321, A
1008	50.5	7.8	361	6	US-10-953-349-27866	Sequence 27866, A	1084	50	7.8	267	6	US-10-953-349-31474	Sequence 31474, A
1009	50.5	7.8	361	7	US-11-056-355B-10726	Sequence 10726, A	1085	50	7.8	278	7	US-11-056-355B-67750	Sequence 67750, A
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1012	50.5	7.8	368	6	US-10-529-931-16	Sequence 16, Appl	1088	50	7.8	303	6	US-10-953-349-266	Sequence 266, App
1013	50.5	7.8	376	7	US-11-056-355B-30978	Sequence 30978, A	1089	50	7.8	303	6	US-10-953-349-3570	Sequence 3570, Ap
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Post-processing: Minimum Match 0%

Maximum Match 100%

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12: gb htg.*

13: gb in.*

14: gb om.*

15: gb ba.*

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SUMMARIES

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8	870	100.0	870	2	AR757309 Sequence
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47	312	35.9	312	2	AR272331	AR272331 Sequence
48	312	35.9	312	2	AR275912	AR275912 Sequence
49	312	35.9	312	2	AR406187	AR406187 Sequence
50	312	35.9	312	2	AR440037	AR440037 Sequence
51	312	35.9	312	2	AR472196	AR472196 Sequence
52	312	35.9	312	2	AR542848	AR542848 Sequence
53	312	35.9	312	2	AR638006	AR638006 Sequence
54	312	35.9	312	2	AR694679	AR694679 Sequence
55	312	35.9	312	2	AR707266	AR707266 Sequence
56	312	35.9	312	2	AX062416	AX062416 Sequence
57	312	35.9	312	2	AX367333	AX367333 Sequence
58	291	33.4	291	2	E40584	E40584 Novel prote
59	261.8	30.1	829	2	AX930425	AX930425 Sequence
60	261.8	30.1	829	6	AY598463	AY598463 Mus muscu
61	256.6	29.5	808	6	BC024561	BC024561 Mus muscu
62	245.6	28.2	357	2	E40583	E40583 Novel prote
63	238	27.4	242	2	CQ462946	CQ462946 Sequence
64	230	26.4	235	2	BD076800	BD076800 5' EST of
65	228	26.2	357	2	E40582	E40582 Novel prote
66	200.4	23.0	291	2	E40586	E40586 Novel prote
67	189.2	21.7	291	2	E40585	E40585 Novel prote
68	166	19.1	44332	5	AC005794	AC005794 Homo sapi
69	153.8	17.7	214674	12	AC164341	AC164341 Bos tauru
70	104.8	12.0	40520	5	AC011513	AC011513 Homo sapi
71	97.6	11.2	43593	5	AC022516	AC022516 Homo sapi
72	86.2	9.9	402	2	CQ737691	CQ737691 Sequence
73	81	9.3	81	2	CS188626	CS188626 Sequence
74	79.4	9.1	108	2	CQ749236	CQ749236 Sequence
75	78.8	9.1	176520	6	AC162443	AC162443 Mus muscu
76	78.8	9.1	190860	12	AC073803	AC073803 Mus muscu
77	78.8	9.1	215234	12	AC073745	AC073745 Mus muscu
78	73.4	8.4	97	2	AX182077	AX182077 Sequence
79	66.4	7.6	218925	12	AC109038	AC109038 Rattus no
80	66.4	7.6	229745	12	AC121639	AC121639 Rattus no
81	66.4	7.6	242596	12	AC134759	AC134759 Rattus no
82	56.8	6.5	7218	2	I66494	I66494 Sequence 14
83	48.4	5.6	168858	12	AC167507	AC167507 Oryctolag
84	48.4	5.6	174371	12	AC167082	AC167082 Oryctolag
85	46	5.3	4519	6	BC049240	BC049240 Mus muscu
86	45.8	5.3	518	2	AX185599	AX185599 Sequence
87	45.4	5.2	168525	6	AC126415	AC126415 Mus muscu
88	45.2	5.2	3214	13	AF019980	AF019980 Dicyoste
89	45.2	5.2	179378	12	AC141011	AC141011 Rattus no
90	45	5.2	2363	6	BC052195	BC052195 Mus muscu
91	45	5.2	4060	6	BC050017	BC050017 Mus muscu

92	44.8	5.1	1665	5	BC041446	BC041446 Homo sapi	165	40.8	4.7	85039	11	BX548062	BX548062 Zebrafish
93	44.6	5.1	51	2	E40591	E40591 Novel prote	c 166	40.8	4.7	174787	12	AC142375	AC142375 Rattus no
94	44.2	5.1	2281	5	AB168896	AB168896 Macaca fa	167	40.8	4.7	219175	5	AC092641	AC092641 Homo sapi
95	44.2	5.1	180040	12	AC148489	AC148489 Saimiri b	168	40.6	4.7	875	13	DQ369263	DQ369263 Anopheles
96	44.2	5.1	226319	12	AC153307	AC153307 Saimiri b	169	40.6	4.7	1030	6	RNTRANGEL	X64422 R.norvegicu
97	44	5.1	110000	12	BCX901936_1	Continuation (2 of	170	40.6	4.7	1130	6	BC061770	BC061770 Rattus no
98	44	5.1	125020	5	AF429315	AF429315 Homo sapi	171	40.6	4.7	1458	6	BC061969	BC061969 Rattus no
99	44	5.1	182631	11	EX649518	EX649518 Zebrafish	c 172	40.6	4.7	1588	2	CQ413503	CQ413503 Sequence
100	44	5.1	209887	12	AC079424	AC079424 Mus muscu	173	40.6	4.7	1649	13	AY058385	AY058385 Drosophil
101	43.8	5.0	181699	12	AC178101	AC178101 Strongylo	174	40.6	4.7	1841	13	BT023838	BT023838 Drosophil
102	43.8	5.0	340625	12	AC117847	AC117847 Rattus no	175	40.6	4.7	2619	2	AX780504	AX780504 Sequence
103	43.6	5.0	125020	5	AF429315	AF429315 Homo sapi	176	40.6	4.7	3574	11	BC084744	BC084744 Xenopus 1
104	43.4	5.0	112712	12	AC144380	AC144380 Pan trogl	c 177	40.6	4.7	110000	13	AC116957_2	Continuation (3 of
105	43.4	5.0	223529	6	AC153513	AC153513 Mus muscu	c 178	40.6	4.7	123014	12	AC179264	AC179264 Strongylo
106	43.4	5.0	228302	6	AC107711	AC107711 Mus muscu	c 179	40.6	4.7	128857	12	AC181354	AC181354 Strongylo
107	43.2	5.0	110000	13	AC16305_2	Continuation (3 of	c 180	40.6	4.7	131946	12	AC160603	AC160603 Loxodonta
108	43.2	5.0	213309	6	AC158553	AC158553 Mus muscu	c 181	40.6	4.7	146117	12	AC160609	AC160609 Loxodonta
109	43.2	5.0	234787	12	AC073780	AC073780 Mus muscu	c 182	40.6	4.7	170212	5	AC058822	AC058822 Homo sapi
110	43.2	5.0	243517	12	AC111219	AC111219 Rattus no	c 183	40.6	4.7	198614	6	AL596127	AL596127 Mouse DNA
111	43	4.9	1199	4	AY234412	AY234412 Arabidops	184	40.6	4.7	211844	12	AC048370	AC048370 Homo sapi
112	42.8	4.9	456	2	AX187025	AX187025 Sequence	185	40.6	4.7	218238	12	CR936243	CR936243 Danio rer
113	42.8	4.9	192187	13	AC117072	AC117072 Dictyoste	186	40.6	4.7	223585	6	AC154474	AC154474 Mus muscu
114	42.6	4.9	145715	12	AC158434	AC158434 Lemur cat	187	40.6	4.7	236260	12	AC168761	AC168761 Strongylo
115	42.6	4.9	169283	12	AC044820	AC044820 Homo sapi	188	40.6	4.7	252707	12	AC165036	AC165036 Bos tauru
116	42.6	4.9	217207	12	AC133132	AC133132 Rattus no	189	40.6	4.7	266544	13	AC116956	AC116956 Dictyoste
117	42.4	4.9	161363	6	AL645535	AL645535 Mouse DNA	c 190	40.4	4.6	6171	2	AX345913	AX345913 Sequence
118	42.2	4.9	1867	13	DMLBTRF	Y08822 D.melanogas	191	40.4	4.6	104806	4	AC006228	AC006228 Genomic s
119	42.2	4.9	4234	13	AF465311	AF465311 Dictyoste	192	40.4	4.6	217989	6	AC113599	AC113599 Mus muscu
120	42.2	4.9	256879	13	AC116982	AC116982 Dictyoste	c 193	40.2	4.6	1522	13	AY701231	AY701231 Orconecte
121	42	4.8	1300	11	AP324209	AP324209 Hoplobatr	194	40.2	4.6	1963	13	AB124840	AB124840 Bombyx mo
122	42	4.8	1827	11	CR760807	CR760807 Xenopus t	195	40.2	4.6	4752	5	AB179302	AB179302 Macaca fa
123	42	4.8	2000	2	AX655393	AX655393 Sequence	196	40.2	4.6	71571	6	BX530028	BX530028 Mouse DNA
124	42	4.8	48876	6	AL928841	AL928841 Mouse DNA	197	40.2	4.6	138307	6	AL808014	AL808014 Mouse DNA
125	42	4.8	89515	5	AL353574	AL353574 Human DNA	c 198	40.2	4.6	158475	5	AC097463	AC097463 Homo sapi
126	42	4.8	155198	12	AL357553	AL357553 Homo sapi	c 199	40.2	4.6	168768	11	BX640579	BX640579 Zebrafish
127	42	4.8	283075	6	AC017801	AC017801 Mus muscu	200	40.2	4.6	220999	12	AC153033	AC153033 Bos tauru
128	41.8	4.8	27359	2	AX592483	AX592483 Sequence	201	40	4.6	861	13	DQ097517	DQ097517 Schistos
129	41.8	4.8	45983	12	AC178483	AC178483 Strongylo	202	40	4.6	1299	6	BC021404	BC021404 Mus muscu
130	41.8	4.8	107714	12	AL356306	AL356306 Homo sapi	203	40	4.6	2260	5	AB178978	AB178978 Macaca fa
131	41.8	4.8	139111	5	AL158048	AL158048 Human DNA	204	40	4.6	2759	11	CR848656	CR848656 Xenopus t
132	41.8	4.8	149233	12	AC178399	AC178399 Strongylo	205	40	4.6	3399	5	BC063840	BC063840 Homo sapi
133	41.8	4.8	178599	6	AC160406	AC160406 Mus muscu	206	40	4.6	4091	5	BSM0803794	BSM0803794 Homo sapi
134	41.8	4.8	180339	12	AC161190	AC161190 Mus muscu	c 207	40	4.6	45549	12	AC182099	AC182099 Mus muscu
135	41.8	4.8	238453	6	AC102734	AC102734 Mus muscu	c 208	40	4.6	86826	13	PFMAL3P5	AL034556 Plasmodiu
136	41.6	4.8	171532	12	AC061993	AC061993 Homo sapi	c 209	40	4.6	143240	12	AC181355	AC181355 Strongylo
137	41.6	4.8	186014	6	AC133942	AC133942 Mus muscu	c 210	40	4.6	187377	11	CR933822	CR933822 Zebrafish
138	41.6	4.8	191781	11	BX000480	BX000480 Zebrafish	c 211	40	4.6	205875	6	AC102083	AC102083 Mus muscu
139	41.6	4.8	193256	5	AL445305	AL445305 Human DNA	c 212	40	4.6	349980	2	AX344574	AX344574 Sequence
140	41.6	4.8	238720	12	AC095949	AC095949 Rattus no	213	39.8	4.6	269	13	AB189921	AB189921 Dictyoste
141	41.6	4.8	271339	12	AC131637	AC131637 Rattus no	214	39.8	4.6	571	13	AB189920	AB189920 Dictyoste
142	41.6	4.8	347050	13	FFA929351	FFA929351 Plasmodiu	215	39.8	4.6	663	7	BV237240	BV237240 S23AP6203
143	41.4	4.8	384	2	CQ395463	CQ395463 Sequence	216	39.8	4.6	774	7	BV059932	BV059932 S212P6027
144	41.4	4.8	384	2	CQ401799	CQ401799 Sequence	217	39.8	4.6	2160	5	BC063455	BC063455 Homo sapi
145	41.4	4.8	202913	6	AC139845	AC139845 Mus muscu	218	39.8	4.6	3362	5	BC033679	BC033679 Homo sapi
146	41.4	4.8	215416	6	AC129537	AC129537 Mus muscu	c 219	39.8	4.6	137187	6	AC127249	AC127249 Mus muscu
147	41.4	4.8	219949	12	AC105796	AC105796 Rattus no	c 220	39.8	4.6	217898	12	AC095909	AC095909 Rattus no
148	41.4	4.8	246132	6	AC144783	AC144783 Mus muscu	c 221	39.8	4.6	222866	12	AC126906	AC126906 Rattus no
149	41.4	4.8	251452	12	AC097208	AC097208 Rattus no	c 222	39.8	4.6	240234	12	AC133305	AC133305 Rattus no
150	41.2	4.7	67356	5	AL161658	AL161658 Human DNA	c 223	39.6	4.6	571	7	BV038512	BV038512 S212P6547
151	41.2	4.7	110000	4	AP008218_168	Continuation (169	224	39.6	4.6	1186	6	RATARM22C	BC1107 rat SM22 mr
152	41.2	4.7	110000	4	AP008218_169	Continuation (170	225	39.6	4.6	1735	13	DQ011045	DQ011045 Dictyocau
153	41.2	4.7	150238	4	CNS0809E	Continuation (170	226	39.6	4.6	2024	5	AK024913	AK024913 Homo sapi
154	41.2	4.7	155592	12	AC178903	AC178903 Strongylo	c 227	39.6	4.6	45173	4	ATAC009318	ATAC009318 Arabidops
155	41.2	4.7	174009	6	AC119943	AC119943 Mus muscu	c 228	39.6	4.6	92401	12	AC181901	AC181901 Strongylo
156	41.2	4.7	178876	11	BX323590	BX323590 Zebrafish	c 229	39.6	4.6	121763	4	AC149804	AC149804 Medicago
157	41.2	4.7	180869	6	AC160403	AC160403 Mus muscu	c 230	39.6	4.6	142846	6	AL845280	AL845280 Mouse DNA
158	41.2	4.7	186567	12	AC084417	AC084417 Homo sapi	c 231	39.6	4.6	172007	5	AC006376	AC006376 Homo sapi
159	41	4.7	2497	11	BC079732	BC079732 Xenopus 1	c 232	39.6	4.6	180823	12	AC176329	AC176329 Strongylo
160	41	4.7	3934	14	RABMEWGLY	L04504 Oryctolagus	c 233	39.6	4.6	182198	12	CT030018	CT030018 Danio rer
161	41	4.7	172924	12	AC170120	AC170120 Bos tauru	c 234	39.6	4.6	183026	11	BX323086	BX323086 Zebrafish
162	41	4.7	190981	12	AC181029	AC181029 Strongylo	c 235	39.6	4.6	214807	12	CR376853	CR376853 Danio rer
163	40.8	4.7	2143	13	AK113048	AK113048 Ciona int	c 236	39.4	4.5	428	2	CQ523955	CQ523955 Sequence
164	40.8	4.7	3338	11	AB197788	AB197788 Pagrus ma	237	39.4	4.5	488	2	CQ519528	CQ519528 Sequence

238	39.4	4.5	541	6	BC046339	Mus muscu	311	4.5	167159	12	AC073481	Homo sapi
239	39.4	4.5	733	11	BC020319	Mus muscu	312	4.5	168154	5	AC012174	Homo sapi
240	39.4	4.5	1022	6	BC071345	Danio rer	313	4.5	169310	11	BX323461	Zebrafish
241	39.4	4.5	1637	6	BC085715	Rattus no	314	4.5	169942	12	AC124793	Homo sapi
242	39.4	4.5	101076	12	AC178032	Strongylo	315	4.5	171239	12	AC10652	Homo sapi
243	39.4	4.5	103610	5	HS024088	Continuation (2 of	316	4.5	173043	12	AC124792	Homo sapi
244	39.4	4.5	110000	13	AC116305_1	Continuation (2 of	317	4.5	174287	5	AC100840	Homo sapi
245	39.4	4.5	141681	12	CR513785	CR388067 Zebrafish	318	4.5	175258	12	AC017098	Homo sapi
246	39.4	4.5	162364	11	CR513785	CR388067 Zebrafish	319	4.5	175258	12	AC017098	Homo sapi
247	39.4	4.5	163519	12	CR388067	CR388067 Zebrafish	320	4.5	178344	6	AC155298	Mus muscu
248	39.4	4.5	165454	5	AL138880	Human DNA	321	4.5	178611	12	AC024631	Homo sapi
249	39.4	4.5	174126	12	AC135552	Canis fam	322	4.5	178810	6	AC099621	Mus muscu
250	39.4	4.5	176042	11	CR589876	CR589876 Zebrafish	323	4.5	184697	6	AL627403	Mouse DNA
251	39.4	4.5	176392	12	AC135954	Papio anu	324	4.5	190333	5	AC092129	Homo sapi
252	39.4	4.5	207504	6	AL670959	AL670959 Mouse DNA	325	4.5	193604	12	AC174144	Medicago
253	39.4	4.5	230186	6	AL731678	AL731678 Mouse DNA	326	4.5	194023	5	AC021541	Homo sapi
254	39.4	4.5	231146	12	AC172467	AC172467 Bos tauru	327	4.5	196416	5	AC006483	Homo sapi
255	39.4	4.5	249136	12	AC106242	AC106242 Rattus no	328	4.5	198019	6	AC116656	Mus muscu
256	39.4	4.5	253001	13	AE014834	AE014834 Plasmodi	329	4.5	201911	12	AC118294	Rattus no
257	39.4	4.5	262388	6	AL670959	AL670959 Mouse DNA	330	4.5	210184	11	BX537272	Zebrafish
258	39.4	4.5	270983	12	AC172936	AC172936 Bos tauru	331	4.5	220857	12	AC178319	Strongylo
259	39.4	4.5	276477	12	AC158009	AC158009 Bos tauru	332	4.5	225611	12	AC111446	Rattus no
260	39.2	4.5	309	2	CQ513146	CQ513146 Sequence	333	4.5	239691	12	AC096274	Rattus no
261	39.2	4.5	337	7	AB134616	AB134616 Homo sapi	334	4.5	254733	13	AC117075	Dicystoste
262	39.2	4.5	424	7	BV237881	BV237881 S234P6478	335	4.5	310779	12	AC005140	Plasmodi
263	39.2	4.5	436	7	BV257903	BV257903 S235P6125	336	4.5	333321	13	AC116986	Dicystoste
264	39.2	4.5	546	14	BC108236	BC108236 Bos tauru	337	4.5	524	7	BV412862	S229P6516
265	39.2	4.5	818	6	BC100523	BC100523 Mus muscu	338	4.5	633	7	BV288848	S232P6214
266	39.2	4.5	913	13	AY542294	AY542294 Bigelowie	339	4.5	667	7	BV221313	S233P6118
267	39.2	4.5	1805	13	DD1PDP5A	L05617 Dictyostelli	340	4.5	1447	5	AC020589	Homo sapi
268	39.2	4.5	1858	5	AB168514	AB168514 Macaca fa	341	4.5	1497	6	BC087038	Rattus no
269	39.2	4.5	1974	6	BC023938	BC023938 Mus muscu	342	4.5	1724	6	BC096761	Mus muscu
270	39.2	4.5	2158	6	BC031195	BC031195 Mus muscu	343	4.5	1743	11	BC061441	Xenopus t
271	39.2	4.5	2433	5	BC041141	BC041141 Homo sapi	344	4.5	1913	5	BC012362	Homo sapi
272	39.2	4.5	2702	5	BC004119	BC004119 Homo sapi	345	4.5	2170	6	BC101874	Rattus no
273	39.2	4.5	3016	13	DDU31631	U31631 Dictyostelli	346	4.5	2363	6	BC083812	Rattus no
274	39.2	4.5	3764	6	BC054483	BC054483 Mus muscu	347	4.5	3863	6	BC088732	Mus muscu
275	39.2	4.5	5321	2	AX348330	AX348330 Sequence	348	4.5	16633	2	AX344576	Sequence
276	39.2	4.5	5321	2	AX356369	AX356369 Sequence	349	4.5	95655	12	AC110069	Homo sapi
277	39.2	4.5	2568	13	AC116955	AC116955 Dicystoste	350	4.5	131633	6	AL713982	Mouse DNA
278	39.2	4.5	35102	5	AL591932	AL591932 Human DNA	351	4.5	162726	12	AC179001	Strongylo
279	39.2	4.5	110000	12	PFMALBP1_00	AL844507 Plasmodi	352	4.5	182151	5	AC011835	Homo sapi
280	39.2	4.5	110000	12	PFMALBP1_01	Continuation (2 of	353	4.5	185463	5	AC016065	Homo sapi
281	39.2	4.5	110000	13	AC116984_2	Continuation (3 of	354	4.5	190623	6	AC121790	Mus muscu
282	39.2	4.5	124464	6	AC123927_2	AC123927 Mus muscu	355	4.5	191377	5	AC018398	Homo sapi
283	39.2	4.5	164611	6	AC156268	AC156268 Mus muscu	356	4.5	201274	6	AC129335	Mus muscu
284	39.2	4.5	167792	12	AC113226	AC113226 Papio anu	357	4.5	204114	12	AC153019	Mus muscu
285	39.2	4.5	171612	5	AC099742	AC099742 Papio anu	358	4.5	226069	12	AC095365	Rattus no
286	39.2	4.5	172335	12	AC181638	AC181638 Strongylo	359	4.5	236105	12	AC165587	Bos tauru
287	39.2	4.5	182141	11	AL954645	AL954645 Zebrafish	360	4.5	250195	13	AE014831	Plasmodi
288	39.2	4.5	187926	6	AC122801	AC122801 Mus muscu	361	4.5	343050	13	PEA929353	Plasmodi
289	39.2	4.5	194207	6	AC163218	AC163218 Mus muscu	362	4.4	582	5	AB168303	Macaca fa
290	39.2	4.5	197397	6	AC113115	AC113115 Mus muscu	363	4.4	631	7	BV221702	Sequence
291	39.2	4.5	200417	12	AC134192	AC134192 Rattus no	364	4.4	2115	4	AY739287	Zea mays
292	39.2	4.5	205150	5	AC005274	AC005274 Homo sapi	365	4.4	2125	2	AX409766	Sequence
293	39.2	4.5	217156	6	AC116393	AC116393 Mus muscu	366	4.4	2125	5	HUMIGFACID	Human IGF b
294	39.2	4.5	232208	12	AC097430	AC097430 Rattus no	367	4.4	2480	6	BC107938	Rattus no
295	39	4.5	259	6	BC093588	BC093588 Mus muscu	368	4.4	6609	2	AX344839	Sequence
296	39	4.5	1575	13	AY069691	AY069691 Drosophil	369	4.4	6609	2	AX346785	Sequence
297	39	4.5	1790	5	AF136630	AF136630 Homo sapi	370	4.4	7218	2	I66494	Sequence 14
298	39	4.5	1999	13	BT004867	BT004867 Drosophil	371	4.4	17598	5	HSJ839811	Human DNA
299	39	4.5	2219	5	BC008719	BC008719 Homo sapi	372	4.4	30849	13	AC117082	Dicystoste
300	39	4.5	2221	5	BC018665	BC018665 Homo sapi	373	4.4	33270	13	AC116921	Dicystoste
301	39	4.5	2221	5	BC018665	BC018665 Homo sapi	374	4.4	110000	13	AC116984_4	Continuation (5 of
302	39	4.5	4446	13	DDU07236	U7236 Dictyostelli	375	4.4	113512	12	AC144377	Pan trogl
303	39	4.5	120809	5	AC007026	AC007026 Homo sapi	376	4.4	134768	11	BX537293	Zebrafish
304	39	4.5	153751	13	AC118551	AC118551 Dicystoste	377	4.4	144109	12	AC176781	Strongylo
305	39	4.5	162626	12	AC138551	AC138551 Danio rer	378	4.4	145600	14	AC151782	Ornithorh
306	39	4.5	164118	12	AC020804	AC020804 Mus muscu	379	4.4	152252	5	AP003039	Homo sapi
307	39	4.5	164496	12	AC147881	AC147881 Xenopus t	380	4.4	152179	12	AC012545	Homo sapi
308	39	4.5	165641	6	AC135469	AC135469 Mus muscu	381	4.4	155949	5	AC091022	Homo sapi
309	39	4.5	166236	5	AC022832	AC022832 Homo sapi	382	4.4	156863	12	AC069249	Homo sapi
310	39	4.5	166411	12	AC178635	AC178635 Strongylo	383	4.4	159036	12	AC180339	Strongylo

384	38.6	4.4	159336	5	AC020584	Homo sapi	AC020584 Homo sapi	457	38.2	4.4	1939	2	BD276277	BD276277 Serine pr
385	38.6	4.4	159850	12	AC177167	Strongylo	AC177167 Strongylo	458	38.2	4.4	3519	6	AF144082	AF144082 Rattus no
386	38.6	4.4	160872	6	AC131782	Mus muscu	AC131782 Mus muscu	459	38.2	4.4	3782	11	BC072923	BC072923 Xenopus l
387	38.6	4.4	161775	5	AC099512	Homo sapi	AC099512 Homo sapi	c 459	38.2	4.4	6424	13	AC115608	AC115608 Dictyoste
388	38.6	4.4	168097	12	AC177377	Strongylo	AC177377 Strongylo	461	38.2	4.4	29143	13	AC115594	AC115594 Dictyoste
389	38.6	4.4	170005	6	AC122297	Mus muscu	AC122297 Mus muscu	462	38.2	4.4	40611	13	AC116987	AC116987 Dictyoste
390	38.6	4.4	172503	12	AC181053	Strongylo	AC181053 Strongylo	c 463	38.2	4.4	57183	12	AC113330	AC113330 Homo sapi
391	38.6	4.4	176564	6	AC141869	Mus muscu	AC141869 Mus muscu	c 464	38.2	4.4	99291	4	ATF7M19	ATF7M19 Arabidops
392	38.6	4.4	179077	11	EX537140	Zebrafish	EX537140 Zebrafish	465	38.2	4.4	110000	12	EX004762	EX004762 Mus muscu
393	38.6	4.4	187574	5	AC018622	Homo sapi	AC018622 Homo sapi	466	38.2	4.4	110000	12	PFMAL11_00	PFMAL11_00 Plasmodiu
394	38.6	4.4	196431	5	CNS01DU5	Human chr	AL133162 Human chr	c 467	38.2	4.4	135666	14	AC152492	AC152492 Rhinoph
395	38.6	4.4	196590	12	AC156839	Pan trogl	AC156839 Pan trogl	c 468	38.2	4.4	143468	5	AC113331	AC113331 Homo sapi
396	38.6	4.4	197360	5	AP004372	Homo sapi	AP004372 Homo sapi	469	38.2	4.4	149951	5	AC018375	AC018375 Homo sapi
397	38.6	4.4	198017	6	AC012314	Homo sapi	AC012314 Homo sapi	c 470	38.2	4.4	159370	12	AL161633	AL161633 Bos tauru
398	38.6	4.4	202949	6	AC159271	Mus muscu	AC159271 Mus muscu	c 471	38.2	4.4	159319	12	AL590419	AL590419 Homo sapi
399	38.6	4.4	205307	12	AC009968	Homo sapi	AC009968 Homo sapi	c 472	38.2	4.4	172637	12	CR855265	CR855265 Danio rer
400	38.6	4.4	205823	5	AC161477	Pan trogl	AC161477 Pan trogl	473	38.2	4.4	173156	6	AC159965	AC159965 Mus muscu
401	38.6	4.4	212675	12	AC073904	Homo sapi	AC073904 Homo sapi	c 474	38.2	4.4	186999	12	AC020597	AC020597 Homo sapi
402	38.6	4.4	213049	12	AC079370	Mus muscu	AC079370 Mus muscu	475	38.2	4.4	187284	6	AC104102	AC104102 Mus muscu
403	38.6	4.4	229590	12	AC162406	Bos tauru	AC162406 Bos tauru	c 476	38.2	4.4	191524	5	AC090893	AC090893 Homo sapi
404	38.6	4.4	232568	6	AC129605	Mus muscu	AC129605 Mus muscu	c 477	38.2	4.4	192581	12	PFMAL113P1	PFMAL113P1 Plasmodiu
405	38.6	4.4	273275	13	AE014828	Plasmodiu	AE014828 Plasmodiu	478	38.2	4.4	194140	5	AF000752	AF000752 Homo sapi
406	38.6	4.4	293451	12	AC157311	Bos tauru	AC157311 Bos tauru	479	38.2	4.4	19053	12	AC167784	AC167784 Glycine m
407	38.6	4.4	337203	13	CR382401	Plasmodiu	CR382401 Plasmodiu	480	38.2	4.4	219212	6	AC124502	AC124502 Mus muscu
408	38.6	4.4	337	2	CO419009	Sequence	CO419009 Sequence	481	38.2	4.4	22092	12	AC108641	AC108641 Rattus no
409	38.4	4.4	447	5	AF242452	Homo sapi	AF242452 Homo sapi	c 482	38.2	4.4	233094	12	AC134131	AC134131 Rattus no
410	38.4	4.4	947	14	BC109934	Bos tauru	BC109934 Bos tauru	c 483	38.2	4.4	235682	11	EX088646	EX088646 Zebrafish
411	38.4	4.4	1072	4	BT009536	Triticum	BT009536 Triticum	c 484	38.2	4.4	241144	12	CT573229	CT573229 Danio rer
412	38.4	4.4	1150	5	HS4420575	Homo sapi	AJ4780471 Homo sapi	c 485	38.2	4.4	243457	11	CR388143	CR388143 Zebrafish
413	38.4	4.4	1815	2	AX780471	Sequence	AX780471 Sequence	486	38.2	4.4	251443	12	AC096251	AC096251 Rattus no
414	38.4	4.4	1815	5	BC006440	Homo sapi	BC006440 Homo sapi	c 487	38.2	4.4	256575	12	AC105807	AC105807 Rattus no
415	38.4	4.4	2064	5	AC025491	Homo sapi	AC025491 Homo sapi	c 488	38.2	4.4	265985	12	AC087226	AC087226 Mus muscu
416	38.4	4.4	2211	6	BC049860	Mus muscu	BC049860 Mus muscu	c 489	38	4.4	408	2	AX300942	AX300942 Sequence
417	38.4	4.4	2253	6	BC010651	Mus muscu	BC010651 Mus muscu	c 490	38	4.4	514	7	G90722	G90722 S08P6777RD
418	38.4	4.4	2329	5	BC051762	Homo sapi	BC051762 Homo sapi	491	38	4.4	600	5	BC058843	BC058843 Homo sapi
419	38.4	4.4	2766	14	BC103000	Bos tauru	BC103000 Bos tauru	492	38	4.4	722	6	MMU300659	MMU300659 Mus muscu
420	38.4	4.4	2909	13	AX116710	Ciona int	AX116710 Ciona int	493	38	4.4	1139	6	BC058435	BC058435 Mus muscu
421	38.4	4.4	5195	2	AX346499	Sequence	AX346499 Sequence	494	38	4.4	1411	13	AY069237	AY069237 Drosophil
422	38.4	4.4	5325	13	AX160094	Dictyoste	AX160094 Dictyoste	495	38	4.4	1474	2	BD270518	BD270518 Novel mai
423	38.4	4.4	15743	2	AC323781	Sequence	AC323781 Sequence	496	38	4.4	1474	2	AX494846	AX494846 Sequence
424	38.4	4.4	110000	12	AC151717_0	Mus muscu	AC151717 Mus muscu	497	38	4.4	1474	2	AX494846	AX494846 Sequence
425	38.4	4.4	110000	13	AC116957_2	Continuation (3 of	Continuation (3 of	498	38	4.4	1481	14	BC102072	BC102072 Bos tauru
426	38.4	4.4	113417	12	AC176319	Strongylo	AC176319 Strongylo	499	38	4.4	2158	13	BT010124	BT010124 Drosophil
427	38.4	4.4	118543	6	AL928615	Mouse DNA	AL928615 Mouse DNA	500	38	4.4	2323	5	BC092417	BC092417 Homo sapi
428	38.4	4.4	138978	11	CR388214	Zebrafish	CR388214 Zebrafish	501	38	4.4	2381	5	AB168314	AB168314 Macaca fa
429	38.4	4.4	156672	6	AC131332	Mus muscu	AC131332 Mus muscu	502	38	4.4	2542	11	BC084868	BC084868 Xenopus t
430	38.4	4.4	164559	5	AL450312	Human DNA	AL450312 Human DNA	503	38	4.4	2972	5	BC051810	BC051810 Homo sapi
431	38.4	4.4	173781	12	AC169543	Bos tauru	AC169543 Bos tauru	504	38	4.4	3486	6	BC043451	BC043451 Mus muscu
432	38.4	4.4	176917	12	CT025872	Danio rer	CT025872 Danio rer	505	38	4.4	3505	6	BC068304	BC068304 Mus muscu
433	38.4	4.4	180200	11	BX927279	Zebrafish	BX927279 Zebrafish	506	38	4.4	4230	13	AF465310	AF465310 Dictyoste
434	38.4	4.4	187214	12	AL354724	Homo sapi	AL354724 Homo sapi	507	38	4.4	4296	13	AF228873	AF228873 Strongylo
435	38.4	4.4	196173	6	AC151988	Mus muscu	AC151988 Mus muscu	c 508	38	4.4	5164	2	AX458606	AX458606 Sequence
436	38.4	4.4	198752	11	BX957279	Zebrafish	BX957279 Zebrafish	c 509	38	4.4	6319	2	AX465444	AX465444 Sequence
437	38.4	4.4	206813	12	AC103518	Rattus no	AC103518 Rattus no	c 510	38	4.4	9751	13	AF465309	AF465309 Dictyoste
438	38.4	4.4	209390	12	AC176766	Strongylo	AC176766 Strongylo	c 511	38	4.4	14287	13	AC115588	AC115588 Dictyoste
439	38.4	4.4	214951	12	AC178655	Strongylo	AC178655 Strongylo	c 512	38	4.4	82797	12	BX890561_3	Continuation (4 of
440	38.4	4.4	220809	6	AC157592	Mus muscu	AC157592 Mus muscu	c 513	38	4.4	89004	13	CEY59H2	CEY59H2 Caenorhabdi
441	38.4	4.4	222297	12	AC133350	Rattus no	AC133350 Rattus no	514	38	4.4	110000	12	AC095760_0	Rattus no
442	38.4	4.4	222394	6	AC115762	Mus muscu	AC115762 Mus muscu	c 515	38	4.4	110000	12	BX890561_0	Danio rer
443	38.4	4.4	228460	13	AC130637	Rattus no	AC130637 Rattus no	516	38	4.4	120757	4	AC119412	Continuation (6 of
444	38.4	4.4	254733	13	AC117075	Dictyoste	AC117075 Dictyoste	517	38	4.4	136876	5	AC119412	AC119412 Medicago
445	38.4	4.4	281198	12	AC099106	Rattus no	AC099106 Rattus no	518	38	4.4	141721	12	AC149953	AC149953 Strongylo
446	38.4	4.4	314002	12	AC131824	Rattus no	AC131824 Rattus no	c 519	38	4.4	145105	12	AC180462	AC180462 Strongylo
447	38.4	4.4	331039	13	AC116979	Dictyoste	AC116979 Dictyoste	c 520	38	4.4	145105	12	AC180462	AC180462 Strongylo
448	38.4	4.4	349980	2	AC334453	Sequence	AC334453 Sequence	521	38	4.4	148267	5	AC067940	AC067940 Homo sapi
449	38.2	4.4	279	2	C0523287	Sequence	C0523287 Sequence	522	38	4.4	157139	12	AC180507	AC180507 Strongylo
450	38.2	4.4	335	2	AR503392	Sequence	AR503392 Sequence	c 523	38	4.4	160321	6	AL772321	AL772321 Mouse chr
451	38.2	4.4	335	2	AR503392	Sequence	AR503392 Sequence	524	38	4.4	161261	5	CNS05TE3	AL358332 Human chr
452	38.2	4.4	335	5	BC035289	Homo sapi	BC035289 Homo sapi	525	38	4.4	162020	6	AC124814	AC124814 Mus muscu
453	38.2	4.4	875	4	BT019284	Zea mays	BT019284 Zea mays	526	38	4.4	163229	12	AC011587	AC011587 Homo sapi
454	38.2	4.4	1557	2	BD191955	Human tol	BD191955 Human tol	c 527	38	4.4	168748	12	AC180313	AC180313 Strongylo
455	38.2	4.4	1557	2	C0870724	Sequence	C0870724 Sequence	c 528	38	4.4	170604	11	BX005481	BX005481 Zebrafish
456	38.2	4.4	1557	2	AX399024	Sequence	AX399024 Sequence	c 529	38	4.4	177957	12	AC025298	AC025298 Homo sapi

C 530	38	4.4	181351	12	AC0211471	AC0211471 Homo sapi	603	37.6	4.3	1807	14	BC109511	BC109511 Bos tauru
C 531	38	4.4	182321	5	AL356866	AL356866 Human DNA	604	37.6	4.3	1817	5	BC038370	BC038370 Homo sapi
C 532	38	4.4	183670	12	AC109485	AC109485 Homo sapi	605	37.6	4.3	2018	11	CR761244	CR761244 Xenopus t
C 533	38	4.4	184528	12	AC167463	AC167463 Mus muscu	606	37.6	4.3	2103	6	BC063757	BC063757 Mus muscu
C 534	38	4.4	185255	6	AC127359	AC127359 Mus muscu	607	37.6	4.3	2731	13	AY058318	AY058318 Drosophil
C 535	38	4.4	190598	6	AC135017	AC135017 Mus muscu	608	37.6	4.3	3133	6	BC058693	BC058693 Mus muscu
C 536	38	4.4	196842	12	AC178756	AC178756 Strongylo	609	37.6	4.3	3151	2	CS150684	CS150684 Sequence
C 537	38	4.4	204400	6	AC159812	AC159812 Mus muscu	610	37.6	4.3	3258	4	AB030491	AB030491 Glycine m
C 538	38	4.4	209529	6	AL691427	AL691427 Mouse DNA	611	37.6	4.3	8649	2	AX251083	AX251083 Sequence
C 539	38	4.4	213090	6	AL691427	AL691427 Mouse DNA	612	37.6	4.3	8649	2	AX251856	AX251856 Sequence
C 540	38	4.4	215559	12	AC141086	AC141086 Mus muscu	613	37.6	4.3	8649	2	AX344242	AX344242 Sequence
C 541	38	4.4	238427	12	CR774193	CR774193 Danio rer	C 614	37.6	4.3	8649	2	AX348633	AX348633 Sequence
C 542	38	4.4	239995	12	CR774193	CR774193 Danio rer	C 615	37.6	4.3	35080	13	U29382	U29382 Caenorhabdi
C 543	38	4.4	245210	12	AC137771	AC137771 Homo sapi	616	37.6	4.3	36731	13	AC110142	AC110142 Mus muscu
C 544	38	4.4	246196	12	AC105641	AC105641 Rattus no	617	37.6	4.3	57203	13	AC115581	AC115581 Dictyoste
C 545	38	4.4	250029	13	AE014830	AE014830 Plasmodiu	618	37.6	4.3	57538	13	AC115682	AC115682 Dictyoste
C 546	38	4.4	259691	12	AC166835	AC166835 Mus muscu	619	37.6	4.3	79904	6	AL589767	AL589767 Mouse DNA
C 547	38	4.4	260085	12	AC164859	AC164859 Bos tauru	C 620	37.6	4.3	89306	12	AC181498	AC181498 Strongylo
C 548	38	4.4	282899	12	AC095879	AC095879 Rattus no	C 621	37.6	4.3	98204	11	AL645800	AL645800 Zebrafish
C 549	38	4.4	289192	12	AC139506	AC139506 Homo sapi	622	37.6	4.3	106568	12	AC139803	AC139803 Continuation (4 of
C 550	38	4.4	304391	12	AC158106	AC158106 Bos tauru	623	37.6	4.3	110000	12	AC139803	AC139803 Continuation (2 of
C 551	38	4.4	329599	12	AC162572	AC162572 Bos tauru	624	37.6	4.3	110000	12	AC140020	AC140020 Continuation (3 of
C 552	38	4.4	337265	12	AC175878	AC175878 Strongylo	625	37.6	4.3	116280	12	AC179096	AC179096 Strongylo
C 553	37.8	4.3	664	11	CT025311	CT025311 Xenopus t	C 626	37.6	4.3	124498	12	AC141194	AC141194 Rattus no
C 554	37.8	4.3	817	14	BC102542	BC102542 Bos tauru	C 627	37.6	4.3	125587	12	AC179714	AC179714 Strongylo
C 555	37.8	4.3	818	11	CT025519	CT025519 Xenopus t	C 628	37.6	4.3	127449	12	AC180443	AC180443 Strongylo
C 556	37.8	4.3	851	6	BC024348	BC024348 Mus muscu	C 629	37.6	4.3	136695	12	AC168810	AC168810 Strongylo
C 557	37.8	4.3	1006	14	BC111143	BC111143 Bos tauru	C 630	37.6	4.3	143124	12	AC176835	AC176835 Strongylo
C 558	37.8	4.3	1065	6	BC049634	BC049634 Mus muscu	C 631	37.6	4.3	144072	6	CT030882	CT030882 Mouse DNA
C 559	37.8	4.3	1443	6	BC061219	BC061219 Mus muscu	C 632	37.6	4.3	147954	12	AC177640	AC177640 Strongylo
C 560	37.8	4.3	1500	5	BC036796	BC036796 Homo sapi	C 633	37.6	4.3	149129	12	CT027791	CT027791 Danio rer
C 561	37.8	4.3	1571	14	BC102904	BC102904 Bos tauru	C 634	37.6	4.3	151555	12	AC139276	AC139276 Homo sapi
C 562	37.8	4.3	1910	5	BC043519	BC043519 Homo sapi	C 635	37.6	4.3	157780	12	AC179634	AC179634 Strongylo
C 563	37.8	4.3	2170	11	BC067704	BC067704 Danio rer	C 636	37.6	4.3	163349	12	AC168256	AC168256 Strongylo
C 564	37.8	4.3	2446	5	BC046497	BC046497 Homo sapi	C 637	37.6	4.3	166824	11	EX470265	EX470265 Zebrafish
C 565	37.8	4.3	2627	11	XLA440222	AJ440222 Xenopus l	C 638	37.6	4.3	169056	12	AC145104	AC145104 Homo sapi
C 566	37.8	4.3	68805	12	AC101557	AC101557 Mus muscu	C 639	37.6	4.3	171745	12	AC138935	AC138935 Homo sapi
C 567	37.8	4.3	94454	12	AC178937	AC178937 Strongylo	C 640	37.6	4.3	174329	6	AC140981	AC140981 Mus muscu
C 568	37.8	4.3	110000	12	AC178937	AC178937 Strongylo	C 641	37.6	4.3	177492	12	AC168350	AC168350 Strongylo
C 569	37.8	4.3	125081	12	CR854824	CR854824 Danio rer	C 642	37.6	4.3	180261	12	AC180779	AC180779 Strongylo
C 570	37.8	4.3	138038	5	AL591435	AL591435 Human DNA	C 643	37.6	4.3	180480	12	AC140174	AC140174 Homo sapi
C 571	37.8	4.3	140466	5	AL355529	AL355529 Human DNA	C 644	37.6	4.3	180958	12	AC025779	AC025779 Homo sapi
C 572	37.8	4.3	143057	12	AC176229	AC176229 Strongylo	C 645	37.6	4.3	183309	11	EX572641	EX572641 Zebrafish
C 573	37.8	4.3	144500	12	AC010231	AC010231 Homo sapi	C 646	37.6	4.3	185162	5	AC140132	AC140132 Homo sapi
C 574	37.8	4.3	149529	12	AC177084	AC177084 Strongylo	C 647	37.6	4.3	185370	12	CR513788	CR513788 Danio rer
C 575	37.8	4.3	162564	6	AC127575	AC127575 Mus muscu	C 648	37.6	4.3	185336	12	AC139837	AC139837 Homo sapi
C 576	37.8	4.3	165490	14	CR925799	CR925799 Wallaby D	C 649	37.6	4.3	191038	6	AC124719	AC124719 Mus muscu
C 577	37.8	4.3	171722	12	AC162117	AC162117 Ovis arie	C 650	37.6	4.3	193305	12	AC177326	AC177326 Strongylo
C 578	37.8	4.3	172477	12	CR936378	CR936378 Danio rer	C 651	37.6	4.3	194268	6	AC107863	AC107863 Mus muscu
C 579	37.8	4.3	174019	12	AC025734	AC025734 Homo sapi	C 652	37.6	4.3	196432	11	EX936462	EX936462 Zebrafish
C 580	37.8	4.3	174627	5	AC022138	AC022138 Homo sapi	C 653	37.6	4.3	197523	12	AC018883	AC018883 Homo sapi
C 581	37.8	4.3	176451	12	AC147930	AC147930 Ovis arie	C 654	37.6	4.3	198615	6	AC123678	AC123678 Mus muscu
C 582	37.8	4.3	177308	5	AC009560	AC009560 Homo sapi	C 655	37.6	4.3	199128	5	AC091946	AC091946 Homo sapi
C 583	37.8	4.3	178233	12	AC182141	AC182141 Bos tauru	C 656	37.6	4.3	200362	5	AC115865	AC115865 Mus muscu
C 584	37.8	4.3	183412	12	AP001899	AP001899 Homo sapi	C 657	37.6	4.3	205782	6	AC124402	AC124402 Mus muscu
C 585	37.8	4.3	185203	12	AL161649	AL161649 Homo sapi	C 658	37.6	4.3	210297	12	AC168246	AC168246 Strongylo
C 586	37.8	4.3	206254	5	AC093283	AC093283 Homo sapi	C 659	37.6	4.3	212827	6	AC137970	AC137970 Mus muscu
C 587	37.8	4.3	211576	6	AC110564	AC110564 Mus muscu	C 660	37.6	4.3	217621	12	EX901924	EX901924 Danio rer
C 588	37.8	4.3	215018	12	AC139113	AC139113 Pongo pyg	C 661	37.6	4.3	220025	12	AC155769	AC155769 Bos tauru
C 589	37.8	4.3	224076	12	AC119090	AC119090 Rattus no	C 662	37.6	4.3	220171	12	AC113111	AC113111 Mus muscu
C 590	37.8	4.3	228004	12	AC094278	AC094278 Rattus no	C 663	37.6	4.3	223342	12	AC094125	AC094125 Rattus no
C 591	37.8	4.3	228925	12	AC158278	AC158278 Canis fam	C 664	37.6	4.3	225302	6	AC109205	AC109205 Mus muscu
C 592	37.8	4.3	240344	12	AC127886	AC127886 Rattus no	C 665	37.6	4.3	229305	12	AC165535	AC165535 Bos tauru
C 593	37.8	4.3	256172	12	AC005139	AC005139 Plasmodiu	C 666	37.6	4.3	230536	12	AC176874	AC176874 Strongylo
C 594	37.8	4.3	257109	13	AC116963	AC116963 Dictyoste	C 667	37.6	4.3	232159	12	AC182457	AC182457 Gallus ga
C 595	37.8	4.3	266837	12	AC171870	AC171870 Bos tauru	C 668	37.6	4.3	233321	6	AL732546	AL732546 Mouse DNA
C 596	37.8	4.3	279836	12	AC117954	AC117954 Rattus no	C 669	37.6	4.3	236376	12	AC170244	AC170244 Bos tauru
C 597	37.8	4.3	346939	15	EX842643	EX842643 Mycoplasma	C 670	37.6	4.3	238123	12	AC136571	AC136571 Rattus no
C 598	37.6	4.3	332	2	CQ524615	CQ524615 Sequence	C 671	37.6	4.3	238598	6	AC117570	AC117570 Mus muscu
C 599	37.6	4.3	650	4	AY731584	AY731584 Arachnis h	C 672	37.6	4.3	244471	12	AC106677	AC106677 Rattus no
C 600	37.6	4.3	983	5	HSW802179	AL137463 Homo sapi	C 673	37.6	4.3	257109	13	AC116963	AC116963 Dictyoste
C 601	37.6	4.3	999	5	BC073929	BC073929 Homo sapi	C 674	37.6	4.3	257757	13	AE014837	AE014837 Plasmodiu
C 602	37.6	4.3	1240	5	BC055418	BC055418 Homo sapi	C 675	37.6	4.3	288857	12	AC128817	AC128817 Rattus no

676	37.4	4.3	158	2	AX2033305	AX2033305 Sequence	c 749	37.4	4.3	210010	12	AC146135	AC146135 Pan trogl
677	37.4	4.3	774	7	BV638413	BV638413 S215P6060	c 750	37.4	4.3	213717	6	AL929228	AL929228 Mouse DNA
678	37.4	4.3	911	6	BC061126	BC061126 Mus muscu	c 751	37.4	4.3	214189	5	BS000022	BS000022 Pan trogl
679	37.4	4.3	913	6	BC100331	BC100331 Mus muscu	c 752	37.4	4.3	223232	6	AC164312	AC164312 Mus muscu
680	37.4	4.3	989	11	BC083533	BC083533 Danio rer	c 753	37.4	4.3	225196	6	AL672067	AL672067 Mouse DNA
681	37.4	4.3	1113	6	BC100322	BC100322 Mus muscu	c 754	37.4	4.3	228709	12	AC020620	AC020620 Mus muscu
682	37.4	4.3	1138	11	BC046570	BC046570 Xenopus l	c 755	37.4	4.3	229410	12	AC172241	AC172241 Bos tauru
683	37.4	4.3	1367	5	AB179271	AB179271 Macaca fa	c 756	37.4	4.3	230204	12	CR933860	CR933860 Danio rer
684	37.4	4.3	1431	13	AK116801	AK116801 Ciona int	c 757	37.4	4.3	231530	6	AL671975	AL671975 Mouse DNA
685	37.4	4.3	1458	5	BC063635	BC063635 Homo sapi	c 758	37.4	4.3	239450	12	AC106212	AC106212 Rattus no
686	37.4	4.3	1570	5	BC036920	BC036920 Homo sapi	c 759	37.4	4.3	240562	12	AC166667	AC166667 Bos tauru
687	37.4	4.3	1641	5	AK024802	AK024802 Homo sapi	c 760	37.4	4.3	246070	12	AC135737	AC135737 Mus muscu
688	37.4	4.3	1641	5	AK223414	AK223414 Homo sapi	c 761	37.4	4.3	246348	6	AC138611	AC138611 Mus muscu
689	37.4	4.3	1767	4	AF062467	AF062467 Cucumis m	c 762	37.4	4.3	256298	6	AC153651	AC153651 Mus muscu
690	37.4	4.3	1793	4	AY598342	AY598342 Solanum t	c 763	37.4	4.3	277028	12	AC161977	AC161977 Bos tauru
691	37.4	4.3	1973	13	AK116690	AK116690 Ciona int	c 764	37.4	4.3	283992	12	AC096048	AC096048 Rattus no
692	37.4	4.3	2150	13	BT010126	BT010126 Drosophila	c 765	37.4	4.3	307657	13	AE003468	AE003468 Drosophila
693	37.4	4.3	2219	5	BC091490	BC091490 Homo sapi	c 766	37.4	4.3	307657	13	AE003468	AE003468 Drosophila
694	37.4	4.3	2398	2	CS135310	CS135310 Sequence	c 767	37.2	4.3	993	6	BC085939	BC085939 Rattus no
695	37.4	4.3	2398	5	AK000197	AK000197 Homo sapi	c 768	37.2	4.3	1204	5	BC014356	BC014356 Homo sapi
696	37.4	4.3	2601	14	RABTRB2	Me1124 Rabbit gcrm	c 769	37.2	4.3	1212	13	AF019112	AF019112 Dictyoste
697	37.4	4.3	2601	14	S60737	S60737 T-cell rece	c 770	37.2	4.3	1303	13	BT024358	BT024358 Drosophila
698	37.4	4.3	2633	5	HS0804701	AL833388 Homo sapi	c 771	37.2	4.3	1340	11	BC054234	BC054234 Xenopus l
699	37.4	4.3	2641	6	BC044860	BC044860 Mus muscu	c 772	37.2	4.3	1609	11	BC057515	BC057515 Danio rer
700	37.4	4.3	3084	11	CR942351	CR942351 Xenopus t	c 773	37.2	4.3	1864	11	BC084240	BC084240 Xenopus l
701	37.4	4.3	5054	13	AF298204	AF298204 Dictyoste	c 774	37.2	4.3	1980	5	BC015791	BC015791 Homo sapi
702	37.4	4.3	6013	13	BT012520	BT012520 Drosophila	c 775	37.2	4.3	2085	5	AB168378	AB168378 Macaca fa
703	37.4	4.3	8047	2	AX344916	AX344916 Sequence	c 776	37.2	4.3	2477	14	BC112800	BC112800 Bos tauru
704	37.4	4.3	8111	2	AX347438	AX347438 Sequence	c 777	37.2	4.3	2811	5	BC018650	BC018650 Homo sapi
705	37.4	4.3	8111	2	AX349159	AX349159 Sequence	c 778	37.2	4.3	2986	11	BC084243	BC084243 Xenopus l
706	37.4	4.3	8111	2	AX657810	AX657810 Sequence	c 779	37.2	4.3	3075	13	AF118151	AF118151 Dictyoste
707	37.4	4.3	8111	2	AX659084	AX659084 Sequence	c 780	37.2	4.3	3363	11	CR942633	CR942633 Xenopus t
708	37.4	4.3	14950	2	AX346159	AX346159 Sequence	c 781	37.2	4.3	3890	5	AB097511	AB097511 Macaca fa
709	37.4	4.3	3544	13	U43375	U43375 Caenorhabdi	c 782	37.2	4.3	3993	6	BC060090	BC060090 Mus muscu
710	37.4	4.3	46739	4	AP002052	AP002052 Arabidopsi	c 783	37.2	4.3	6577	2	AX251920	AX251920 Sequence
711	37.4	4.3	80226	2	CQ597458	CQ597458 Sequence	c 784	37.2	4.3	6577	2	AX346258	AX346258 Sequence
712	37.4	4.3	82139	13	AC115684	AC115684 Dictyoste	c 785	37.2	4.3	6577	2	AX348993	AX348993 Sequence
713	37.4	4.3	109321	12	AC117866	AC117866 Strongylo	c 786	37.2	4.3	9323	6	AJ616838	AJ616838 Mus muscu
714	37.4	4.3	110000	12	AC117108	AC117108 Rattus no	c 787	37.2	4.3	38194	11	BX571725	BX571725 Carp DNA
715	37.4	4.3	110000	12	BX322642_0	BX322642_0 Mus muscu	c 788	37.2	4.3	44851	6	AC004404	AC004404 Mus muscu
716	37.4	4.3	110000	12	BX322642_1	BX322642_1 Mus muscu	c 789	37.2	4.3	46443	12	AC102078	AC102078 Mus muscu
717	37.4	4.3	110000	12	BX322642_3	Continuation (2 of	c 790	37.2	4.3	46443	12	AC102078	AC102078 Mus muscu
718	37.4	4.3	110826	5	AC009743	Continuation (4 of	c 791	37.2	4.3	88549	13	AC116924	AC116924 Dictyoste
719	37.4	4.3	115022	5	AC009743	AC009743 Arabidopsi	c 792	37.2	4.3	95359	5	AC078903	AC078903 Homo sapi
720	37.4	4.3	127508	5	AP002264	AP002264 Homo sapi	c 793	37.2	4.3	103275	12	AC136252	AC136252 Rattus no
721	37.4	4.3	130435	5	HS17807	AL021886 Human DNA	c 794	37.2	4.3	110000	6	AE008686_3	Continuation (4 of
722	37.4	4.3	136119	5	HS1028D15	AL021886 Human DNA	c 795	37.2	4.3	110000	12	AC112368_3	Continuation (4 of
723	37.4	4.3	147934	6	AC164113	AC164113 Mus muscu	c 796	37.2	4.3	120448	6	AC174651	AC174651 Mus muscu
724	37.4	4.3	149264	6	AC140283	AC140283 Mus muscu	c 797	37.2	4.3	126804	12	AC179202	AC179202 Strongylo
725	37.4	4.3	149291	6	AC116328	AC116328 Mus muscu	c 798	37.2	4.3	137911	6	AC115015	AC115015 Mus muscu
726	37.4	4.3	151643	6	AC127227	AC127227 Mus muscu	c 799	37.2	4.3	142781	12	AC141934	AC141934 Rattus no
727	37.4	4.3	159426	12	AC178902	AC178902 Strongylo	c 800	37.2	4.3	148361	12	AC179290	AC179290 Strongylo
728	37.4	4.3	159980	12	AC149021	AC149021 Daesypus n	c 801	37.2	4.3	150385	11	BX511147	BX511147 Zebrafish
729	37.4	4.3	162921	12	AC013528	AC013528 Homo sapi	c 802	37.2	4.3	153083	6	CR936849	CR936849 Mouse DNA
730	37.4	4.3	164399	13	PMAL3P6	Z98551 Plasmodium	c 803	37.2	4.3	155132	12	AC080148	AC080148 Homo sapi
731	37.4	4.3	170575	12	AC013758	AC013758 Drosophila	c 804	37.2	4.3	160295	6	AC140358	AC140358 Mus muscu
732	37.4	4.3	170705	12	AC178099	AC178099 Strongylo	c 805	37.2	4.3	168698	5	AC068138	AC068138 Homo sapi
733	37.4	4.3	170788	12	AC139387	AC139387 Rattus no	c 806	37.2	4.3	169599	12	AC180326	AC180326 Strongylo
734	37.4	4.3	172472	5	AC095058	AC095058 Homo sapi	c 807	37.2	4.3	171785	12	AC176265	AC176265 Strongylo
735	37.4	4.3	176086	6	AC124729	AC124729 Mus muscu	c 808	37.2	4.3	172465	12	BX344192	BX344192 Mus muscu
736	37.4	4.3	176455	12	AC178313	AC178313 Strongylo	c 809	37.2	4.3	173134	11	AL935282	AL935282 Zebrafish
737	37.4	4.3	179776	13	AC010026	AC010026 Drosophila	c 810	37.2	4.3	176533	12	AC179122	AC179122 Strongylo
738	37.4	4.3	181076	6	AC110803	AC110803 Mus muscu	c 811	37.2	4.3	176793	12	AC167130	AC167130 Mus muscu
739	37.4	4.3	181179	6	AC102031	AC102031 Mus muscu	c 812	37.2	4.3	177363	5	AC073856	AC073856 Homo sapi
740	37.4	4.3	181308	12	CR030718	CR030718 Danio rer	c 813	37.2	4.3	177745	6	AC144923	AC144923 Mus muscu
741	37.4	4.3	183533	5	BS000021	BS000021 Pan trogl	c 814	37.2	4.3	185146	6	AC102573	AC102573 Mus muscu
742	37.4	4.3	186197	12	AL627384	AL627384 Homo sapi	c 815	37.2	4.3	185517	6	AC140231	AC140231 Mus muscu
743	37.4	4.3	195837	4	ATCHRIV21	AL161509 Arabidops	c 816	37.2	4.3	186218	6	AC129592	AC129592 Mus muscu
744	37.4	4.3	201073	6	AC158903	AC158903 Mus muscu	c 817	37.2	4.3	189063	6	AC123736	AC123736 Mus muscu
745	37.4	4.3	202001	6	AL772303	AL772303 Mouse DNA	c 818	37.2	4.3	195662	12	AC173888	AC173888 Bos tauru
746	37.4	4.3	205310	12	AC134491	AC134491 Rattus no	c 819	37.2	4.3	196377	14	AC105306	AC105306 Bos tauru
747	37.4	4.3	208914	12	BX927237	BX927237 Danio rer	c 820	37.2	4.3	196902	6	AC153381	AC153381 Mus muscu
748	37.4	4.3	209251	5	AC100848	AC100848 Homo sapi	c 821	37.2	4.3	197913	6	AC163657	AC163657 Mus muscu

822	37.2	4.3	200477	12	AC158221	AC158221 Mus muscu	895	37	4.3	140288	12	CR631128	CR631128 Danio rer
823	37.2	4.3	203296	12	AC152839	Bos tauru	c 896	37	4.3	140288	12	CR631128	CR631128 Danio rer
824	37.2	4.3	203628	6	AC160633	Mus muscu	897	37	4.3	140288	12	CR954190	CR954190 Medicago
c 825	37.2	4.3	204465	6	AC117232	Mus muscu	898	37	4.3	143996	12	AC068859	AC068859 Homo sapi
826	37.2	4.3	205870	11	BX088695		899	37	4.3	154402	12	AC139634	AC139634 Gallus ga
827	37.2	4.3	207354	6	AL671857	Mouse DNA	900	37	4.3	154847	5	AL357894	AL357894 Human DNA
828	37.2	4.3	208625	12	AC164605	Mus muscu	901	37	4.3	155023	11	CR354440	CR354440 Zebrafish
c 829	37.2	4.3	214911	12	CT009578	Mus muscu	902	37	4.3	161881	12	CT033841	CT033841 Danio rer
830	37.2	4.3	215095	12	AC126729	Rattus no	903	37	4.3	162826	11	BX248393	BX248393 Zebrafish
c 831	37.2	4.3	215566	6	AC119805	Mus muscu	904	37	4.3	168027	12	AC177170	AC177170 Strongylo
c 832	37.2	4.3	217361	12	AC159695	Bos tauru	905	37	4.3	169330	6	AC162869	AC162869 Mus muscu
c 833	37.2	4.3	226664	12	AC157175	Bos tauru	c 906	37	4.3	175003	6	AC159000	AC159000 Mus muscu
c 834	37.2	4.3	231934	12	AC169709	Bos tauru	907	37	4.3	176702	12	AC011206	AC011206 Homo sapi
835	37.2	4.3	233274	12	AC106465	Rattus no	c 908	37	4.3	182043	6	AC102166	AC102166 Mus muscu
836	37.2	4.3	233692	12	AC119690	Rattus no	c 909	37	4.3	182303	11	BX470267	BX470267 Zebrafish
c 837	37.2	4.3	239426	12	AC111207	Rattus no	910	37	4.3	183648	13	AC117081	AC117081 Dictyoste
c 838	37.2	4.3	240825	2	AX087869	Sequence	911	37	4.3	186842	6	AC154553	AC154553 Mus muscu
c 839	37.2	4.3	240825	2	AX523960	Sequence	912	37	4.3	187725	5	AC146205	AC146205 Pan trogl
840	37.2	4.3	245802	12	AC006279	Plasmodiu	c 913	37	4.3	190210	12	AC022318	AC022318 Homo sapi
c 841	37.2	4.3	250707	13	AE014848	Plasmodiu	c 914	37	4.3	192915	12	AC181115	AC181115 Strongylo
c 842	37.2	4.3	253540	12	AC095829	Rattus no	915	37	4.3	193531	12	AC181266	AC181266 Strongylo
c 843	37.2	4.3	254175	12	AC122615	Rattus no	c 916	37	4.3	193623	12	AC117843	AC117843 Rattus no
c 844	37.2	4.3	260929	13	AE014852	Plasmodiu	c 917	37	4.3	193882	6	AC161231	AC161231 Mus muscu
845	37.2	4.3	262212	12	AC103198	Rattus no	918	37	4.3	197147	12	AC172910	AC172910 Bos tauru
846	37.2	4.3	279278	12	AC158093	Bos tauru	c 919	37	4.3	199549	5	AC100773	AC100773 Homo sapi
c 847	37.2	4.3	281723	13	PFA929359	Plasmodiu	c 920	37	4.3	199782	6	AC134985	AC134985 Mus muscu
c 848	37.2	4.3	301168	12	AC172631	Bos tauru	c 921	37	4.3	199914	5	BS000009	BS000009 Pan trogl
c 849	37.2	4.3	319485	12	AC078979	Homo sapi	922	37	4.3	200205	12	CR388366	CR388366 Danio rer
c 850	37	4.3	127	2	CQ777636	Sequence	923	37	4.3	200631	6	AC134867	AC134867 Mus muscu
851	37	4.3	518	4	QSAJ692	Quercus s	924	37	4.3	201739	6	AC123698	AC123698 Mus muscu
c 852	37	4.3	602	7	BV252778	BV479961 qhg30g10.	925	37	4.3	202336	6	AC087727	AC087727 Mus muscu
c 853	37	4.3	810	7	BV479961		c 926	37	4.3	204569	6	AC169384	AC169384 Mus muscu
c 854	37	4.3	1040	13	AY069658	Drosophila	927	37	4.3	211183	6	AL731771	AL731771 Mouse DNA
c 855	37	4.3	1085	11	CT025478	Xenopus t	928	37	4.3	241400	6	AL646093	AL646093 Mouse DNA
856	37	4.3	1172	11	BC088527	Xenopus t	c 929	37	4.3	243036	12	AC112103	AC112103 Rattus no
857	37	4.3	1291	5	BC093090	BC093090 Homo sapi	c 930	37	4.3	245012	13	AC131444	AC131444 Rattus no
858	37	4.3	1315	11	BC084499	BC084499 Xenopus t	c 931	37	4.3	250022	13	AE014824	AE014824 Plasmodiu
859	37	4.3	1356	6	BC034886	BC034886 Mus muscu	932	37	4.3	250823	13	AE014821	AE014821 Plasmodiu
c 860	37	4.3	1555	11	BC064241	BC064241 Xenopus t	933	37	4.3	257581	12	AC157013	AC157013 Bos tauru
c 861	37	4.3	2171	2	CS113396	CS113396 Sequence	c 934	37	4.3	271629	12	AC143316	AC143316 Macaca mu
c 862	37	4.3	2171	2	CS113514	CS113514 Sequence	935	36.8	4.2	282	2	CQ515927	CQ515927 Sequence
c 863	37	4.3	2249	5	BC092410	BC092410 Homo sapi	936	36.8	4.2	360	2	CQ527206	CQ527206 Sequence
864	37	4.3	2274	6	BC096371	BC096371 Mus muscu	c 937	36.8	4.2	370	2	CQ476082	CQ476082 Sequence
865	37	4.3	2307	13	AY095053	AY095053 Drosophila	938	36.8	4.2	400	5	AF041005	AF041005 Homo sapi
866	37	4.3	2587	11	BC926175	BC926175 Xenopus t	939	36.8	4.2	441	2	AR506593	AR506593 Sequence
c 867	37	4.3	2820	13	BT010288	BT010288 Drosophila	c 940	36.8	4.2	445	2	CQ410337	CQ410337 Sequence
868	37	4.3	2723	5	BC042178	BC042178 Homo sapi	941	36.8	4.2	533	6	BC090389	BC090389 Mus muscu
869	37	4.3	2783	11	BC081012	BC081012 Xenopus l	c 942	36.8	4.2	565	14	BC105433	BC105433 Bos tauru
870	37	4.3	3238	6	BC069041	BC069041 Mus muscu	943	36.8	4.2	672	7	BV426135	BV426135 S237P6520
871	37	4.3	3348	11	BC066759	BC066759 Danio rer	944	36.8	4.2	1046	5	AB168908	AB168908 Macaca fa
c 872	37	4.3	3973	2	AX345073	AX345073 Sequence	945	36.8	4.2	1166	11	BC097178	BC097178 Danio rer
c 873	37	4.3	5397	2	AX347107	AX347107 Sequence	946	36.8	4.2	1182	6	BC049567	BC049567 Mus muscu
c 874	37	4.3	6136	2	AX348428	AX348428 Sequence	947	36.8	4.2	1257	13	BT001395	BT001395 Drosophila
c 875	37	4.3	6232	11	BC084088	BC084088 Xenopus l	948	36.8	4.2	1290	2	CQ981351	CQ981351 Sequence
876	37	4.3	7686	5	HSN808085	HSN808085 Homo sapi	949	36.8	4.2	1290	5	BC007024	BC007024 Homo sapi
c 877	37	4.3	8234	2	AX346551	AX346551 Sequence	950	36.8	4.2	1316	5	HSN801735	HSN801735 Homo sapi
c 878	37	4.3	10039	5	AX346944	AX346944 Sequence	951	36.8	4.2	1508	2	AR264367	AR264367 Sequence
c 879	37	4.3	34516	5	BS001885	BS001885 Human DNA	952	36.8	4.2	1607	5	BC068273	BC068273 Homo sapi
c 880	37	4.3	3969	12	AC180530	AC180530 Strongylo	953	36.8	4.2	1633	11	BC084760	BC084760 Xenopus l
881	37	4.3	79976	4	AB008264	AB008264 Arabidops	954	36.8	4.2	1697	2	AR310263	AR310263 Sequence
c 882	37	4.3	84821	6	BT076123	BT076123 Mouse DNA	955	36.8	4.2	1697	2	AR640306	AR640306 Sequence
c 883	37	4.3	89995	5	AC133794	AC133794 Homo sapi	956	36.8	4.2	1725	2	AR451632	AR451632 Sequence
c 884	37	4.3	91319	5	AC172456	AC172456 Bos tauru	957	36.8	4.2	1841	4	AF387639	AF387639 Arabidops
c 885	37	4.3	92815	5	AC067990	AC067990 Homo sapi	958	36.8	4.2	1877	5	BC062584	BC062584 Homo sapi
c 886	37	4.3	94153	12	AC139443	AC139443 Rattus no	959	36.8	4.2	1898	2	I46765	I46765 Sequence l
c 887	37	4.3	97428	11	BX323028	BX323028 Zebrafish	960	36.8	4.2	1933	5	HSN806724	HSN806724 Homo sapi
888	37	4.3	105682	6	AL929160	Continuation (4 of	961	36.8	4.2	2141	5	BC053352	BC053352 Homo sapi
c 889	37	4.3	107366	6	AL929160	Continuation (4 of	962	36.8	4.2	2196	5	HSN801403	HSN801403 Homo sapi
c 890	37	4.3	110000	12	AC115497	AC115497 Rattus no	963	36.8	4.2	2219	13	AY061258	AY061258 Drosophila
c 891	37	4.3	110000	15	BS008798	Continuation (19 o	964	36.8	4.2	2245	6	BC005686	BC005686 Mus muscu
c 892	37	4.3	113880	13	PFNAL3P4	AL008970 Plasmodiu	965	36.8	4.2	2262	5	BC041668	BC041668 Homo sapi
c 893	37	4.3	117343	12	AC177694	AC177694 Strongylo	966	36.8	4.2	2294	11	BC045728	BC045728 Xenopus l
c 894	37	4.3	129256	12	BX927183	BX927183 Danio rer	967	36.8	4.2	2291	5	BC045767	BC045767 Homo sapi

968	36.8	4.2	3000	11	BC068787	Xenopus t
969	36.8	4.2	3066	11	BC074642	Xenopus t
970	36.8	4.2	4346	13	BT016106	Drosophila
c 971	36.8	4.2	5511	6	AX346773	Sequence
c 972	36.8	4.2	5742	6	BC060122	Mus muscu
c 973	36.8	4.2	7742	2	AX348912	Sequence
c 974	36.8	4.2	13135	5	AL589908	Human DNA
c 975	36.8	4.2	13670	13	AY380531	Biophala
c 976	36.8	4.2	13670	13	AY380567	Biophala
c 977	36.8	4.2	14112	2	AX251232	Sequence
c 978	36.8	4.2	14112	2	AX344329	Sequence
c 979	36.8	4.2	14112	2	AX346345	Sequence
c 980	36.8	4.2	14112	2	AX458464	Sequence
c 981	36.8	4.2	29571	13	AF077541	Caenorhab
c 982	36.8	4.2	36454	13	AC006670	Caenorhab
c 983	36.8	4.2	57705	12	AC104245	Homo sapi
c 984	36.8	4.2	57817	12	AC173970	Strongylo
c 985	36.8	4.2	64491	5	AL365188	Human DNA
c 986	36.8	4.2	68190	12	AC090604	Homo sapi
c 987	36.8	4.2	73572	12	AC170406	Rattus no
c 988	36.8	4.2	78579	12	AC177634	Strongylo
c 989	36.8	4.2	85916	13	AC117080	Dictyoste
c 990	36.8	4.2	87485	11	AL627170	Zebrafish
c 991	36.8	4.2	90578	5	AC128686	Homo sapi
c 992	36.8	4.2	93831	11	AL627163	Zebrafish
c 993	36.8	4.2	99216	12	AC179582	Strongylo
c 994	36.8	4.2	100923	11	AC002124	Homo sapi
c 995	36.8	4.2	105480	11	BX537356	Zebrafish
c 996	36.8	4.2	108780	5	AC021945	Homo sapi
c 997	36.8	4.2	108994	5	HS124K22	Human DNA
c 998	36.8	4.2	109573	12	AC007555	Homo sapi
c 999	36.8	4.2	110000	12	AC105546	Continuation (3 of
1000	36.8	4.2	110000	13	AC116984	Continuation (5 of
1001	36.8	4.2	110010	15	AB017243	Continuation (6 of
c1002	36.8	4.2	111035	5	AC022405	Homo sapi
c1003	36.8	4.2	114664	4	AC130809	Medicago
c1004	36.8	4.2	119944	5	AC111162	Homo sapi
c1005	36.8	4.2	125855	4	AC151823	Medicago
c1006	36.8	4.2	127831	12	AC177469	Strongylo
c1007	36.8	4.2	133263	12	AC126235	Canis fam
c1008	36.8	4.2	134640	13	AC181778	Strongylo
c1009	36.8	4.2	136240	12	AC117070	Dictyoste
c1010	36.8	4.2	136285	12	AC160608	Lorodonta
c1011	36.8	4.2	139640	11	BX511108	Zebrafish
c1012	36.8	4.2	139852	5	AC146567	Human DNA
c1013	36.8	4.2	141672	4	AC146567	Medicago
c1014	36.8	4.2	143137	12	AC180304	Strongylo
c1015	36.8	4.2	143585	12	AC013349	Homo sapi
c1016	36.8	4.2	145271	12	AC169089	Medicago
c1017	36.8	4.2	147160	12	AC181723	Strongylo
c1018	36.8	4.2	148782	12	CT573397	Danio rer
c1019	36.8	4.2	148890	12	AC022614	Homo sapi
c1020	36.8	4.2	150963	12	AC006727	Caenorhab
c1021	36.8	4.2	151763	12	AC001715	Homo sapi
c1022	36.8	4.2	153439	5	AL138914	Human DNA
c1023	36.8	4.2	154071	13	AC115598	Dictyoste
c1024	36.8	4.2	154883	5	AC154914	Pan trogl
c1025	36.8	4.2	155270	5	AL391384	Human DNA
c1026	36.8	4.2	156328	12	AL148280	Sorex ara
c1027	36.8	4.2	156466	12	AL139181	Homo sapi
c1028	36.8	4.2	157054	12	AC021782	Homo sapi
c1029	36.8	4.2	157402	12	AC034161	Homo sapi
c1030	36.8	4.2	159723	12	AC021862	Homo sapi
c1031	36.8	4.2	160748	5	AC001234	Homo sapi
c1032	36.8	4.2	165254	6	AC117189	Mus muscu
c1033	36.8	4.2	165287	5	AC090599	Homo sapi
c1034	36.8	4.2	167196	12	CT025585	Danio rer
c1035	36.8	4.2	168492	5	AC092989	Homo sapi
c1036	36.8	4.2	169054	12	AC068444	Homo sapi
c1037	36.8	4.2	169135	11	BX649325	Zebrafish
c1038	36.8	4.2	169150	12	AC026141	Homo sapi
c1039	36.8	4.2	169418	5	AC104163	Homo sapi
1040	36.8	4.2	169546	12	AC004157	Plasmodiu

36.8	4.2	170233	5	AC147091	AC147091 Pan trogl
36.8	4.2	170998	5	AL390071	AL390071 Human DNA
36.8	4.2	171430	12	AC110599	AC110599 Homo sapi
36.8	4.2	173547	12	AC073637	AC073637 Homo sapi
36.8	4.2	173614	6	AC125122	AC125122 Mus muscu
36.8	4.2	175166	12	AC128626	AC128626 Rattus no
36.8	4.2	175315	5	AC021049	AC021049 Homo sapi
36.8	4.2	176045	6	AC122370	AC122370 Mus muscu
36.8	4.2	178129	12	AC179763	AC179763 Strongylo
36.8	4.2	178273	12	AC005308	AC005308 Plasmodiu
36.8	4.2	180465	6	AC163390	AC163390 Mus muscu
36.8	4.2	180854	5	AC107960	AC107960 Homo sapi
36.8	4.2	181313	6	AC124332	AC124332 Mus muscu
36.8	4.2	181519	6	AC112968	AC112968 Mus muscu
36.8	4.2	181796	12	AC178482	AC178482 Strongylo
36.8	4.2	182871	13	AC117176	AC117176 Dictyoste
36.8	4.2	185938	6	AC122802	AC122802 Mus muscu
36.8	4.2	186717	12	AC147894	AC147894 Xenopus t
36.8	4.2	188449	12	CR381660	CR381660 Danio rer
36.8	4.2	189038	12	AC120323	AC120323 Rattus no
36.8	4.2	197092	12	AC036155	AC036155 Homo sapi
36.8	4.2	201389	12	CT485674	CT485674 Danio rer
36.8	4.2	202967	12	AC175374	AC175374 Colobus g
36.8	4.2	204840	12	CR753862	CR753862 Danio rer
36.8	4.2	205273	6	AL845364	AL845364 Mouse DNA
36.8	4.2	205429	12	AC005506	AC005506 Plasmodiu
36.8	4.2	205508	6	AC079243	AC079243 Mus muscu
36.8	4.2	206489	12	CR956401	CR956401 Danio rer
36.8	4.2	207400	6	AC155261	AC155261 Mus muscu
36.8	4.2	212973	6	AL683847	AL683847 Mouse DNA
36.8	4.2	214419	6	AC101932	AC101932 Mus muscu
36.8	4.2	216008	12	AC178129	AC178129 Strongylo
36.8	4.2	221584	12	AC177229	AC177229 Strongylo
36.8	4.2	221990	12	AC161923	AC161923 Mus muscu
36.8	4.2	222981	6	AL669981	AL669981 Mouse DNA
36.8	4.2	224108	12	AC182012	AC182012 Otolemur
36.8	4.2	225545	12	AC110659	AC110659 Rattus no
36.8	4.2	225873	12	AC111240	AC111240 Rattus no
36.8	4.2	227450	12	AC103214	AC103214 Rattus no
36.8	4.2	232225	6	AL662876	AL662876 Mouse DNA
36.8	4.2	233783	6	AC118698	AC118698 Mus muscu
36.8	4.2	236076	12	AC181741	AC181741 Strongylo
36.8	4.2	236652	12	AC129111	AC129111 Rattus no
36.8	4.2	236690	6	AC109202	AC109202 Mus muscu
36.8	4.2	239522	12	AC095395	AC095395 Rattus no
36.8	4.2	245030	12	AC106061	AC106061 Rattus no
36.8	4.2	245472	12	AC137473	AC137473 Rattus no
36.8	4.2	247979	12	AC092261	AC092261 Mus muscu
36.8	4.2	250421	13	AE014849	AE014849 Plasmodiu
36.8	4.2	250531	13	AE014845	AE014845 Plasmodiu
36.8	4.2	250713	13	AE014850	AE014850 Plasmodiu
36.8	4.2	251814	6	AL591882	AL591882 Mouse DNA
36.8	4.2	252394	13	AE014833	AE014833 Plasmodiu
36.6	4.2	265	2	CQ516973	CQ516973 Sequence
36.6	4.2	545	2	AX185705	AX185705 Sequence
36.6	4.2	743	6	BC034898	BC034898 Mus muscu
36.6	4.2	765	6	BC091177	BC091177 Rattus no
36.6	4.2	892	11	CR848247	CR848247 Xenopus t
36.6	4.2	1019	6	BC027418	BC027418 Mus muscu
36.6	4.2	1038	6	BC013496	BC013496 Mus muscu
36.6	4.2	1102	2	AR110206	AR110206 Sequence
36.6	4.2	1102	2	AR169965	AR169965 Sequence
36.6	4.2	1102	2	AR171774	AR171774 Sequence
36.6	4.2	1102	2	BD009002	BD009002 Promoter
36.6	4.2	1102	2	BD189471	BD189471 PROMOTER
36.6	4.2	1102	2	AR264114	AR264114 Sequence
36.6	4.2	1165	11	BC095695	BC095695 Danio rer
36.6	4.2	1342	2	CQ981633	CQ981633 Sequence
36.6	4.2	1342	5	BC016808	BC016808 Homo sapi
36.6	4.2	1464	13	AK134486	AK134486 Ciona int
36.6	4.2	1501	6	BC103477	BC103477 Rattus no
36.6	4.2	1543	6	BC052355	BC052355 Mus muscu
36.6	4.2	1710	14	BC102907	BC102907 Bos tauru

[illegible]

c1260	36.4	4.2	2865	2	AX251074	Sequence	1333	36.4	4.2	171510	6	AC154102
c1261	36.4	4.2	2865	2	AX344643	Sequence	1334	36.4	4.2	171551	4	OSJN00177
1262	36.4	4.2	3000	5	BC036812	Homo sapi	1335	36.4	4.2	175037	12	AC180563
c1263	36.4	4.2	3416	11	BC076684	Xenopus t	c1336	36.4	4.2	175372	5	AC009659
c1264	36.4	4.2	3531	13	AF447572	Plasmidieu	c1337	36.4	4.2	176223	5	AC034192
c1265	36.4	4.2	3700	13	DGGR80G	X66483 D.discoidieu	c1338	36.4	4.2	178860	11	BX001036
1266	36.4	4.2	4424	6	BC050125	Mus muscu	1339	36.4	4.2	179058	6	AC122420
1267	36.4	4.2	4815	5	HSM803690	AL832382 Homo sapi	c1340	36.4	4.2	180629	6	AL670939
1268	36.4	4.2	4930	5	HSM805943	BS37846 Homo sapi	c1341	36.4	4.2	182870	13	AC116960
c1269	36.4	4.2	6636	2	AX344614	Sequence	c1342	36.4	4.2	184483	12	AC182175
c1270	36.4	4.2	8305	2	AX346470	Sequence	c1343	36.4	4.2	186218	5	AC093865
1271	36.4	4.2	12940	13	AE001386	Plasmodiou	c1344	36.4	4.2	187088	6	AC133876
1272	36.4	4.2	16148	13	AC116100	Dictyoste	c1345	36.4	4.2	187548	11	AL929031
c1273	36.4	4.2	41070	12	AC171812	AC171812 Spermophi	c1346	36.4	4.2	189148	12	AC068262
c1274	36.4	4.2	64707	13	AC115607	AC115607 Dictyoste	c1347	36.4	4.2	190180	6	AC117766
1275	36.4	4.2	68256	4	AP005842	AP005842 Oryza sat	c1348	36.4	4.2	190426	14	AC149571
1276	36.4	4.2	80339	11	BX663495	BX663495 Zebrafish	c1349	36.4	4.2	191921	12	AC175656
c1277	36.4	4.2	84506	5	AL591867	AL591867 Human DNA	c1350	36.4	4.2	192187	13	AC117072
c1278	36.4	4.2	85781	5	AL663074	AL663074 Human DNA	c1351	36.4	4.2	193117	5	AC163767
c1279	36.4	4.2	99228	5	AL133376	AL133376 Human DNA	c1352	36.4	4.2	195151	6	AC154357
c1280	36.4	4.2	101080	12	BX004860	Danio rer	c1353	36.4	4.2	196024	6	AC114602
c1281	36.4	4.2	101241	11	AL845510	AL845510 Zebrafish	c1354	36.4	4.2	198089	12	AC176755
c1282	36.4	4.2	103888	12	AC149916	AC149916 Strongylo	c1355	36.4	4.2	201418	12	AC144493
1283	36.4	4.2	110000	4	AP008208	Continuation (190	c1356	36.4	4.2	203351	12	AC171851
1284	36.4	4.2	110000	4	AP008210	Continuation (265	c1357	36.4	4.2	210405	12	AC172537
1285	36.4	4.2	110000	12	AC098456	AC098456 Rattus no	c1358	36.4	4.2	211803	12	AC117813
1286	36.4	4.2	110000	12	PFMAU13_22	Continuation (23 o	c1359	36.4	4.2	213482	6	AC164971
c1287	36.4	4.2	110000	13	AC116984	AC116984 Dictyoste	c1360	36.4	4.2	214285	12	AC125812
1288	36.4	4.2	110000	13	AC116984	Continuation (2 of	c1361	36.4	4.2	220203	6	AC116584
1289	36.4	4.2	111167	12	AC171545	AC171545 Bos tauru	c1362	36.4	4.2	220671	11	BX276106
c1290	36.4	4.2	113547	12	AC152350	AC152350 Medicago	c1363	36.4	4.2	221053	12	AC166447
1291	36.4	4.2	114870	12	AC010755	AC010755 Homo sapi	c1364	36.4	4.2	223402	12	AC175067
c1292	36.4	4.2	117886	12	AC178818	AC178818 Strongylo	c1365	36.4	4.2	223545	12	AC100545
1293	36.4	4.2	123282	12	OSJN01004	AL607096 Oryza sat	c1366	36.4	4.2	224141	6	AC110576
1294	36.4	4.2	124231	12	AC016466	AC016466 Homo sapi	c1367	36.4	4.2	228633	11	BX649600
c1295	36.4	4.2	126004	11	BX914219	BX914219 Zebrafish	c1368	36.4	4.2	228869	6	BX470109
1296	36.4	4.2	132131	5	AB045357	AB045357 Homo sapi	c1369	36.4	4.2	229686	12	BX927087
c1297	36.4	4.2	134328	12	AC181359	AC181359 Strongylo	c1370	36.4	4.2	230215	12	AC152328
c1298	36.4	4.2	135124	12	AC177676	AC177676 Strongylo	c1371	36.4	4.2	230283	12	AC160055
c1299	36.4	4.2	135955	5	HSI35814	AJ010598 Homo sapi	c1372	36.4	4.2	230853	12	AC161842
1300	36.4	4.2	140454	4	OSJN00183	AL662984 Oryza sat	c1373	36.4	4.2	231435	12	AC130519
1301	36.4	4.2	140484	11	CR854834	CR854834 Zebrafish	c1374	36.4	4.2	231797	6	AC121848
c1302	36.4	4.2	140523	12	AC173432	AC173432 Muntiacu	c1375	36.4	4.2	232491	11	BX908747
c1303	36.4	4.2	141646	12	AC179856	AC179856 Strongylo	c1376	36.4	4.2	232594	11	BX005006
1304	36.4	4.2	142704	6	AC157558	AC157558 Mus muscu	c1377	36.4	4.2	234483	12	AC098407
1305	36.4	4.2	143573	12	CF7573424	CF7573424 Danio rer	c1378	36.4	4.2	235237	6	AC160995
c1306	36.4	4.2	149596	12	CR391909	CR391909 Danio rer	c1379	36.4	4.2	241428	12	BX649537
1307	36.4	4.2	150313	12	AC179580	AC179580 Strongylo	c1380	36.4	4.2	243770	12	AC123492
c1308	36.4	4.2	150434	5	AL138784	AL138784 Human DNA	c1381	36.4	4.2	245403	12	AC133063
c1309	36.4	4.2	151349	12	ALJ353647	ALJ353647 Homo sapi	c1382	36.4	4.2	246577	12	AC136124
1310	36.4	4.2	151923	6	AL845499	AL845499 Mouse DNA	c1383	36.4	4.2	247073	12	AC160164
1311	36.4	4.2	152742	12	AC022381	AC022381 Homo sapi	c1384	36.4	4.2	249982	12	AC108661
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RESULT 2
LOCUS      CS257510
DEFINITION Sequence 25 from Patent EP1623991.
ACCESSION  CS257510
VERSION     CS257510.1 GI:87159018
KEYWORDS   Homo sapiens (human)
SOURCE     Homo sapiens
ORGANISM   Homo sapiens
REFERENCE  1.
AUTHORS    Eaton, D.L.
TITLE      Secreted and transmembrane polypeptides and nucleic acids encoding
JOURNAL    Patent: EP 1623991-A 25 08-FEB-2006;
GENENTECH, INC. (US)
FEATURES   Location/Qualifiers
source     1..870
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ORIGIN
Query Match 100.0%; Score 870; DB 2; Length 870;
Best Local Similarity 100.0%; Pred. No. 9.9e-268;
Matches 870; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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RESULT 3
LOCUS      CS257680
DEFINITION Sequence 25 from Patent EP1623993.
ACCESSION  CS257680
VERSION     CS257680.1 GI:87159104
KEYWORDS   Homo sapiens (human)
SOURCE     Homo sapiens
ORGANISM   Homo sapiens
REFERENCE  1.
AUTHORS    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE      Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
JOURNAL    Hominidae; Homo.
GENENTECH, INC. (US)
FEATURES   Location/Qualifiers
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/mol_type="Homo sapiens"
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ORIGIN
Query Match 100.0%; Score 870; DB 2; Length 870;
Best Local Similarity 100.0%; Pred. No. 9.9e-268;
Matches 870; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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REFERENCE 1
AUTHORS Baton,D.L.
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding the same
JOURNAL Patent: EP 1623993-A 25 08-FEB-2006;
Genetech, Inc. (US)
FEATURES Location/Qualifiers
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Query Match 100.0%; Score 870; DB 2; Length 870;
Best Local Similarity 100.0%; Pred. No. 9.9e-268;
Matches 870; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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LOCUS CS257850
DEFINITION Sequence 25 from Patent EP1623992.
ACCESSION CS257850
VERSION CS257850.1 GI:87159190
KEYWORDS Homo sapiens (human)
SOURCE
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS Baton,D.L.
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding the same
JOURNAL Patent: EP 1623992-A 25 08-FEB-2006;
GENENTECH, INC. (US)
FEATURES Location/Qualifiers
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Query Match 100.0%; Score 870; DB 2; Length 870;
Best Local Similarity 100.0%; Pred. No. 9.9e-268;
Matches 870; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DEFINITION Sequence 164 from patent US 6478825.
ACCESSION AR252494
VERSION AR252494.1 GI:27300402
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 870)
AUTHORS Winterbottom,J.M., Shimp,L., Boyce,T.M. and Kaes,D.
TITLE Implant, method of making same and use of the implant for the
JOURNAL treatment of bone defects
Patent: US 6478825-A 164 12-NOV-2002;
Osteotech, Inc.; Eatontown, NJ
FEATURES
source Location/Qualifiers
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ORIGIN
Query Match 100.0%; Score 870; DB 2; Length 870;
Best Local Similarity 100.0%; Pred. No. 9.9e-268;
Matches 870; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 6
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LOCUS AR693384 870 bp DNA linear PAT 14-SEP-2005
DEFINITION Sequence 164 from patent US 6913919.
ACCESSION AR693384
VERSION AR693384.1 GI:75183789
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 870)
AUTHORS Botstein,D., Goddard,A., Godowski,P.J., Gurney,A.L., Roy,M.A. and Wood,W.I.
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding
JOURNAL the same
Patent: US 6913919-A 164 05-JUL-2005;
Genetech, Inc.; South San Francisco, CA
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source Location/Qualifiers
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LOCUS AR776123 870 bp DNA linear PAT 08-DEC-2005
DEFINITION Sequence 164 from patent US 6972185.
ACCESSION AR776123
VERSION AR776123.1 GI:83353462
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 870)
AUTHORS Desnoyers, L., Goddard, A., Godowski, P.J., Gurney, A.L. and Wood, W.I.
TITLE Nucleic acids encoding PRO844 polypeptides
JOURNAL Patent: US 6972185-A 164 06-DEC-2005;
Genentech, Inc.; South San Francisco, CA

FEATURES
source Location/Qualifiers
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Matches 870; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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LOCUS AX092294 870 bp DNA linear PAT 21-MAR-2001
DEFINITION Sequence 25 from Patent WO0116318.
ACCESSION AX092294
VERSION AX092294.1 GI:13444461
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Eaton, D.L., Filvaroff, E., Gerritsen, M.E., Goddard, A., and Godowski, P.J., Grimaldi, C.J., Gurney, A.L., Watanabe, C.K. and Wood, W.I.
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding the same
JOURNAL Patent: WO 0116318-A 25 08-MAR-2001;
Genentech, Inc. (US)
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Db 841 TTTTAAATGTCAAAAAAAAAAAAAA 870

RESULT 12
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LOCUS AX376072 870 bp DNA linear PAT 01-MAR-2002
DEFINITION Sequence 139 from Patent WO0168848.
ACCESSION AX376072
VERSION AX376072.1 GI:19170428
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS Baker,K.P., Chen,J., Desnoyers,L., Goddard,A., Godowski,P.J.,
Gurney,A.L., Pan,J., Smith,V., Watanabe,C.K., Wood,W.I. and
Zhang,Z.
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding
the same
JOURNAL Patent: WO 0168848-A 139 20-SEP-2001;
Genentech, Inc. (US)
FEATURES
Location/Qualifiers
source 1..870

ORIGIN
Query Match 100.0%; Score 870; DB 2; Length 870;
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AX403277 870 bp DNA linear PAT 14-JUN-2002
LOCUS AX403277
RESULT 13
AX403277
LOCUS

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ACCESSION	AX403277.1	GI:21436848	
VERSION			
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SOURCE	Homo sapiens		
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REFERENCE	Ashkenazi,A.J., Baker,K.P., Botstein,D., Desnovers,L., Eaton,D., Ferrara,N., Gerber,H., Gerritsen,M., Goddard,A., Godowski,P., Grimaldi,C.D., Gurney,A.B., Kijavins,I., Napier,R.A., Pan,J., Paoni,N.F., Roy,M., Stewart,T.A., Tamas,D., Watanabe,C.K., Williams,P., Wood,W.I. and Zhang,Z. Secreted and transmembrane polypeptides and nucleic acids encoding the same Patent: WO 0073454-A 164 07-DEC-2000;		
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SUMMARIES
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ID AAZ65001 standard; cDNA; 870 BP.
DE Membrane-bound protein PRO842 encoding cDNA.
PN WO9963088-A2.
PD 09-DEC-1999.
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Best Local Similarity 100.0%; Pred. No. 4.3e-229;
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DE Human DNA encoding PRO polypeptide sequence #70.
PN WO200168848-A2.
PD 20-SEP-2001.
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Best Local Similarity 100.0%; Pred. No. 4.3e-229;
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DE Human PRO842 cDNA.
PN WO200116318-A2.
PD 08-MAR-2001.
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DE Human PRO842 (UNQ473) nucleotide sequence SEQ ID NO:164.
PN WO200073454-A1.
PD 07-DEC-2000.
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Best Local Similarity 100.0%; Pred. No. 4.3e-229;
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ID ABS74390 standard; cDNA; 870 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO842.
PN US2002119130-A1.
PD 29-AUG-2002.
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ID ABV73914 standard; cDNA; 870 BP.
DE Human cytokine PRO842 (CK27) cDNA.
PN WO200270706-A2.
PD 12-SEP-2002.
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Best Local Similarity 100.0%; Pred. No. 4.3e-229;
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ID ACAB9444 standard; cDNA; 870 BP.
DE cDNA encoding human PRO polypeptide #70.
PN US2003036141-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
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PN US2003036146-A1.
PD 20-FEB-2003.
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Best Local Similarity 100.0%; Pred. No. 4.3e-229;
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PN US2003036162-A1.
PD 20-FEB-2003.
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Best Local Similarity 100.0%; Pred. No. 4.3e-229;
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PN US2003036137-A1.
PD 20-FEB-2003.
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Best Local Similarity 100.0%; Pred. No. 4.3e-229;
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DE Novel human secreted and transmembrane protein PRO842 cDNA.
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Best Local Similarity 100.0%; Pred. No. 4.3e-229;
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DE Novel human secreted and transmembrane protein PRO842 cDNA.
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PD 23-JAN-2003.
PA (GETH ) GENENTECH INC.
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DE Human cDNA encoding secreted/transmembrane protein PRO842.
PN US2003009013-A1.
PD 09-JAN-2003.
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PN US2003040083-A1.
PD 27-FEB-2003.
PA (GETH ) GENENTECH INC.
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PN US2003027267-A1.
PD 06-FEB-2003.
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Best Local Similarity 100.0%; Pred. No. 4.3e-229;
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DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003036160-A1.
PD 20-FEB-2003.
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PN US2003044925-A1.
PD 06-MAR-2003.
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Best Local Similarity 100.0%; Pred. No. 4.3e-229;
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DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003054474-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
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Best Local Similarity 100.0%; Pred. No. 4.3e-229;
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DE Novel human secreted and transmembrane protein PRO842 cDNA.
PN US2003018183-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 8; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 21
ID ACA72226 standard; cDNA; 870 BP.
DE Novel human secreted and transmembrane protein PRO842 cDNA.
PN US2003032114-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 870; DB 8; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 22
ID ACD04750 standard; cDNA; 870 BP.
DE Novel human secreted and transmembrane protein PRO842 cDNA.
PN US2003032101-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 870; DB 8; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 23
ID ACD18211 standard; cDNA; 870 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #70.
PN US2003036124-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 870; DB 8; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 24
ID ACD08218 standard; cDNA; 870 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #70.
PN US2003040054-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 870; DB 8; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 25

ID ACA88652 standard; cDNA; 870 BP.
DE Novel human secreted and transmembrane protein PRO842 cDNA.
PN US2003036133-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 870; DB 8; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 26
ID ACA70094 standard; cDNA; 870 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #70.
PN US2003036134-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 870; DB 8; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 27
ID ACD12316 standard; cDNA; 870 BP.
DE Novel human secreted and transmembrane protein PRO842 cDNA.
PN US2003022294-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 870; DB 8; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 28
ID ACC74231 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003027275-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 870; DB 8; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 29
ID ACD15859 standard; cDNA; 870 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #70.
PN US2003027324-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 870; DB 8; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 30
ID ACD25427 standard; cDNA; 870 BP.
DE Novel human secreted and transmembrane protein PRO842 cDNA.
PN US2003036118-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 8; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 31
ID ACD17904 standard; cDNA; 870 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #70.
PN US2003036123-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 870; DB 8; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 32
ID ACC88191 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003036148-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 870; DB 8; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 33
ID ACD21545 standard; cDNA; 870 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #70.
PN US2003040060-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 870; DB 8; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 34
ID ACD18612 standard; cDNA; 870 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #70.
PN US2003044916-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 870; DB 8; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 35
ID ACA58822 standard; cDNA; 870 BP.
DE cDNA encoding human secreted polypeptide PRO842.

PN US2003013855-A1.
PD 16-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 8; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 36
ID ABX98222 standard; cDNA; 870 BP.
DE Human cDNA encoding a secreted/transmembrane protein, SEQ ID 139.
PN US2003036156-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 870; DB 8; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 37
ID ACD13973 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003032117-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 870; DB 8; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 38
ID ACD09753 standard; cDNA; 870 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #70.
PN US2003036128-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 870; DB 8; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 39
ID ACC88498 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003027266-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 870; DB 8; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 40
ID ACD21238 standard; cDNA; 870 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #70.
PN US2003054483-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 8; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 41
ID ABX75610 standard; cDNA; 870 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO842.
PN US2003022298-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 870; DB 8; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 42
ID ACA63998 standard; cDNA; 870 BP.
DE cDNA encoding human PRO polypeptide #13.
PN US2002182638-A1.
PD 05-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 8; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 43
ID ABX97813 standard; cDNA; 870 BP.
DE Human PRO polynucleotide #70.
PN US2003032102-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 870; DB 8; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 44
ID ACA97289 standard; cDNA; 870 BP.
DE Novel human secreted and transmembrane protein PRO842 cDNA.
PN US2003036117-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 870; DB 8; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 45
ID ACA57752 standard; cDNA; 870 BP.
DE Human PRO842 cDNA.

PN US2003036143-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 870; DB 8; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 46
ID ACD14280 standard; cDNA; 870 BP.
DE Human PRO polynucleotide #70.
PN US2003032130-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 870; DB 8; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 47
ID ACC91063 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003032138-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 8; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 48
ID ACC88805 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003036132-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 870; DB 8; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 49
ID ACD07002 standard; cDNA; 870 BP.
DE Human PRO polynucleotide #70.
PN US2003008353-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 8; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 50
ID ACA67453 standard; cDNA; 870 BP.
DE Human PRO polynucleotide #70.
PN US2003017542-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 870; DB 8; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 51
ID ACC81508 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003032137-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 870; DB 8; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 52
ID ACA91262 standard; cDNA; 870 BP.
DE cDNA encoding human PRO polypeptide #13.
PN US2003018168-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 8; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 53
ID ACC89112 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003027269-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 870; DB 8; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 54
ID ACC86468 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003027268-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 870; DB 8; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 55
ID ACC89726 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.

PN US2003027274-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 870; DB 8; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 56
ID ACC92905 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003032135-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 8; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 57
ID ABX80736 standard; cDNA; 870 BP.
DE Human secreted/transmembrane protein cDNA, #61.
PN US2003027162-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 870; DB 8; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 58
ID ACAY2533 standard; cDNA; 870 BP.
DE Human PRO polynucleotide #70.
PN US2003022295-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 870; DB 8; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 59
ID ACAR89051 standard; cDNA; 870 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #70.
PN US2003022297-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 870; DB 8; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 60
ID ACAG9787 standard; cDNA; 870 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #70.
PN US2003032105-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 870; DB 8; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 61
ID ACA96930 standard; cDNA; 870 BP.
DE Novel human secreted and transmembrane protein PRO842 cDNA.
PN US2003032123-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 870; DB 8; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 62
ID ACA90926 standard; cDNA; 870 BP.
DE Novel human secreted and transmembrane protein PRO842 cDNA.
PN US2003032108-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 870; DB 8; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 63
ID ACA70708 standard; cDNA; 870 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #70.
PN US2003032111-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 870; DB 8; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 64
ID ACA95218 standard; cDNA; 870 BP.
DE Novel human secreted and transmembrane protein PRO842 cDNA.
PN US2003032119-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 8; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 65
ID ACDA4245 standard; cDNA; 870 BP.
DE cDNA encoding human PRO842 polypeptide.
PN US2002127576-A1.

PD 12-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 8; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 66
ID ACC86161 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003027263-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 870; DB 8; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 67
ID ACD45161 standard; cDNA; 870 BP.
DE Human secreted/transmembrane polypeptide PRO842 cDNA.
PN US2003009012-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 8; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 68
ID ACC90033 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003027271-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 870; DB 8; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 69
ID ACD12641 standard; cDNA; 870 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #70.
PN US2003036125-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 870; DB 8; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 70
ID ACF19871 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003040068-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 870; DB 8; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 71
ID ABX76815 standard; cDNA; 870 BP.
DE Human PRO polynucleotide #70.
PN US2003027280-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 870; DB 8; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 72
ID ACA73147 standard; cDNA; 870 BP.
DE Novel human secreted and transmembrane protein PRO842 cDNA.
PN US2003022300-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 870; DB 8; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 73
ID ACA68690 standard; cDNA; 870 BP.
DE Novel human secreted and transmembrane protein PRO842 cDNA.
PN US2003036136-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 870; DB 8; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 74
ID ACA74534 standard; cDNA; 870 BP.
DE cDNA encoding human PRO polypeptide #70.
PN US2003036138-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 870; DB 8; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 75
ID ACA70401 standard; cDNA; 870 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #70.
PN US2003032109-A1.
PD 13-FEB-2003.

Query Match 100.0%; Score 870; DB 8; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 76
ID ACD14587 standard; cDNA; 870 BP.
DE Novel human secreted and transmembrane protein PRO842.
PN US2003040066-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 870; DB 8; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 77
ID ACA93709 standard; cDNA; 870 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO842.
PN US2003045684-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 8; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 78
ID ACA68259 standard; cDNA; 870 BP.
DE Novel human secreted and transmembrane protein PRO842.
PN US2003032104-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 870; DB 8; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 79
ID ABX98724 standard; cDNA; 870 BP.
DE Novel human secreted and transmembrane protein PRO842.
PN US2003036157-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 870; DB 8; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 80
ID ACA67283 standard; cDNA; 870 BP.
DE cDNA encoding human secreted polypeptide PRO842.
PN US2003027212-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 8; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 81
ID ACC81201 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003032120-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 870; DB 8; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 82
ID ACA95525 standard; cDNA; 870 BP.
DE Novel human secreted and transmembrane protein PRO842.
PN US2003036155-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 870; DB 8; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 83
ID ACD04443 standard; cDNA; 870 BP.
DE Novel human secreted and transmembrane protein PRO842.
PN US2003022296-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 870; DB 8; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 84
ID ACC87884 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003027281-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 8; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 85
ID ACF12546 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003040058-A1.
PD 27-FEB-2003.

Query Match 100.0%; Score 870; DB 8; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 86
ID ACH66256 standard; cDNA; 870 BP.
DE Novel human secreted and transmembrane protein PRO842.
PN US2003027986-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 8; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 87
ID ABX79416 standard; cDNA; 870 BP.
DE Human secreted/transmembrane protein cDNA, #61.
PN US2002142961-A1.
PD 03-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 8; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 88
ID ACA96261 standard; cDNA; 870 BP.
DE Human PRO polynucleotide #70.
PN US2003017540-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 870; DB 8; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 89
ID ACA65035 standard; cDNA; 870 BP.
DE Human PRO polynucleotide #70.
PN US2003032106-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 870; DB 8; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 90
ID ACA73761 standard; cDNA; 870 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #70.
PN US2003032129-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 870; DB 8; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 91
ID ACA74173 standard; cDNA; 870 BP.
DE Novel human secreted and transmembrane protein PRO842.
PN US2003032131-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 870; DB 8; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 92
ID ACA96568 standard; cDNA; 870 BP.
DE Human PRO polynucleotide #70.
PN US2003032103-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 870; DB 8; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 93
ID ACD10674 standard; cDNA; 870 BP.
DE cDNA encoding human PRO polypeptide #70.
PN US2003032107-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 870; DB 8; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 94
ID ACC91370 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003032139-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 870; DB 8; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 95
ID ACA93437 standard; cDNA; 870 BP.
DE Novel human secreted and transmembrane protein PRO842.
PN US2003022187-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 870; DB 8; Length 870;


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Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 96
ID AC020705 standard; cDNA; 870 BP.
DE CDNA encoding human PRO polypeptide #70.
PN US2003022301-A1.
PD 30-JAN-2003.
Query Match
Best Local Similarity 100.0%; Score 870; DB 8; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 97
ID ACC87270 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003036165-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 870; DB 8; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 98
ID ACC85854 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003027282-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 870; DB 8; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 99
ID ABX81119 standard; DNA; 870 BP.
DE Novel human secreted or transmembrane protein PRO839 DNA.
PN US2003027985-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 870; DB 8; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 100
ID ACA85342 standard; cDNA; 870 BP.
DE Human PRO polynucleotide #70.
PN US2003032110-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 870; DB 8; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 101
ID ACA94159 standard; cDNA; 870 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #70.
PN US2003036142-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 870; DB 8; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 102
ID ACA97903 standard; cDNA; 870 BP.
DE Human PRO polynucleotide #70.
PN US2003036145-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 870; DB 8; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 103
ID ACA91405 standard; cDNA; 870 BP.
DE Novel human secreted and transmembrane protein PRO842 cDNA.
PN US2003036154-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 870; DB 8; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 104
ID ACA90619 standard; cDNA; 870 BP.
DE Novel human secreted and transmembrane protein PRO842 cDNA.
PN US2003036153-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 870; DB 8; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 105
ID ACD16166 standard; cDNA; 870 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #70.
PN US2003044931-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 870; DB 8; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 106
ID ACD17327 standard; cDNA; 870 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #70.
PN US2003036150-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 870; DB 8; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 107
ID ACC91984 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003040069-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 870; DB 8; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 108
ID ACD02310 standard; cDNA; 870 BP.
DE Novel human secreted and transmembrane protein PRO842 cDNA.
PN US2002183493-A1.
PD 05-DEC-2002.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 870; DB 8; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 109
ID ACA74841 standard; cDNA; 870 BP.
DE cDNA encoding human PRO polypeptide #70.
PN US2003022293-A1.
PD 30-JAN-2003.
Query Match
Best Local Similarity 100.0%; Score 870; DB 8; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 110
ID ACA91712 standard; cDNA; 870 BP.
DE Human PRO polynucleotide #70.
PN US2003032128-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 870; DB 8; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 111
ID ACA89301 standard; cDNA; 870 BP.
DE Novel human secreted and transmembrane protein PRO842 cDNA.
PN US2003036634-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 870; DB 8; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 112
ID ACA71356 standard; cDNA; 870 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #70.
PN US2003032116-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 870; DB 8; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 113
ID ACC90756 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003032122-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 870; DB 8; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 114
ID ACA65766 standard; cDNA; 870 BP.
DE cDNA encoding human PRO protein #70.
PN US2003036139-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 870; DB 8; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 115
ID ACA68938 standard; cDNA; 870 BP.
DE Novel human secreted and transmembrane protein PRO842 cDNA.
PN US2002183494-A1.
PD 05-DEC-2002.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 870; DB 8; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 116
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ID ACA92935 standard; cDNA; 870 BP.
DE Novel human secreted and transmembrane protein PRO842 cDNA.
PN US2003017476-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 870; DB 8; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 117
ID ACA94911 standard; cDNA; 870 BP.
DE cDNA encoding human PRO polypeptide #70.
PN US2003017541-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 870; DB 8; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 118
ID ACD16473 standard; cDNA; 870 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #70.
PN US2003017543-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 870; DB 8; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 119
ID ACD15552 standard; cDNA; 870 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #70.
PN US2003036152-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 870; DB 8; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 120
ID ACA98460 standard; cDNA; 870 BP.
DE Human PRO polynucleotide #13.
PN US2003027993-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 8; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 121
ID ABX17019 standard; cDNA; 870 BP.
DE Human PRO polynucleotide #38.
PN US2002123463-A1.
PD 05-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 8; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 122
ID ABX16655 standard; cDNA; 870 BP.
DE Human cDNA encoding secreted/transmembrane protein #70.
PN US2002127584-A1.
PD 12-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 8; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 123
ID ACA67874 standard; cDNA; 870 BP.
DE Novel human secreted and transmembrane protein PRO842 cDNA.
PN US2002177164-A1.
PD 28-NOV-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 124
ID ACA63385 standard; cDNA; 870 BP.
DE cDNA encoding human PRO polypeptide #13.
PN US2003023042-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 125
ID ACA97596 standard; cDNA; 870 BP.
DE Human PRO polynucleotide #70.
PN US2003032115-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 870; DB 9; Length 870;

Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 126
ID ACA99045 standard; cDNA; 870 BP.
DE Novel human secreted and transmembrane protein PRO842 cDNA.
PN US2003032140-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 127
ID ACC91677 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003040076-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 128
ID ACD11088 standard; cDNA; 870 BP.
DE Novel human secreted and transmembrane protein PRO842 cDNA.
PN US2003008352-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 129
ID ACD14938 standard; cDNA; 870 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #70.
PN US2003044922-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 130
ID ACA88323 standard; cDNA; 870 BP.
DE Human secreted and transmembrane polypeptide PRO842 cDNA.
PN US2002197615-A1.
PD 26-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 131
ID ACD81830 standard; cDNA; 870 BP.
DE cDNA encoding human PRO842 polypeptide.
PN US2003017981-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 132
ID ACD11702 standard; cDNA; 870 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #70.
PN US2003032118-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 133
ID ACC95831 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003036135-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 134
ID ACF16394 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003054455-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 135
ID ACF02512 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003049741-A1.
PD 13-MAR-2003.


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PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 136
ID ACF02819 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003049743-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 137
ID ACF21406 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003049769-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 138
ID ACF10090 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003068743-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 139
ID ACF77983 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003054479-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 140
ID ACD46688 standard; cDNA; 870 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #70.
PN US2003068685-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 141
ID ACD49451 standard; cDNA; 870 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #70.
PN US2003068725-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 142
ID ACF28218 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003068752-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 143
ID ACD88908 standard; cDNA; 870 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #70.
PN US2003068682-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 144
ID ACD84303 standard; cDNA; 870 BP.
DE Human PRO polynucleotide #70.
PN US2003068701-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 145
ID ACD99077 standard; cDNA; 870 BP.
DE cDNA encoding human PRO polypeptide #70.
PN US2003068755-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 146
ID ADA77891 standard; cDNA; 870 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #70.
PN US2003073180-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 147
ID ACF48819 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003104539-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 148
ID ACD09139 standard; cDNA; 870 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #70.
PN US2003036131-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 149
ID ACF11932 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003040075-A1.
PD 27-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 150
ID ACF41166 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003054459-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 151
ID ACF15780 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003044930-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 152
ID ACF16087 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003040071-A1.
PD 27-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 153
ID ADB17082 standard; cDNA; 870 BP.
DE Human cDNA clone (SeqID 25) encoding the transmembrane PRO protein.
PN US2003050462-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 154
ID ACD31914 standard; cDNA; 870 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #70.
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PN US2003054471-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 155
ID ACF18722 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003064452-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 156
ID ACF09169 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003068705-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 157
ID ACF78290 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003054473-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 158
ID ACF51889 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003064440-A1.
PD 03-APR-2003.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 159
ID ACF26376 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003068704-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 160
ID ACF24169 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003068722-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 161
ID ACF63480 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003073183-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 162
ID ACF50354 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003104549-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 163
ID ACH07825 standard; cDNA; 870 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #70.
PN US2003049749-A1.
PD 13-MAR-2003.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 164
ID ACF13631 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003064462-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 165
ID ACDA1557 standard; cDNA; 870 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #70.
PN US2003065159-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 166
ID ADA37675 standard; cDNA; 870 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO842.
PN US2003008297-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 167
ID ACF31970 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003064447-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 168
ID ACF23248 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003073184-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 169
ID ACF39938 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003064463-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 170
ID ACD45460 standard; cDNA; 870 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #70.
PN US2003064451-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 171
ID ACF53117 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003068721-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 172
ID ACF27297 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003068699-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 173
ID ACF45135 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003068707-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 174
ID ACF29753 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003073175-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 175
ID ACD9829 standard; cDNA; 870 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #70.
PN US2003068695-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 176
ID ACD84610 standard; cDNA; 870 BP.
DE Human PRO polynucleotide #70.
PN US2003068703-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 177
ID ACD98770 standard; cDNA; 870 BP.
DE cDNA encoding human PRO polypeptide #70.
PN US2003068732-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 178
ID ACF77062 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003082717-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 179
ID ACF76755 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003104548-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 180
ID ACF49740 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003104542-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 181
ID ACF50047 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003104543-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 182
ID ADA21361 standard; cDNA; 870 BP.

DE Human cDNA encoding secreted/transmembrane polypeptide PRO842.
PN US2003054404-A1.
PD 20-MAR-2003.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 183
ID ACD09446 standard; cDNA; 870 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #70.
PN US2003036127-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 184
ID ACD08525 standard; cDNA; 870 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #70.
PN US2003040061-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 185
ID ACH03588 standard; cDNA; 870 BP.
DE Human secreted/transmembrane polypeptide PRO 842 cDNA.
PN US2003018172-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 186
ID ACF12239 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003036130-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 187
ID ACC94747 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003054468-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 188
ID ACD22466 standard; cDNA; 870 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #70.
PN US2003054470-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 189
ID ACF15166 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003044917-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 190
ID ACC97261 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003044929-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 191
ID ACC92291 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003059880-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 192

ID ACF13938 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003064465-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 193
ID ACF14245 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003054478-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 194
ID ADA10148 standard; cDNA; 870 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO842.
PN US2003059831-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 195
ID ACF09476 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003068718-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 196
ID ACD45767 standard; cDNA; 870 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #70.
PN US2003064454-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 197
ID ACD47916 standard; cDNA; 870 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #70.
PN US2003064461-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 198
ID ACD67647 standard; cDNA; 870 BP.
DE cDNA encoding human PRO polypeptide #70.
PN US2003068724-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 199
ID ACF25455 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003068727-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 200
ID ACF29139 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003068772-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 201
ID ACD84917 standard; cDNA; 870 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #70.

PN US2003068714-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 202
ID ACD81996 standard; cDNA; 870 BP.
DE Human PRO polynucleotide #70.
PN US2003068758-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 203
ID ACD87987 standard; cDNA; 870 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #70.
PN US2003068776-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 204
ID ACF30674 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003069407-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 205
ID ACF32277 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003104555-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 206
ID ACH11937 standard; cDNA; 870 BP.
DE cDNA encoding human PRO polypeptide #70.
PN US2003049768-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 207
ID ACH12244 standard; cDNA; 870 BP.
DE cDNA encoding human PRO polypeptide #70.
PN US2003049771-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 208
ID ADA19887 standard; cDNA; 870 BP.
DE Novel human secreted and transmembrane protein PRO842 cDNA.
PN US2003059394-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 209
ID ACD40636 standard; cDNA; 870 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #70.
PN US2003032134-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 210
ID ADB17270 standard; cDNA; 870 BP.
DE Human cDNA clone (SeqID 25) encoding the transmembrane PRO protein.
PN US2003050465-A1.
PD 13-MAR-2003.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 211
ID ADA17692 standard; cDNA; 870 BP.
DE cDNA encoding human PRO842 polypeptide.
PN US20030543987-A1.
PD 20-MAR-2003.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 212
ID ACF18108 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003054481-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 213
ID ACF08555 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003049778-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 214
ID ACF31356 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003049782-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 215
ID ACF52196 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003054476-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 216
ID ACD50065 standard; cDNA; 870 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #70.
PN US2003068733-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 217
ID ACF38768 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003068692-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 218
ID ACF26683 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003068709-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 219
ID ACF24783 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003068716-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;

Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 220
ID ACF46363 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003068740-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 221
ID ACF27911 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003068751-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 222
ID ACD89215 standard; cDNA; 870 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #70.
PN US2003068684-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 223
ID ACF63787 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003073179-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 224
ID ACF60427 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003087374-A1.
PD 08-MAY-2003.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 225
ID ACH12551 standard; cDNA; 870 BP.
DE cDNA encoding human PRO polypeptide #70.
PN US2003049773-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 226
ID ACH09974 standard; cDNA; 870 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #70.
PN US2003049777-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 227
ID ACD03829 standard; cDNA; 870 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #70.
PN US2003040055-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 228
ID ACD10367 standard; cDNA; 870 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #70.
PN US2003036164-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 229
ID ACD12009 standard; cDNA; 870 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #70.

PN US2003040074-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 870; DB 9; Length 870;
Pred. No. 4.3e-229;
RESULT 230
ID ACF42394 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003054480-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 870; DB 9; Length 870;
Pred. No. 4.3e-229;
RESULT 231
ID ADA27800 standard; cDNA; 870 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO842.
PN US2003054359-A1.
PD 20-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 870; DB 9; Length 870;
Pred. No. 4.3e-229;
RESULT 232
ID ACF18415 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003059885-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 870; DB 9; Length 870;
Pred. No. 4.3e-229;
RESULT 233
ID ACF02205 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003049740-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 870; DB 9; Length 870;
Pred. No. 4.3e-229;
RESULT 234
ID ACF21713 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003049770-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 870; DB 9; Length 870;
Pred. No. 4.3e-229;
RESULT 235
ID ACF10397 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003073169-A1.
PD 17-APR-2003.
Query Match
Best Local Similarity 100.0%; Score 870; DB 9; Length 870;
Pred. No. 4.3e-229;
RESULT 236
ID ACF33849 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003064457-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 870; DB 9; Length 870;
Pred. No. 4.3e-229;
RESULT 237
ID ACF44811 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003068711-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 870; DB 9; Length 870;
Pred. No. 4.3e-229;
RESULT 238
ID ACD90443 standard; cDNA; 870 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #70.
PN US2003049745-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 870; DB 9; Length 870;
Pred. No. 4.3e-229;

Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 239
ID ACD91056 standard; cDNA; 870 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #70.
PN US2003049751-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 870; DB 9; Length 870;
Pred. No. 4.3e-229;
RESULT 240
ID ACF10367 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003067478-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 870; DB 9; Length 870;
Pred. No. 4.3e-229;
RESULT 241
ID ACD87066 standard; cDNA; 870 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #70.
PN US2003068773-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 870; DB 9; Length 870;
Pred. No. 4.3e-229;
RESULT 242
ID ACF60120 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003073185-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 870; DB 9; Length 870;
Pred. No. 4.3e-229;
RESULT 243
ID ACF46670 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003087373-A1.
PD 08-MAY-2003.
Query Match
Best Local Similarity 100.0%; Score 870; DB 9; Length 870;
Pred. No. 4.3e-229;
RESULT 244
ID ACF75527 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003096353-A1.
PD 22-MAY-2003.
Query Match
Best Local Similarity 100.0%; Score 870; DB 9; Length 870;
Pred. No. 4.3e-229;
RESULT 245
ID ADA79683 standard; cDNA; 870 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #70.
PN US2003073173-A1.
PD 17-APR-2003.
Query Match
Best Local Similarity 100.0%; Score 870; DB 9; Length 870;
Pred. No. 4.3e-229;
RESULT 246
ID ACF17187 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003054458-A1.
PD 20-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 870; DB 9; Length 870;
Pred. No. 4.3e-229;
RESULT 247
ID ACF22941 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003059886-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 870; DB 9; Length 870;
Pred. No. 4.3e-229;
RESULT 248
ID ACF07941 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003049758-A1.


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PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 870; DB 9; Length 870;
RESULT 249
ID ACF08248 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003049772-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 870; DB 9; Length 870;
RESULT 250
ID ACF40552 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003064448-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 870; DB 9; Length 870;
RESULT 251
ID ACF53731 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003064456-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 870; DB 9; Length 870;
RESULT 252
ID ACD46995 standard; cDNA; 870 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #70.
PN US2003068693-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 870; DB 9; Length 870;
RESULT 253
ID ACF47898 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003068735-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 870; DB 9; Length 870;
RESULT 254
ID ACF47284 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003068753-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 870; DB 9; Length 870;
RESULT 255
ID ACF46056 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003068742-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 870; DB 9; Length 870;
RESULT 256
ID ACD86145 standard; cDNA; 870 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #70.
PN US2003068756-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 870; DB 9; Length 870;
RESULT 257
ID ACF52503 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003082715-A1.
PD 01-MAY-2003.

Query Match
Best Local Similarity 100.0%; Score 870; DB 9; Length 870;
RESULT 258
ID ACF52810 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003082716-A1.
PD 01-MAY-2003.
Query Match
Best Local Similarity 100.0%; Score 870; DB 9; Length 870;
RESULT 259
ID ACF64803 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003068737-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 870; DB 9; Length 870;
RESULT 260
ID ACF76448 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003104547-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 870; DB 9; Length 870;
RESULT 261
ID ACF61348 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003096359-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 870; DB 9; Length 870;
RESULT 262
ID ACF61655 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003100061-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 870; DB 9; Length 870;
RESULT 263
ID ACD30686 standard; cDNA; 870 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #70.
PN US2003032125-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 870; DB 9; Length 870;
RESULT 264
ID ACD31607 standard; cDNA; 870 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #70.
PN US2003054454-A1.
PD 20-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 870; DB 9; Length 870;
RESULT 265
ID ACD32528 standard; cDNA; 870 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #70.
PN US2003054477-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 870; DB 9; Length 870;
RESULT 266
ID ADA20059 standard; cDNA; 870 BP.
DE Novel human secreted and transmembrane protein PRO842 cDNA.
PN US2003055222-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 870; DB 9; Length 870;
RESULT 267
ID ACD82102 standard; cDNA; 870 BP.
```


DE Human secreted/transmembrane polypeptide PRO 842 cDNA, SEQ ID NO:139.
PN US2003060601-A1.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 268
ID ACF17494 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003054460-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 269
ID ADA94380 standard; cDNA; 870 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO842.
PN US2003059832-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 270
ID ACF07327 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003049753-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 271
ID ACF20485 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003049763-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 272
ID ACF21099 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003073172-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 273
ID ACF20792 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003073172-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 274
ID ACDA7609 standard; cDNA; 870 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #70.
PN US2003068700-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 275
ID ACF47591 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003068736-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 276
ID ACF53424 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003068679-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 277
ID ACDB6759 standard; cDNA; 870 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #70.
PN US2003068767-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 278
ID ACH05007 standard; cDNA; 870 BP.
DE cDNA encoding human PRO polypeptide #70.
PN US2003073182-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 279
ID ACF44504 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003104557-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 280
ID ADA81410 standard; cDNA; 870 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #70.
PN US2003092121-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 281
ID ACD22159 standard; cDNA; 870 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #70.
PN US2003027276-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 282
ID ACD24506 standard; cDNA; 870 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #70.
PN US2003044920-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 283
ID ACD39709 standard; cDNA; 870 BP.
DE cDNA encoding human PRO polypeptide #70.
PN US2003027285-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 284
ID ACD40016 standard; cDNA; 870 BP.
DE cDNA encoding human PRO polypeptide #70.
PN US2003054461-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 285
ID ACF13324 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003064446-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 286
ID ACF03126 standard; cDNA; 870 BP.

DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003049744-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 870; DB 9; Length 870;
RESULT 287
ID ACP78597 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003049783-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 870; DB 9; Length 870;
RESULT 288
ID ACF11318 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003073171-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 870; DB 9; Length 870;
RESULT 289
ID ACF50661 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003032121-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 870; DB 9; Length 870;
RESULT 290
ID ACF34156 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003064458-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 870; DB 9; Length 870;
RESULT 291
ID ACD46381 standard; cDNA; 870 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #70.
PN US2003064460-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 870; DB 9; Length 870;
RESULT 292
ID ACD48223 standard; cDNA; 870 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #70.
PN US2003064464-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 870; DB 9; Length 870;
RESULT 293
ID ACF27604 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003068702-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 870; DB 9; Length 870;
RESULT 294
ID ACF24476 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003068734-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 870; DB 9; Length 870;
RESULT 295
ID ACD85531 standard; cDNA; 870 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #70.
PN US2003068719-A1.
PD 10-APR-2003.

PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 870; DB 9; Length 870;
RESULT 296
ID ACD90136 standard; cDNA; 870 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #70.
PN US2003068729-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 870; DB 9; Length 870;
RESULT 297
ID ACD83689 standard; cDNA; 870 BP.
DE Human PRO polynucleotide #70.
PN US2003068738-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 870; DB 9; Length 870;
RESULT 298
ID ACF49126 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003104540-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 870; DB 9; Length 870;
RESULT 299
ID ACH07211 standard; cDNA; 870 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #70.
PN US2003049742-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 870; DB 9; Length 870;
RESULT 300
ID ACH07518 standard; cDNA; 870 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #70.
PN US2003049747-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 870; DB 9; Length 870;
RESULT 301
ID ACH08132 standard; cDNA; 870 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #70.
PN US2003049750-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 870; DB 9; Length 870;
RESULT 302
ID ACH11323 standard; cDNA; 870 BP.
DE cDNA encoding human PRO polypeptide #70.
PN US2003049766-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 870; DB 9; Length 870;
RESULT 303
ID ACH11630 standard; cDNA; 870 BP.
DE cDNA encoding human PRO polypeptide #70.
PN US2003049767-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 870; DB 9; Length 870;
RESULT 304
ID ACH10281 standard; cDNA; 870 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #70.
PN US2003049779-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 870; DB 9; Length 870;
RESULT 305
ID ACH10281 standard; cDNA; 870 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #70.
PN US2003049779-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 870; DB 9; Length 870;

Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 305
ID ACF01284 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003040059-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 306
ID ACF40859 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003040078-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 307
ID ACD24199 standard; cDNA; 870 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #70.
PN US2003044918-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 308
ID ACD31300 standard; cDNA; 870 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #70.
PN US2003032132-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 309
ID ACF17801 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003054462-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 310
ID ADA38605 standard; cDNA; 870 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO842.
PN US2003059780-A1.
PD 27-MAR-2003.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 311
ID ACF32584 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003064445-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 312
ID ACF40245 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003064449-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 313
ID ACF48205 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003064441-A1.
PD 03-APR-2003.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 314
ID ACF38154 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003068696-A1.
PD 10-APR-2003.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 315
ID ACF25090 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003068712-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 316
ID ACF26990 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003068730-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 317
ID ACF29446 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003073174-A1.
PD 17-APR-2003.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 318
ID ACD87680 standard; cDNA; 870 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #70.
PN US2003068775-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 319
ID ACF76141 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003104545-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 320
ID ACF49433 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003104541-A1.
PD 05-JUN-2003.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 321
ID ACF43890 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003104554-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 322
ID ACH06235 standard; cDNA; 870 BP.
DE cDNA encoding human PRO polypeptide #70.
PN US2003049762-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 323
ID ACH06542 standard; cDNA; 870 BP.
DE cDNA encoding human PRO polypeptide #70.
PN US2003049765-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 329
ID ACH06542 standard; cDNA; 870 BP.
DE cDNA encoding human PRO polypeptide #70.
PN US2003049765-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;

RESULT 324
ID ADA83208 standard; cDNA; 870 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #70.
PN US2003049752-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 325
ID ACC92598 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003032133-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 326
ID ACC93212 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003032136-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 327
ID ACF19257 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003036129-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 328
ID ACD12948 standard; cDNA; 870 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #70.
PN US2003040053-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 329
ID ACF06406 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003040057-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 330
ID ACC94440 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003054467-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 331
ID ACC97868 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003044932-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 332
ID ACC94133 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003027270-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 333
ID ACF42087 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003054469-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;

RESULT 334
ID ACD30993 standard; cDNA; 870 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #70.
PN US2003032126-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 335
ID ACD43022 standard; cDNA; 870 BP.
DE cDNA encoding human PRO polypeptide #70.
PN US2003054463-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 336
ID ACD43329 standard; cDNA; 870 BP.
DE cDNA encoding human PRO polypeptide #70.
PN US2003054466-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 337
ID ACF14859 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003059879-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 338
ID ADA92726 standard; cDNA; 870 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO842.
PN US2003060407-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 339
ID ACF01591 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003049738-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 340
ID ACF31663 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003064469-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 341
ID ACD67340 standard; cDNA; 870 BP.
DE cDNA encoding human PRO polypeptide #70.
PN US2003064453-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 342
ID ACD48530 standard; cDNA; 870 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #70.
PN US2003064466-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 343
ID ACD48837 standard; cDNA; 870 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #70.
PN US2003064468-A1.

PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 344
ID ACF51275 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003068760-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 345
ID ACF54038 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003068769-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 346
ID ACF25762 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003045700-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 347
ID ACF39075 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003068698-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 348
ID ACF28832 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003068759-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 349
ID ACD90749 standard; cDNA; 870 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #70.
PN US2003049748-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 350
ID ACD86452 standard; cDNA; 870 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #70.
PN US2003068765-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 351
ID ACH05314 standard; cDNA; 870 BP.
DE cDNA encoding human PRO polypeptide #70.
PN US2003049754-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 352
ID ACF65110 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003068698-A1.
PD 10-APR-2003.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 353
ID ADB20251 standard; cDNA; 870 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #70.
PN US2003082767-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 354
ID ACF43583 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003104552-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 355
ID ACH09053 standard; cDNA; 870 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #70.
PN US2003049774-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 356
ID ACH09360 standard; cDNA; 870 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #70.
PN US2003049775-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 357
ID ADA78503 standard; cDNA; 870 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #70.
PN US2003073181-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 358
ID ACF09783 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003068720-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 359
ID ADA00356 standard; cDNA; 870 BP.
DE Human secreted/transmembrane polypeptide PRO 842 cDNA.
PN US2003027992-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 360
ID ACF50968 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003068739-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 361
ID ACF23862 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003068763-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;


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Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 362
ID ACD88294 standard; cDNA; 870 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #70.
PN US2003068689-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 363
ID ACH09667 standard; cDNA; 870 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #70.
PN US2003049776-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 364
ID ACH10588 standard; cDNA; 870 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #70.
PN US2003049780-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 365
ID ACD11395 standard; cDNA; 870 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #70.
PN US2003036126-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 366
ID ACC96445 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003044924-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 367
ID ACC98475 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003044927-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 368
ID ACF41780 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003040072-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 369
ID ACF16701 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003040073-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 370
ID ACD32221 standard; cDNA; 870 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #70.
PN US2003054475-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 371
ID ACD30379 standard; cDNA; 870 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #70.
PN US2003032124-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 372
ID ACD41250 standard; cDNA; 870 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #70.
PN US2003064467-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 373
ID ACF07634 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003049759-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 374
ID ACF31049 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003064455-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 375
ID ACF77369 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003054465-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 376
ID ACF11011 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003073170-A1.
PD 17-APR-2003.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 377
ID ACF32891 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003073176-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 378
ID ACF26069 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003068717-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 379
ID ACD83382 standard; cDNA; 870 BP.
DE Human PRO polynucleotide #70.
PN US2003068728-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 380
ID ACF23555 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003068764-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
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RESULT 381
ID ACF42969 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003104550-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 382
ID ACF43276 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003104551-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 383
ID ACH05928 standard; cDNA; 870 BP.
DE cDNA encoding human PRO polypeptide #70.
PN US2003049761-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 384
ID ACH08746 standard; cDNA; 870 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #70.
PN US2003049757-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 385
ID ACC90340 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003027273-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 386
ID ACF10704 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003036119-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 387
ID ACC93519 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003036120-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 388
ID ACC96138 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003036161-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 389
ID ACD24813 standard; cDNA; 870 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #70.
PN US2003044921-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 390
ID ACF01898 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003049739-A1.
PD 13-MAR-2003.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 391
ID ACF22020 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003059892-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 392
ID ACF22634 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003059894-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 393
ID ACF08862 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003068687-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 394
ID ACF33198 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003073186-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 395
ID ACF54652 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003064443-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 396
ID ACF48512 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003064444-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 397
ID ACD47302 standard; cDNA; 870 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #70.
PN US2003068697-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 398
ID ACD49144 standard; cDNA; 870 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #70.
PN US2003068710-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 399
ID ACF37847 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003068686-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 400
ID ACF30060 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003073178-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 401
ID AC087373 standard; cDNA; 870 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #70.
PN US2003068774-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 402
ID ACF61962 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003104538-A1.
PD 05-JUN-2003.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 403
ID ACH10895 standard; cDNA; 870 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #70.
PN US2003049781-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 404
ID ACD10060 standard; cDNA; 870 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #70.
PN US2003036158-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 405
ID ACD16785 standard; cDNA; 870 BP.
DE CDNA encoding human PRO polypeptide #70.
PN US2003036151-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 406
ID ACH65391 standard; cDNA; 870 BP.
DE Human CDNA encoding secreted/transmembrane protein PRO842.
PN US2003044806-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 407
ID ACC99082 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003040067-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 408
ID ACF00476 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003054456-A1.
PD 20-MAR-2003.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 409
ID ACD40943 standard; cDNA; 870 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #70.
PN US2003054482-A1.
PD 20-MAR-2003.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 410
ID ACF14552 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003054457-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 411
ID ACF22327 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003059883-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 412
ID ACF78904 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003049764-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 413
ID ACF11625 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003073177-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 414
ID ADA22287 standard; cDNA; 870 BP.
DE Human CDNA encoding secreted/transmembrane polypeptide PRO842.
PN US2003040473-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 415
ID ACF51582 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003064442-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 416
ID ACF33505 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003064450-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 417
ID ACD49758 standard; cDNA; 870 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #70.
PN US2003068731-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 418
ID ACF37540 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003068683-A1.
PD 10-APR-2003.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;

RESULT 419
ID ACF28525 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003068754-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
ID ACD20624 standard; cDNA; 870 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #70.
PN US2003044919-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
ID ACD88601 standard; cDNA; 870 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #70.
PN US2003068681-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
ID ACF75220 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003096351-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
ID ACF61041 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003096358-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
ID ACF44197 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003104556-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
ID ACF44197 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003104556-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
ID ACH08439 standard; cDNA; 870 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #70.
PN US2003049756-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
ID ACD39381 standard; cDNA; 870 BP.
DE Human cDNA encoding PRO839.
PN US2003017982-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
ID ACC93826 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003036122-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
ID ACD20931 standard; cDNA; 870 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #70.
PN US2003036121-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
ID ACF06713 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003040065-A1.

PD 27-FEB-2003.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 429
ID ACD20624 standard; cDNA; 870 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #70.
PN US2003044919-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
ID ACD22773 standard; cDNA; 870 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #70.
PN US2003040077-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
ID ACF41473 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003044928-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
ID ADA06453 standard; cDNA; 870 BP.
DE Human secreted/transmembrane PRO polypeptide cDNA #38.
PN US2003049638-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
ID ADA39146 standard; cDNA; 870 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO842.
PN US2003059782-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
ID ACF07020 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003049746-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
ID ACF77676 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003054464-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
ID ACD46074 standard; cDNA; 870 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #70.
PN US2003084459-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
ID ACF46977 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003068757-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
ID ACF54345 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.

PN US2003068723-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 870; DB 9; Length 870;
RESULT 439
ID ACF45749 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003068741-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 870; DB 9; Length 870;
RESULT 440
ID ACF45442 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003068744-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 870; DB 9; Length 870;
RESULT 441
ID ACF38461 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003068766-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 870; DB 9; Length 870;
RESULT 442
ID ACD89522 standard; cDNA; 870 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #70.
PN US2003068694-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 870; DB 9; Length 870;
RESULT 443
ID ACD85224 standard; cDNA; 870 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #70.
PN US2003068715-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 870; DB 9; Length 870;
RESULT 444
ID ACD85838 standard; cDNA; 870 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #70.
PN US2003068726-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 870; DB 9; Length 870;
RESULT 445
ID ACF75834 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003104544-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 870; DB 9; Length 870;
RESULT 446
ID ACF60734 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003096357-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 870; DB 9; Length 870;
RESULT 447
ID ACH05621 standard; cDNA; 870 BP.
DE cDNA encoding human PRO polypeptide #70.
PN US2003049760-A1.

PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 870; DB 9; Length 870;
RESULT 448
ID ADA82574 standard; cDNA; 870 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #70.
PN US2003049755-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 870; DB 9; Length 870;
RESULT 449
ID ADB85598 standard; cDNA; 870 BP.
DE Novel human secreted and transmembrane protein PRO842 cDNA.
PN US2003049735-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 870; DB 9; Length 870;
RESULT 450
ID ADB96172 standard; cDNA; 870 BP.
DE Human PRO polynucleotide #38.
PN US2003054403-A1.
PD 20-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 870; DB 9; Length 870;
RESULT 451
ID ACF55880 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003068680-A1.
PD 10-APR-2003.
Query Match
Best Local Similarity 100.0%; Score 870; DB 9; Length 870;
RESULT 452
ID ACF55266 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003068762-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 870; DB 10; Length 870;
RESULT 453
ID ADB85882 standard; cDNA; 870 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #70.
PN US2003054472-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 870; DB 10; Length 870;
RESULT 454
ID ACF56187 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003068708-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 870; DB 10; Length 870;
RESULT 455
ID ACF56494 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003068713-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 870; DB 10; Length 870;
RESULT 456
ID ADB88277 standard; cDNA; 870 BP.
DE Human PRO842 cDNA.
PN US2003065161-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 870; DB 10; Length 870;

Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 457
ID ADB68084 standard; cDNA; 870 BP.
DE Human PRO842 cDNA.
PN US200306060-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 10; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 458
ID ACF55573 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003068761-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 10; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 459
ID ACF54959 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003068771-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 10; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 460
ID ADB90901 standard; cDNA; 870 BP.
DE Novel human secreted and transmembrane protein PRO842 cDNA.
PN US2003083473-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 10; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 461
ID ADC57644 standard; cDNA; 870 BP.
DE Human PRO polynucleotide #38.
PN US2003027754-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 870; DB 10; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 462
ID ADC55008 standard; cDNA; 870 BP.
DE Human PRO polynucleotide #38.
PN US2003045463-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 870; DB 10; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 463
ID ADC11875 standard; cDNA; 870 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO842.
PN US2003049681-A1.
PD 13-MAR-2003.
Query Match 100.0%; Score 870; DB 10; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 464
ID ADC06981 standard; cDNA; 870 BP.
DE Human PRO842 cDNA.
PN US2003060602-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 10; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 465
ID ADC56297 standard; cDNA; 870 BP.
DE Human PRO polynucleotide #38.
PN US2003064375-A1.
PD 03-APR-2003.
Query Match 100.0%; Score 870; DB 10; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 466
ID ADC17160 standard; cDNA; 870 BP.
DE cDNA sequence encoding a PRO polypeptide (SeqID 25).
PN US2003065143-A1.

PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 10; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 467
ID ADC07352 standard; cDNA; 870 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO842.
PN US2003068647-A1.
PD 10-APR-2003.
Query Match 100.0%; Score 870; DB 10; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 468
ID ADC11342 standard; cDNA; 870 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO842.
PN US2003069403-A1.
PD 10-APR-2003.
Query Match 100.0%; Score 870; DB 10; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 469
ID ADC14858 standard; cDNA; 870 BP.
DE Novel human secreted and transmembrane protein PRO842 cDNA.
PN US2003073208-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 10; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 470
ID ADC52353 standard; cDNA; 870 BP.
DE Novel human secreted and transmembrane protein PRO842 cDNA.
PN US2003138882-A1.
PD 24-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 10; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 471
ID ADC14464 standard; cDNA; 870 BP.
DE Novel human secreted and transmembrane protein PRO842 cDNA.
PN US2003082546-A1.
PD 01-MAY-2003.
Query Match 100.0%; Score 870; DB 10; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 472
ID ADD07996 standard; cDNA; 870 BP.
DE Novel human secreted and transmembrane protein PRO842 cDNA.
PN US2003068623-A1.
PD 10-APR-2003.
Query Match 100.0%; Score 870; DB 10; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 473
ID ADC81821 standard; cDNA; 870 BP.
DE Human PRO polynucleotide #38.
PN US2003083461-A1.
PD 01-MAY-2003.
Query Match 100.0%; Score 870; DB 10; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 474
ID ADD07463 standard; cDNA; 870 BP.
DE Novel human secreted and transmembrane protein PRO842 cDNA.
PN US2002193299-A1.
PD 19-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 10; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 475
ID ADC82354 standard; cDNA; 870 BP.
DE Human PRO polynucleotide #38.
PN US2003059833-A1.
PD 27-MAR-2003.
Query Match 100.0%; Score 870; DB 10; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 476
ID ADD05612 standard; cDNA; 870 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #70.

PN US2003087376-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 870; DB 10; Length 870;
RESULT 477
ID ADD08534 standard; cDNA; 870 BP.
DE Novel human secreted and transmembrane protein PRO842 cDNA.
PN US2003073090-A1.
PD 17-APR-2003.
Query Match
Best Local Similarity 100.0%; Score 870; DB 10; Length 870;
RESULT 478
ID ADD06783 standard; cDNA; 870 BP.
DE Novel human secreted and transmembrane protein PRO842 cDNA.
PN US2002193300-A1.
PD 19-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 870; DB 10; Length 870;
RESULT 479
ID ADC83030 standard; cDNA; 870 BP.
DE Human PRO polynucleotide #38.
PN US2003059783-A1.
PD 27-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 870; DB 10; Length 870;
RESULT 480
ID ADD55137 standard; cDNA; 870 BP.
DE Human PRO polynucleotide #38.
PN US2003077593-A1.
PD 24-APR-2003.
Query Match
Best Local Similarity 100.0%; Score 870; DB 10; Length 870;
RESULT 481
ID ADD36029 standard; cDNA; 870 BP.
DE Novel human secreted and transmembrane protein PRO842 cDNA.
PN US2003105298-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 870; DB 10; Length 870;
RESULT 482
ID ADD56095 standard; cDNA; 870 BP.
DE Human PRO polynucleotide #38.
PN US2003077594-A1.
PD 24-APR-2003.
Query Match
Best Local Similarity 100.0%; Score 870; DB 10; Length 870;
RESULT 483
ID ADD54533 standard; cDNA; 870 BP.
DE Human PRO polynucleotide #38.
PN US2002132253-A1.
PD 19-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 870; DB 10; Length 870;
RESULT 484
ID ADE26687 standard; cDNA; 870 BP.
DE Novel human secreted and transmembrane protein PRO842 cDNA.
PN US2003087304-A1.
PD 08-MAY-2003.
Query Match
Best Local Similarity 100.0%; Score 870; DB 10; Length 870;
RESULT 485
ID ADE26154 standard; cDNA; 870 BP.
DE Novel human secreted and transmembrane protein PRO842 cDNA.
PN US2003087305-A1.
PD 08-MAY-2003.
Query Match
Best Local Similarity 100.0%; Score 870; DB 10; Length 870;
RESULT 486
ID ADF67091 standard; cDNA; 870 BP.

DE Human PRO842 nucleotide sequence SEQ ID NO:164.
PN US2002198148-A1.
PD 26-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 870; DB 10; Length 870;
RESULT 487
ID ADG01030 standard; cDNA; 870 BP.
DE Novel human secreted and transmembrane protein PRO842 cDNA.
PN US2003078387-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 870; DB 10; Length 870;
RESULT 488
ID ADG08583 standard; cDNA; 870 BP.
DE Novel human secreted and transmembrane protein PRO842 cDNA.
PN US2003180793-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 870; DB 10; Length 870;
RESULT 489
ID ADG02607 standard; cDNA; 870 BP.
DE Novel human secreted and transmembrane protein PRO842 cDNA.
PN US2003207397-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 870; DB 10; Length 870;
RESULT 490
ID ADG01314 standard; cDNA; 870 BP.
DE Novel human secreted and transmembrane protein PRO842 cDNA.
PN US2003207399-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 870; DB 10; Length 870;
RESULT 491
ID ADF95489 standard; cDNA; 870 BP.
DE Novel human secreted and transmembrane protein PRO842 cDNA.
PN US2003207398-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 870; DB 10; Length 870;
RESULT 492
ID ADF95204 standard; cDNA; 870 BP.
DE Novel human secreted and transmembrane protein PRO842 cDNA.
PN US2003180795-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 870; DB 10; Length 870;
RESULT 493
ID ADG12304 standard; cDNA; 870 BP.
DE Novel human secreted and transmembrane protein PRO842 cDNA.
PN US2003207392-A1.
PD 06-NOV-2003.
Query Match
Best Local Similarity 100.0%; Score 870; DB 10; Length 870;
RESULT 494
ID ADH24057 standard; cDNA; 870 BP.
DE Novel human secreted and transmembrane protein PRO842 cDNA.
PN US2003180918-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 870; DB 10; Length 870;
RESULT 495
ID ADH34083 standard; cDNA; 870 BP.
DE Novel human secreted and transmembrane protein PRO842 cDNA.
PN US2003180858-A1.

PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 10; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 496
ID ADH29916 standard; cDNA; 870 BP.
DE Novel human secreted and transmembrane protein PRO842 cDNA.
PN US2003180859-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 10; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 497
ID ADH23887 standard; cDNA; 870 BP.
DE Novel human secreted and transmembrane protein PRO842 cDNA.
PN US2003180919-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 10; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 498
ID ADH08964 standard; cDNA; 870 BP.
DE Human PRO polynucleotide #70.
PN US2003207395-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 10; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 499
ID ADG85291 standard; cDNA; 870 BP.
DE Novel human secreted and transmembrane protein PRO842 cDNA.
PN US2003180904-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 10; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 500
ID ADH24567 standard; cDNA; 870 BP.
DE Novel human secreted and transmembrane protein PRO842 cDNA.
PN US2003180907-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 10; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 501
ID ADH37423 standard; cDNA; 870 BP.
DE Human secreted and transmembrane protein PRO842 cDNA.
PN US2003181646-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 10; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 502
ID ADH02012 standard; cDNA; 870 BP.
DE Human PRO polynucleotide #13.
PN US2003180837-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 10; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 503
ID ADH37593 standard; cDNA; 870 BP.
DE Human secreted and transmembrane protein PRO842 cDNA.
PN US2003181648-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 10; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 504
ID ADG85631 standard; cDNA; 870 BP.
DE Novel human secreted and transmembrane protein PRO842 cDNA.
PN US2003180905-A1.
PD 25-SEP-2003.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 10; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 505
ID ADH24227 standard; cDNA; 870 BP.
DE Novel human secreted and transmembrane protein PRO842 cDNA.
PN US2003180914-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 10; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 506
ID ADH38521 standard; cDNA; 870 BP.
DE Novel human secreted and transmembrane protein PRO842 cDNA.
PN US2003181643-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 10; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 507
ID ADG83642 standard; cDNA; 870 BP.
DE Human PRO polynucleotide #13.
PN US2003180794-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 10; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 508
ID ADH29450 standard; cDNA; 870 BP.
DE Novel human secreted and transmembrane protein PRO842 cDNA.
PN US2003180860-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 10; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 509
ID ADH27566 standard; cDNA; 870 BP.
DE Novel human secreted and transmembrane protein PRO842 cDNA.
PN US2003180906-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 10; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 510
ID ADH37663 standard; cDNA; 870 BP.
DE Human secreted and transmembrane protein PRO842 cDNA.
PN US2003181647-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 10; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 511
ID ADH37940 standard; cDNA; 870 BP.
DE Human secreted and transmembrane protein PRO842 cDNA.
PN US2003181649-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 10; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 512
ID ADH57360 standard; cDNA; 870 BP.
DE Novel human secreted and transmembrane protein PRO842 cDNA.
PN US2003180920-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 10; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 513
ID ADH33502 standard; cDNA; 870 BP.
DE Novel human secreted and transmembrane protein PRO842 cDNA.
PN US2003181636-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.

DE Human PRO polynucleotide #70.
PN US2003027272-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 870; DB 10; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 533
ID ACA75569 standard; cDNA; 870 BP.
DE Novel human secreted and transmembrane protein PRO842 cDNA.
PN US2003032127-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 870; DB 10; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 534
ID ACA71049 standard; cDNA; 870 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #70.
PN US2003032112-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 870; DB 10; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 535
ID ACC87577 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003027278-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 870; DB 10; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 536
ID ACC86963 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003036159-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 870; DB 10; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 537
ID ACD04136 standard; cDNA; 870 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #70.
PN US2003040070-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 870; DB 10; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 538
ID ABX77820 standard; cDNA; 870 BP.
DE Human PRO polynucleotide #38.
PN US2003027163-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 870; DB 10; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 539
ID ABX80232 standard; DNA; 870 BP.
DE Novel human secreted or transmembrane protein PRO839 DNA.
PN US2002132252-A1.
PD 19-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 10; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 540
ID ACA69138 standard; cDNA; 870 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO842.
PN US2003032023-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 870; DB 10; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 541
ID ACA69467 standard; cDNA; 870 BP.
DE cDNA encoding human PRO polypeptide #70.
PN US2003032113-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 870; DB 10; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 542
ID ACA90312 standard; cDNA; 870 BP.
DE Novel human secreted and transmembrane protein PRO842 cDNA.
PN US2003036147-A1.

PD 20-FEB-2003.
Query Match 100.0%; Score 870; DB 10; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 543
ID ACC89419 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003027264-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 870; DB 10; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 544
ID ABX90209 standard; cDNA; 870 BP.
DE Human secreted/transmembrane protein cDNA, #61.
PN US2002160384-A1.
PD 31-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 10; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 545
ID ACA98210 standard; cDNA; 870 BP.
DE Novel human secreted and transmembrane protein PRO842 cDNA.
PN US2003036144-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 870; DB 10; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 546
ID ACA93852 standard; cDNA; 870 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #70.
PN US2003036149-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 870; DB 10; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 547
ID ACD15245 standard; cDNA; 870 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #70.
PN US2003044923-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 870; DB 10; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 548
ID ACD08832 standard; cDNA; 870 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #70.
PN US2003040062-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 870; DB 10; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 549
ID ACC96752 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003040056-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 870; DB 10; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 550
ID ACF15473 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003044926-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 870; DB 10; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 551
ID ABX64055 standard; cDNA; 870 BP.
DE cDNA encoding human PRO842 polypeptide.
PN US2002103125-A1.
PD 01-AUG-2002.
PA (GETH) GENENTECH LTD.
Query Match 100.0%; Score 870; DB 10; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 552
ID ACA72840 standard; cDNA; 870 BP.
DE Human PRO polynucleotide #70.
PN US2003036140-A1.
PD 20-FEB-2003.


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PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 870; DB 10; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 553
ID AC03012 standard; cDNA; 870 BP.
DE Novel human secreted and transmembrane protein PRO842 cDNA.
PN US2003013153-A1.
PD 16-JAN-2003.
Query Match 100.0%; Score 870; DB 10; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 554
ID AC01827 standard; cDNA; 870 BP.
DE Novel human secreted and transmembrane protein PRO842 cDNA.
PN US2003017544-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 870; DB 10; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 555
ID ACA92019 standard; cDNA; 870 BP.
DE Novel human secreted and transmembrane protein PRO842 cDNA.
PN US2003027277-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 870; DB 10; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 556
ID ADI05045 standard; cDNA; 870 BP.
DE Novel human secreted and transmembrane protein PRO842 cDNA.
PN US2003180848-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 870; DB 10; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 557
ID ADI03395 standard; cDNA; 870 BP.
DE Novel human secreted and transmembrane protein PRO842 cDNA.
PN US2003181654-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 870; DB 10; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 558
ID ADI04790 standard; cDNA; 870 BP.
DE Novel human secreted and transmembrane protein PRO842 cDNA.
PN US2003181657-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 870; DB 10; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 559
ID ADH78244 standard; cDNA; 870 BP.
DE Human PRO polynucleotide #13.
PN US2003181658-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 870; DB 10; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 560
ID ADI19598 standard; cDNA; 870 BP.
DE Novel human secreted and transmembrane protein PRO842 cDNA.
PN US2003181676-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 870; DB 10; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 561
ID ADH90336 standard; cDNA; 870 BP.
DE Novel human secreted and transmembrane protein PRO842 cDNA.
PN US2003181699-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 870; DB 10; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 562
ID ADI05389 standard; cDNA; 870 BP.
DE Novel human secreted and transmembrane protein PRO842 cDNA.
PN US2003181655-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 870; DB 10; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 563
ID ADI03055 standard; cDNA; 870 BP.
DE Novel human secreted and transmembrane protein PRO842 cDNA.
PN US2003181653-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 870; DB 10; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 564
ID ADH77904 standard; cDNA; 870 BP.
DE Human PRO polynucleotide #13.
PN US2003181666-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 870; DB 10; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 565
ID ADH97887 standard; cDNA; 870 BP.
DE Novel human secreted and transmembrane protein PRO842 cDNA.
PN US2003181674-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 870; DB 10; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 566
ID ADI01967 standard; cDNA; 870 BP.
DE Novel human secreted and transmembrane protein PRO842 cDNA.
PN US2003181652-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 870; DB 10; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 567
ID ADI03225 standard; cDNA; 870 BP.
DE Novel human secreted and transmembrane protein PRO842 cDNA.
PN US2003181655-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 870; DB 10; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 568
ID ADI11412 standard; cDNA; 870 BP.
DE Human PRO polynucleotide #13.
PN US2003181681-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 870; DB 10; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 569
ID ADI02314 standard; cDNA; 870 BP.
DE Novel human secreted and transmembrane protein PRO842 cDNA.
PN US2003181650-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 870; DB 10; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 570
ID ADI11752 standard; cDNA; 870 BP.
DE Human PRO polynucleotide #13.
PN US2003181685-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 870; DB 10; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 571
ID ADI05389 standard; cDNA; 870 BP.
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DE Novel human secreted and transmembrane protein PRO842 cDNA.
PN US2003190716-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 10; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 572
ID ADH79461 standard; cDNA; 870 BP.
DE Novel human secreted and transmembrane protein PRO842 cDNA.
PN US2003191290-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 10; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 573
ID ADI19418 standard; cDNA; 870 BP.
DE Novel human secreted and transmembrane protein PRO842 cDNA.
PN US2003181675-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 10; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 574
ID ADI05219 standard; cDNA; 870 BP.
DE Novel human secreted and transmembrane protein PRO842 cDNA.
PN US2003181677-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 10; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 575
ID ADH79631 standard; cDNA; 870 BP.
DE Novel human secreted and transmembrane protein PRO842 cDNA.
PN US2003191288-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 10; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 576
ID ADI01457 standard; cDNA; 870 BP.
DE Novel human secreted and transmembrane protein PRO842 cDNA.
PN US2003181678-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 10; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 577
ID ADI01627 standard; cDNA; 870 BP.
DE Novel human secreted and transmembrane protein PRO842 cDNA.
PN US2003181679-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 10; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 578
ID ADI01797 standard; cDNA; 870 BP.
DE Novel human secreted and transmembrane protein PRO842 cDNA.
PN US2003181680-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 10; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 579
ID ADH79801 standard; cDNA; 870 BP.
DE Novel human secreted and transmembrane protein PRO842 cDNA.
PN US2003191289-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 10; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 580
ID ADI04619 standard; cDNA; 870 BP.
DE Novel human secreted and transmembrane protein PRO842 cDNA.

PN US2003171550-A1.
PD 11-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 10; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 581
ID ADI02755 standard; cDNA; 870 BP.
DE Novel human secreted and transmembrane protein PRO842 cDNA.
PN US2003181651-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 10; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 582
ID ADH78074 standard; cDNA; 870 BP.
DE Human PRO polynucleotide #13.
PN US2003181687-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 10; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 583
ID ADI25713 standard; cDNA; 870 BP.
DE Novel human secreted and transmembrane protein PRO842 cDNA.
PN US2003181670-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 10; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 584
ID ADI25883 standard; cDNA; 870 BP.
DE Novel human secreted and transmembrane protein PRO842 cDNA.
PN US2003181671-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 10; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 585
ID ADK65395 standard; cDNA; 870 BP.
DE Novel human secreted and transmembrane protein PRO842 cDNA.
PN US2003073821-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 10; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 586
ID ADH98737 standard; cDNA; 870 BP.
DE Novel human secreted and transmembrane protein PRO842 cDNA.
PN US2003191284-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 10; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 587
ID ADH79978 standard; cDNA; 870 BP.
DE Novel human secreted and transmembrane protein PRO842 cDNA.
PN US2003191287-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 10; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 588
ID ADL32745 standard; cDNA; 870 BP.
DE Novel human secreted and transmembrane protein PRO842 cDNA.
PN US2003207396-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 10; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 589
ID ADL32745 standard; cDNA; 870 BP.
DE Novel human secreted and transmembrane protein PRO842 cDNA.
PN US2003073813-A1.

DE Novel human secreted and transmembrane protein PRO842 cDNA.
PN US2003180846-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 12; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 609
ID ADH39177 standard; cDNA; 870 BP.
DE Novel human secreted and transmembrane protein PRO842 cDNA.
PN US2003180917-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 12; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 610
ID ADH26069 standard; cDNA; 870 BP.
DE Novel human secreted and transmembrane protein PRO842 cDNA.
PN US2003068770-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 12; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 611
ID ADG83917 standard; cDNA; 870 BP.
DE Human PRO polynucleotide #13.
PN US2003180842-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 12; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 612
ID ADH19410 standard; cDNA; 870 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO842.
PN US2003228656-A1.
PD 11-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 12; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 613
ID ADG85461 standard; cDNA; 870 BP.
DE Novel human secreted and transmembrane protein PRO842 cDNA.
PN US2003166848-A1.
PD 04-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 12; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 614
ID ADH06255 standard; cDNA; 870 BP.
DE Novel human secreted and transmembrane protein PRO842 cDNA.
PN US2003180854-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 12; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 615
ID ADH30085 standard; cDNA; 870 BP.
DE Novel human secreted and transmembrane protein PRO842 cDNA.
PN US2003180856-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 12; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 616
ID ADH24397 standard; cDNA; 870 BP.
DE Novel human secreted and transmembrane protein PRO842 cDNA.
PN US2003180910-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 12; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 617
ID ADH33038 standard; cDNA; 870 BP.
DE Human PRO polynucleotide #70.

PN US2003068768-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 12; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 618
ID ADG69526 standard; cDNA; 870 BP.
DE Novel human secreted and transmembrane protein PRO842 cDNA.
PN US2003180844-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 12; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 619
ID ADH07789 standard; cDNA; 870 BP.
DE Novel human secreted and transmembrane protein PRO842 cDNA.
PN US2003180851-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 12; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 620
ID ADG85801 standard; cDNA; 870 BP.
DE Novel human secreted and transmembrane protein PRO842 cDNA.
PN US2003180861-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 12; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 621
ID ADH39347 standard; cDNA; 870 BP.
DE Novel human secreted and transmembrane protein PRO842 cDNA.
PN US2003180916-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 12; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 622
ID ADH33539 standard; cDNA; 870 BP.
DE Human PRO polynucleotide #13.
PN US2003181637-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 12; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 623
ID ADH33879 standard; cDNA; 870 BP.
DE Human PRO polynucleotide #13.
PN US2003181644-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 12; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 624
ID ADH01089 standard; cDNA; 870 BP.
DE Human PRO polynucleotide #13.
PN US2003180838-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 12; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 625
ID ADG49696 standard; cDNA; 870 BP.
DE Novel human secreted and transmembrane protein PRO842 cDNA.
PN US2003180843-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 870; DB 12; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 626
ID ADH20903 standard; cDNA; 870 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO842.
PN US2003224358-A1.


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PD 04-DEC-2003.
Query Match 100.0%; Score 870; DB 12; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 627
ID ADH02182 standard; cDNA; 870 BP.
DE Human PRO polynucleotide #13.
PN US2003180841-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 870; DB 12; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 628
ID ADG69186 standard; cDNA; 870 BP.
DE Novel human secreted and transmembrane protein PRO842 cDNA.
PN US2003180847-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 870; DB 12; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 629
ID ADG85971 standard; cDNA; 870 BP.
DE Novel human secreted and transmembrane protein PRO842 cDNA.
PN US2003180862-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 870; DB 12; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 630
ID ADH24907 standard; cDNA; 870 BP.
DE Novel human secreted and transmembrane protein PRO842 cDNA.
PN US2003180909-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 870; DB 12; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 631
ID ADH39524 standard; cDNA; 870 BP.
DE Novel human secreted and transmembrane protein PRO842 cDNA.
PN US2003180915-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 870; DB 12; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 632
ID ADH19943 standard; cDNA; 870 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO842.
PN US2003219856-A1.
PD 27-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 870; DB 12; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 633
ID ADH02522 standard; cDNA; 870 BP.
DE Human PRO polynucleotide #13.
PN US2003180840-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 870; DB 12; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 634
ID ADG69016 standard; cDNA; 870 BP.
DE Novel human secreted and transmembrane protein PRO842 cDNA.
PN US2003180849-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 870; DB 12; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 635
ID ADH07619 standard; cDNA; 870 BP.
DE Novel human secreted and transmembrane protein PRO842 cDNA.
PN US2003180850-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 870; DB 12; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 636
ID ADG86141 standard; cDNA; 870 BP.
DE Novel human secreted and transmembrane protein PRO842 cDNA.
PN US2003180863-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 870; DB 12; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 637
ID ADH24737 standard; cDNA; 870 BP.
DE Novel human secreted and transmembrane protein PRO842 cDNA.
PN US2003180908-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 870; DB 12; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 638
ID ADH25785 standard; cDNA; 870 BP.
DE Novel human secreted and transmembrane protein PRO842 cDNA.
PN US2003180911-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 870; DB 12; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 639
ID ADH38351 standard; cDNA; 870 BP.
DE Novel human secreted and transmembrane protein PRO842 cDNA.
PN US2003180922-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 870; DB 12; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 640
ID ADH57190 standard; cDNA; 870 BP.
DE Novel human secreted and transmembrane protein PRO842 cDNA.
PN US2003181642-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 870; DB 12; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 641
ID ADH52178 standard; cDNA; 870 BP.
DE Novel human secreted and transmembrane protein PRO842 cDNA.
PN US2003180921-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 870; DB 12; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 642
ID ADH49544 standard; cDNA; 870 BP.
DE Novel human secreted and transmembrane protein PRO842 cDNA.
PN US2003180857-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 870; DB 12; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 643
ID ADH90506 standard; cDNA; 870 BP.
DE Novel human secreted and transmembrane protein PRO842 cDNA.
PN US2003181700-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 870; DB 12; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 644
ID ADI11442 standard; cDNA; 870 BP.
DE Human PRO polynucleotide #13.
PN US2003181683-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 870; DB 12; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
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Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 645
ID ADJ98907 standard; cDNA; 870 BP.
DE Novel human secreted and transmembrane protein PRO842 cDNA.
PN US2003190698-A1.
PD 09-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 870; DB 12; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 646
ID ADJ02137 standard; cDNA; 870 BP.
DE Novel human secreted and transmembrane protein PRO842 cDNA.
PN US2003190699-A1.
PD 09-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 870; DB 12; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 647
ID ADJ90676 standard; cDNA; 870 BP.
DE Novel human secreted and transmembrane protein PRO842 cDNA.
PN US2003181701-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 870; DB 12; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 648
ID ADJ54777 standard; cDNA; 870 BP.
DE Human PRO polynucleotide #70.
PN US2004023321-A1.
PD 05-FEB-2004.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 870; DB 12; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 649
ID ADJ98551 standard; cDNA; 870 BP.
DE Novel human secreted and transmembrane protein PRO842 cDNA.
PN US2003187197-A1.
PD 02-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 870; DB 12; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 650
ID ADJ98721 standard; cDNA; 870 BP.
DE Novel human secreted and transmembrane protein PRO842 cDNA.
PN US2003187228-A1.
PD 02-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 870; DB 12; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 651
ID ADJ78880 standard; cDNA; 870 BP.
DE Novel human secreted and transmembrane protein PRO842 cDNA.
PN US2003181703-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 870; DB 12; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 652
ID ADJ99114 standard; cDNA; 870 BP.
DE Novel human secreted and transmembrane protein PRO842 cDNA.
PN US2003186408-A1.
PD 02-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 870; DB 12; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 653
ID ADJ93284 standard; cDNA; 870 BP.
DE Novel human secreted and transmembrane protein PRO842 cDNA.
PN US2003187196-A1.
PD 02-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 870; DB 12; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 654
ID ADJ98902 standard; cDNA; 870 BP.
DE Novel human secreted and transmembrane protein PRO842 cDNA.
PN US2003187242-A1.
PD 02-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 870; DB 12; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 655
ID ADJ79050 standard; cDNA; 870 BP.
DE Novel human secreted and transmembrane protein PRO842 cDNA.
PN US2003181702-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 870; DB 12; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 656
ID ADK00910 standard; cDNA; 870 BP.
DE Human PRO polynucleotide #13.
PN US2003186407-A1.
PD 02-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 870; DB 12; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 657
ID ADK14431 standard; cDNA; 870 BP.
DE Novel human secreted and transmembrane protein PRO842 cDNA.
PN US2003187229-A1.
PD 02-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 870; DB 12; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 658
ID ADJ64548 standard; cDNA; 870 BP.
DE Human PRO polynucleotide #70.
PN US2004038337-A1.
PD 26-FEB-2004.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 870; DB 12; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 659
ID ADM31444 standard; cDNA; 870 BP.
DE Novel human secreted and transmembrane protein PRO842 cDNA.
PN US2004048334-A1.
PD 11-MAR-2004.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 870; DB 12; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 660
ID ADM36491 standard; cDNA; 870 BP.
DE Novel human secreted and transmembrane protein PRO842 cDNA.
PN US2004053358-A1.
PD 18-MAR-2004.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 870; DB 12; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 661
ID ADM40296 standard; cDNA; 870 BP.
DE Novel human secreted and transmembrane protein PRO842 cDNA.
PN US2004048335-A1.
PD 11-MAR-2004.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 870; DB 12; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 662
ID ADM80880 standard; cDNA; 870 BP.
DE Human PRO polynucleotide #13.
PN US2004058411-A1.
PD 25-MAR-2004.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 870; DB 12; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 663
ID ADM80880 standard; cDNA; 870 BP.
DE Human PRO polynucleotide #13.
PN US2004058411-A1.
PD 25-MAR-2004.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 870; DB 12; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
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ID ADN37904 standard; cDNA; 870 BP.
DE Novel human secreted and transmembrane protein PRO842 cDNA.
PN US2004091959-A1.
PD 13-MAY-2004.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 870; DB 12; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 664
ID ADY77720 standard; cDNA; 870 BP.
DE Neoplastic disease detection cDNA PRO842.
PN US2005059102-A1.
PD 17-MAR-2005.
PA (EATO/) EATON D L.
PA (FILV/) FILVAROFF E.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GRIM/) GRIMALDI J C.
PA (GURN/) GURNEY A L.
PA (WATA/) WATANABE C K.
PA (WOOD/) WOOD W I.
Query Match 100.0%; Score 870; DB 14; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 665
ID AD245056 standard; cDNA; 870 BP.
DE Human PRO842 encoding cDNA SEQ ID NO:1.
PN US2005100544-A1.
PD 12-MAY-2005.
PA (EATO/) EATON D L.
PA (PISA/) PISABARRO M T.
PA (SCHN/) SCHMIDT K N.
PA (VAND/) VANDLEN R.
PA (CHIA/) CHIANG N.
PA (DIEH/) DIEHL L.
Query Match 100.0%; Score 870; DB 14; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 666
ID AEA38433 standard; cDNA; 870 BP.
DE Human secreted/transmembrane protein cDNA, #107.
PN US2005112725-A1.
PD 26-MAY-2005.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 870; DB 14; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 667
ID AED50134 standard; cDNA; 870 BP.
DE Novel human secreted and transmembrane protein PRO842 cDNA.
PN US2005163766-A1.
PD 28-JUL-2005.
Query Match 100.0%; Score 870; DB 14; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 668
ID AEF12551 standard; cDNA; 870 BP.
DE Human PRO842 cDNA SEQ ID NO:25.
PN US2006008901-A1.
PD 12-JAN-2006.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 870; DB 15; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 669
ID AEF74240 standard; cDNA; 870 BP.
DE Human PRO842 encoding cDNA SEQ ID NO:25.
PN US2005260647-A1.
PD 24-NOV-2005.
PA (FILV/) FILVAROFF E.
PA (EATO/) EATON D L.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GRIM/) GRIMALDI J C.
PA (GURN/) GURNEY A L.
PA (WATA/) WATANABE C K.
PA (WOOD/) WOOD W L.
Query Match 100.0%; Score 870; DB 15; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 670
ID ACD27900 standard; cDNA; 868 BP.
DE cDNA encoding human PRO842 polypeptide.
PN US2003065154-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 99.8%; Score 868; DB 9; Length 868;
Best Local Similarity 100.0%; Pred. No. 1.5e-228;
RESULT 671
ID AAZ98202 standard; cDNA; 870 BP.
DE Human signal peptide containing protein HSPP-94 cDNA SEQ ID NO:228.
PN WO200000610-A2.
PD 06-JAN-2000.
PA (INCY-) INCYTE PHARM INC.
Query Match 99.1%; Score 862.4; DB 3; Length 870;
Best Local Similarity 99.9%; Pred. No. 5.3e-227;
RESULT 672
ID ADQ86898 standard; cDNA; 1118 BP.
DE Human tumour-associated antigenic target (TAT) cDNA sequence #3773.
PN WO2004060270-A2.
PD 22-JUL-2004.
PA (GETH ) GENENTECH INC.
PA (WUTD/) WU T D.
PA (ZHOU/) ZHOU Y.
Query Match 98.5%; Score 856.6; DB 12; Length 1118;
Best Local Similarity 99.5%; Pred. No. 2.4e-225;
RESULT 673
ID AAH7951 standard; DNA; 1171 BP.
DE Nucleotide sequence of a human Lng104 polypeptide.
PN WO200161055-A2.
PD 23-AUG-2001.
PA (DIAD-) DIADEXUS INC.
Query Match 98.5%; Score 856.6; DB 4; Length 1171;
Best Local Similarity 99.5%; Pred. No. 2.4e-225;
RESULT 674
ID ADE39934 standard; cDNA; 1171 BP.
DE Human lung disorder-related cDNA - SEQ ID 4.
PN US2003124580-A1.
PD 03-JUL-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 98.5%; Score 856.6; DB 10; Length 1171;
Best Local Similarity 99.5%; Pred. No. 2.4e-225;
RESULT 675
ID ACF58050 standard; cDNA; 1172 BP.
DE Human VCC-1 polypeptide encoding cDNA.
PN WO2003087157-A2.
PD 23-OCT-2003.
PA (PHAA ) PHARMACIA CORP.
Query Match 98.5%; Score 856.6; DB 10; Length 1172;
Best Local Similarity 99.5%; Pred. No. 2.4e-225;
RESULT 676
ID ADL01574 standard; DNA; 1172 BP.
DE Human VEGF co-regulated chemokine-1 (VCC-1) DNA.
PN WO2004016224-A2.
PD 26-FEB-2004.
PA (PHAA ) PHARMACIA CORP.
Query Match 98.5%; Score 856.6; DB 12; Length 1172;
Best Local Similarity 99.5%; Pred. No. 2.4e-225;
RESULT 677
ID ADP07625 standard; DNA; 1214 BP.
DE Human secreted protein encoding DNA, seq id 108.
PN WO2004042000-A2.
PD 21-MAY-2004.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 98.5%; Score 856.6; DB 12; Length 1214;
Best Local Similarity 99.5%; Pred. No. 2.4e-225;
RESULT 678
ID ABA09257 standard; cDNA; 1148 BP.
DE Human TGC-440 homologue-encoding cDNA, SEQ ID NO:1033.
PN WO200157188-A2.
PD 09-AUG-2001.
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PA (HYSE-) HYSEQ INC.
Query Match 98.3%; Score 855; DB 4; Length 1148;
Best Local Similarity 99.4%; Pred. No. 6.6e-225;
RESULT 679
ID AA239726 standard; DNA; 895 BP.
DE Human lung specific gene-3.
PN WO9960160-A1.
PD 25-NOV-1999.
PA (DIAD-) DIADEXUS LLC.
Query Match 97.9%; Score 852; DB 3; Length 895;
Best Local Similarity 100.0%; Pred. No. 3.9e-224;
RESULT 680
ID AAH77949 standard; DNA; 895 BP.
DE Nucleotide sequence of a human Lng104 polypeptide.
PN WO200161055-A2.
PD 23-AUG-2001.
PA (DIAD-) DIADEXUS INC.
Query Match 97.9%; Score 852; DB 4; Length 895;
Best Local Similarity 100.0%; Pred. No. 3.9e-224;
RESULT 681
ID ADK70291 standard; cDNA; 856 BP.
DE Respiratory disease differentially expressed cDNA #27.
PN WO2003101283-A2.
PD 11-DEC-2003.
PA (INCY-) INCYTE CORP.
Query Match 97.7%; Score 850; DB 12; Length 856;
Best Local Similarity 100.0%; Pred. No. 1.4e-223;
RESULT 682
ID ADY30447 standard; DNA; 1131 BP.
DE Human splice variant DNA expressed in ovary cells DEX0487_006.nt.1.
PN WO2005017102-A2.
PD 24-FEB-2005.
PA (DIAD-) DIADEXUS INC.
Query Match 92.2%; Score 802.2; DB 14; Length 1131;
Best Local Similarity 97.8%; Pred. No. 2.3e-210;
RESULT 683
ID ADY30448 standard; DNA; 1111 BP.
DE Human splice variant DNA expressed in ovary cells DEX0487_006.nt.2.
PN WO2005017102-A2.
PD 24-FEB-2005.
PA (DIAD-) DIADEXUS INC.
Query Match 89.3%; Score 777; DB 14; Length 1111;
Best Local Similarity 99.4%; Pred. No. 2e-203;
RESULT 684
ID ADP07697 standard; DNA; 750 BP.
DE Human secreted protein encoding DNA, seq id 180.
PN WO2004042000-A2.
PD 21-MAY-2004.
PA (HUNA-) HUMAN GENOME SCI INC.
Query Match 81.4%; Score 708.6; DB 12; Length 750;
Best Local Similarity 99.4%; Pred. No. 1.2e-184;
RESULT 685
ID AAA08343 standard; DNA; 849 BP.
DE Human TGC-440 secretory protein nucleotide sequence.
PN WO200014226-A1.
PD 16-MAR-2000.
PA (TAXE) TAKEDA CHEM IND LTD.
Query Match 77.1%; Score 670.8; DB 3; Length 849;
Best Local Similarity 89.1%; Pred. No. 3.4e-174;
RESULT 686
ID ADT50719 standard; DNA; 972 BP.
DE Cancer related nucleic acid sequence #23.
PN WO2004092338-A2.
PD 28-OCT-2004.
PA (DIAD-) DIADEXUS INC.
Query Match 73.3%; Score 637.6; DB 13; Length 972;
Best Local Similarity 99.1%; Pred. No. 5.1e-165;
RESULT 687
ID AAC59829 standard; DNA; 654 BP.
DE Human secreted protein encoding DNA clone vq8 1.
PN WO200055375-A1.
PD 21-SEP-2000.
PA (ALPH-) ALPHAGEN INC.

Query Match 72.4%; Score 630; DB 3; Length 654;
Best Local Similarity 100.0%; Pred. No. 5.3e-163;
RESULT 688
ID ADT50720 standard; DNA; 942 BP.
DE Cancer related nucleic acid sequence #24.
PN WO2004092338-A2.
PD 28-OCT-2004.
PA (DIAD-) DIADEXUS INC.
Query Match 71.9%; Score 625.6; DB 13; Length 942;
Best Local Similarity 99.4%; Pred. No. 1e-161;
RESULT 689
ID ADT50721 standard; DNA; 877 BP.
DE Cancer related nucleic acid sequence #25.
PN WO2004092338-A2.
PD 28-OCT-2004.
PA (DIAD-) DIADEXUS INC.
Query Match 65.5%; Score 570; DB 13; Length 877;
Best Local Similarity 97.4%; Pred. No. 2.1e-146;
RESULT 690
ID AAF68195 standard; cDNA; 533 BP.
DE Human lung tumour protein related nucleotide sequence SEQ ID NO:113.
PN WO200100828-A2.
PD 04-JAN-2001.
PA (CORI-) CORIXA CORP.
Query Match 60.4%; Score 525.8; DB 5; Length 533;
Best Local Similarity 99.6%; Pred. No. 2.5e-134;
RESULT 691
ID ABK38106 standard; cDNA; 533 BP.
DE cDNA encoding clone #18471 of lung tumour protein.
PN WO200204514-A2.
PD 17-JAN-2002.
PA (CORI-) CORIXA CORP.
Query Match 60.4%; Score 525.8; DB 6; Length 533;
Best Local Similarity 99.6%; Pred. No. 2.5e-134;
RESULT 692
ID ACA10435 standard; cDNA; 533 BP.
DE Human lung cancer-associated cDNA, SEQ ID 113.
PN US2002197669-A1.
PD 26-DEC-2002.
PA (BANG/) BANGUR C S.
PA (FANG/) FANGER G R.
PA (WANG/) WANG A.
PA (SWIT/) SWITZER A P.
PA (MCNE/) MCNEILL P D.
PA (CLAP/) CLAPPER J D.
Query Match 60.4%; Score 525.8; DB 8; Length 533;
Best Local Similarity 99.6%; Pred. No. 2.5e-134;
RESULT 693
ID ABX99386 standard; cDNA; 533 BP.
DE Lung cancer therapy and diagnosis associated cDNA #113.
PN US2002172952-A1.
PD 21-NOV-2002.
PA (CORI-) CORIXA CORP.
Query Match 60.4%; Score 525.8; DB 8; Length 533;
Best Local Similarity 99.6%; Pred. No. 2.5e-134;
RESULT 694
ID ADH45632 standard; cDNA; 533 BP.
DE Human lung tumour cDNA clone, SEQ ID No 113.
PN WO2003037267-A2.
PD 08-MAY-2003.
PA (CORI-) CORIXA CORP.
Query Match 60.4%; Score 525.8; DB 10; Length 533;
Best Local Similarity 99.6%; Pred. No. 2.5e-134;
RESULT 695
ID ADE72169 standard; cDNA; 533 BP.
DE Human lung tumour protein cDNA #113.
PN US2003125245-A1.
PD 03-JUL-2003.
PA (WANG/) WANG T.
PA (BANG/) BANGUR C S.
Query Match 60.4%; Score 525.8; DB 12; Length 533;
Best Local Similarity 99.6%; Pred. No. 2.5e-134;

RESULT 696
ID ADJ19551 standard; cDNA; 533 BP.
DE Human lung cancer-related cDNA - SEQ ID 113.
PN US2003211510-A1.
PD 13-NOV-2003.
PA (CORI-) CORIXA CORP.
Query Match 60.4%; Score 525.8; DB 13; Length 533;
Best Local Similarity 99.6%; Pred. No. 2.5e-134;
RESULT 697
ID ADP07674 standard; DNA; 569 BP.
DE Human secreted protein encoding DNA, seq id 157.
PN WO2004042000-A2.
PD 21-MAY-2004.
PA (HUNA-) HUMAN GENOME SCI INC.
Query Match 59.7%; Score 519; DB 12; Length 569;
Best Local Similarity 100.0%; Pred. No. 1.9e-132;
RESULT 698
ID ADM67834 standard; DNA; 569 BP.
DE Human secreted protein encoding DNA, seq id 81.
PN WO2004042000-A2.
PD 21-MAY-2004.
PA (HUNA-) HUMAN GENOME SCI INC.
Query Match 59.7%; Score 519; DB 13; Length 569;
Best Local Similarity 100.0%; Pred. No. 1.9e-132;
RESULT 699
ID ADP07670 standard; DNA; 573 BP.
DE Human secreted protein encoding DNA, seq id 153.
PN WO2004042000-A2.
PD 21-MAY-2004.
PA (HUNA-) HUMAN GENOME SCI INC.
Query Match 59.7%; Score 519; DB 12; Length 573;
Best Local Similarity 100.0%; Pred. No. 2e-132;
RESULT 700
ID ADP07619 standard; DNA; 569 BP.
DE Human secreted protein encoding DNA, seq id 102.
PN WO2004042000-A2.
PD 21-MAY-2004.
PA (HUNA-) HUMAN GENOME SCI INC.
Query Match 59.6%; Score 518.2; DB 12; Length 569;
Best Local Similarity 99.6%; Pred. No. 3.2e-132;
RESULT 701
ID ACF58052 standard; DNA; 524 BP.
DE Human VCC-1 expressed sequence tag (EST) fragment.
PN WO2003087157-A2.
PD 23-OCT-2003.
PA (PHAA) PHARMACIA CORP.
Query Match 51.4%; Score 447.2; DB 10; Length 524;
Best Local Similarity 97.7%; Pred. No. 1.2e-112;
RESULT 702
ID ABK87217 standard; DNA; 30709 BP.
DE Human lipase, hormone-sensitive (LHPE) gene sequence.
Query Match 50.9%; Score 443; DB 6; Length 30709;
Best Local Similarity 98.9%; Pred. No. 1e-110;
RESULT 703
ID ABL64634 standard; DNA; 419 BP.
DE Stomach cancer related gene sequence SEQ ID NO:2971.
PN WO200194629-A2.
PD 13-DEC-2001.
PA (AVAL-) AVALON PHARM.
Query Match 47.8%; Score 415.8; DB 6; Length 419;
Best Local Similarity 99.5%; Pred. No. 4.7e-104;
RESULT 704
ID AAV69618 standard; DNA; 511 BP.
DE Human secreted protein gene 8 clone HLHCM89.
PN WO9845712-A2.
PD 15-OCT-1998.
PA (HUNA-) HUMAN GENOME SCI INC.
Query Match 46.2%; Score 402.2; DB 2; Length 511;
Best Local Similarity 97.7%; Pred. No. 2.9e-100;
RESULT 705
ID AAX40454 standard; cDNA; 365 BP.
DE Human secreted protein 5' EST SEQ ID NO: 54.
PN WO9906550-A2.
PD 13-NOV-2003.
PA (CORI-) CORIXA CORP.
Query Match 35.9%; Score 312; DB 12; Length 312;
Best Local Similarity 100.0%; Pred. No. 1.7e-75;
RESULT 706
ID AAA08344 standard; DNA; 357 BP.
DE Human TGC-440 secretory protein nucleotide sequence SEQ ID NO:4.
PN WO200014226-A1.
PD 16-MAR-2000.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 41.0%; Score 357; DB 3; Length 357;
Best Local Similarity 100.0%; Pred. No. 7.1e-88;
RESULT 707
ID AAF68125 standard; cDNA; 312 BP.
DE Human lung tumour protein related nucleotide sequence SEQ ID NO:43.
PN WO200100828-A2.
PD 04-JAN-2001.
PA (CORI-) CORIXA CORP.
Query Match 35.9%; Score 312; DB 5; Length 312;
Best Local Similarity 100.0%; Pred. No. 1.7e-75;
RESULT 708
ID ABK38036 standard; cDNA; 312 BP.
DE cDNA encoding clone #18950 of lung tumour protein.
PN WO200204514-A2.
PD 17-JAN-2002.
PA (CORI-) CORIXA CORP.
Query Match 35.9%; Score 312; DB 6; Length 312;
Best Local Similarity 100.0%; Pred. No. 1.7e-75;
RESULT 709
ID ACA10365 standard; cDNA; 312 BP.
DE Human lung cancer-associated cDNA, SEQ ID 43.
PN US2002197669-A1.
PD 26-DEC-2002.
PA (BANG/) BANGUR C S.
PA (FANG/) FANGER G R.
PA (WANG/) WANG A.
PA (WANG/) WANG T.
PA (SWIT/) SWITZER A P.
PA (MCNE/) MCNEILL P D.
PA (CLAP/) CLAPPER J D.
Query Match 35.9%; Score 312; DB 8; Length 312;
Best Local Similarity 100.0%; Pred. No. 1.7e-75;
RESULT 710
ID ABX99316 standard; cDNA; 312 BP.
DE Lung cancer therapyand diagnosis associated cDNA #43.
PN US2002172952-A1.
PD 21-NOV-2002.
PA (CORI-) CORIXA CORP.
Query Match 35.9%; Score 312; DB 8; Length 312;
Best Local Similarity 100.0%; Pred. No. 1.7e-75;
RESULT 711
ID ADH45562 standard; cDNA; 312 BP.
DE Human lung tumour cDNA clone, SEQ ID No 43.
PN WO2003037267-A2.
PD 08-MAY-2003.
PA (CORI-) CORIXA CORP.
Query Match 35.9%; Score 312; DB 10; Length 312;
Best Local Similarity 100.0%; Pred. No. 1.7e-75;
RESULT 712
ID ADE72099 standard; cDNA; 312 BP.
DE Human lung tumour protein cDNA #43.
PN US2003125245-A1.
PD 03-JUL-2003.
PA (WANG/) WANG T.
PA (BANG/) BANGUR C S.
Query Match 35.9%; Score 312; DB 12; Length 312;
Best Local Similarity 100.0%; Pred. No. 1.7e-75;
RESULT 713
ID ADJ19481 standard; cDNA; 312 BP.
DE Human lung cancer-related cDNA - SEQ ID 43.
PN US2003211510-A1.
PD 13-NOV-2003.
PA (CORI-) CORIXA CORP.

Query Match
Best Local Similarity 35.9%; Score 312; DB 13; Length 312;
RESULT 714
ID ARA08345 standard; DNA; 291 BP.
DE Mature human TGC-440 secretory protein nucleotide sequence SEQ ID NO:10.
PN WO200014226-A1.
PD 16-MAR-2000.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match
Best Local Similarity 100.0%; Score 291; DB 3; Length 291;
RESULT 715
ID AAA08349 standard; DNA; 764 BP.
DE Mouse TGC-440 secretory protein nucleotide sequence.
PN WO200014226-A1.
PD 16-MAR-2000.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match
Best Local Similarity 30.1%; Score 262.2; DB 3; Length 764;
RESULT 716
ID ACF58051 standard; cDNA; 829 BP.
DE Mouse VCC-1 polypeptide encoding cDNA.
PN WO2003087157-A2.
PD 23-OCT-2003.
PA (PHAA) PHARMACIA CORP.
Query Match
Best Local Similarity 30.1%; Score 261.8; DB 10; Length 829;
RESULT 717
ID AAA08350 standard; DNA; 357 BP.
DE Mouse TGC-440 secretory protein nucleotide sequence SEQ ID NO:6.
PN WO200014226-A1.
PD 16-MAR-2000.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match
Best Local Similarity 28.2%; Score 245.6; DB 3; Length 357;
RESULT 718
ID AAA08346 standard; DNA; 959 BP.
DE Rat TGC-440 secretory protein nucleotide sequence.
PN WO200014226-A1.
PD 16-MAR-2000.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match
Best Local Similarity 73.1%; Score 241.8; DB 3; Length 959;
RESULT 719
ID ABL82746 standard; cDNA; 242 BP.
DE Human ovarian cancer related cDNA clone SEQ ID NO:5724.
PN WO200192581-A2.
PD 06-DEC-2001.
PA (CORI-) CORIXA CORP.
Query Match
Best Local Similarity 100.0%; Score 238; DB 6; Length 242;
RESULT 720
ID ABL22573 standard; DNA; 553 BP.
DE Breast cancer marker gene SEQ ID NO 946.
PN WO200285298-A2.
PD 31-OCT-2002.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match
Best Local Similarity 26.6%; Score 231.8; DB 10; Length 553;
RESULT 721
ID AAX40453 standard; cDNA; 235 BP.
DE Human secreted protein 5' EST SEQ ID NO: 53.
PN WO9906550-A2.
PD 11-FEB-1999.
PA (GEST) GENSET.
Query Match
Best Local Similarity 26.3%; Score 228.4; DB 2; Length 235;
RESULT 722
ID AAA08347 standard; DNA; 357 BP.
DE Rat TGC-440 secretory protein nucleotide sequence SEQ ID NO:5.
PN WO200014226-A1.
PD 16-MAR-2000.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match
Best Local Similarity 26.2%; Score 228; DB 3; Length 357;

Best Local Similarity 77.5%; Pred. No. 2.5e-52;
RESULT 723
ID ADL84236 standard; DNA; 403 BP.
DE DNA up-regulated in murine common lymphoid progenitor cells SeqID 629.
PN WO2003093445-A2.
PD 13-NOV-2003.
PA (STOW-) STOWERS INST MEDICAL RES.
Query Match
Best Local Similarity 74.0%; Score 218; DB 12; Length 403;
RESULT 724
ID ADL84235 standard; DNA; 403 BP.
DE DNA up-regulated in murine common lymphoid progenitor cells SeqID 628.
PN WO2003093445-A2.
PD 13-NOV-2003.
PA (STOW-) STOWERS INST MEDICAL RES.
Query Match
Best Local Similarity 25.1%; Score 218; DB 12; Length 403;
RESULT 725
ID ABT22609 standard; DNA; 357 BP.
DE Breast cancer marker gene SEQ ID NO 982.
PN WO200285298-A2.
PD 31-OCT-2002.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match
Best Local Similarity 23.4%; Score 203.2; DB 10; Length 357;
RESULT 726
ID AAA08351 standard; DNA; 291 BP.
DE Mature mouse TGC-440 secretory protein nucleotide sequence SEQ ID NO:12.
PN WO200014226-A1.
PD 16-MAR-2000.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match
Best Local Similarity 23.0%; Score 200.4; DB 3; Length 291;
RESULT 727
ID AAT25820 standard; cDNA to mRNA; 195 BP.
DE Human gene signature HUMGS08049.
PN WO9514772-A1.
PD 01-JUN-1995.
PA (MATS/) MATSUBARA K.
PA (OKUB/) OKUBO K.
Query Match
Best Local Similarity 22.1%; Score 192; DB 2; Length 195;
RESULT 728
ID AAA08348 standard; DNA; 291 BP.
DE Mature rat TGC-440 secretory protein nucleotide sequence SEQ ID NO:11.
PN WO200014226-A1.
PD 16-MAR-2000.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match
Best Local Similarity 21.7%; Score 189.2; DB 3; Length 291;
RESULT 729
ID AED3177 standard; DNA; 81 BP.
DE Contig 510 amplicon.
PN WO2005100606-A2.
PD 27-OCT-2005.
PA (GENO-) GENOMIC HEALTH INC.
Query Match
Best Local Similarity 9.3%; Score 81; DB 14; Length 81;
RESULT 730
ID AAS07713 standard; DNA; 97 BP.
DE Cervical cancer pre-malignant condition DNA marker #12.
PN WO200142792-A2.
PD 14-JUN-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match
Best Local Similarity 8.4%; Score 73.4; DB 4; Length 97;
RESULT 731
ID AAH70020 standard; cDNA; 518 BP.
DE Human cervical cancer marker nucleic acid 1294.
PN WO200142467-A2.
PD 14-JUN-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match
Best Local Similarity 5.3%; Score 45.8; DB 4; Length 518;

Best Local Similarity 74.3%; Pred. No. 0.05;

RESULT 732 ID AAA08356 standard; DNA; 51 BP.

DE Human TGC-440 secretory protein PCR primer SEQ ID NO:17.

PN WO200014226-A1.

PD 16-MAR-2000.

PA (TAKE) TAKEDA CHEM IND LTD.

Query Match 5.1%; Score 44.6; DB 3; Length 51;

Best Local Similarity 92.2%; Pred. No. 0.037;

RESULT 733

ID AAF23906 standard; cDNA; 1484 BP.

DE Human secreted protein cDNA #13.

PN WO20007173-A1.

PD 21-DEC-2000.

PA (HUMA-) HUMAN GENOME SCI INC.

Query Match 5.0%; Score 43.8; DB 4; Length 1484;

Best Local Similarity 62.2%; Pred. No. 0.28;

RESULT 734

ID ABD33526 standard; DNA; 31312 BP.

DE Murine cancer-associated (CA) gene MD07-104.

PN WO2004058146-A2.

PD 15-JUL-2004.

PA (SAGR-) SAGRES DISCOVERY INC.

Query Match 5.0%; Score 43.2; DB 13; Length 31312;

Best Local Similarity 51.6%; Pred. No. 1.7;

RESULT 735

ID AAH71445 standard; cDNA; 456 BP.

DE Human cervical cancer marker nucleic acid 2719.

PN WO200142467-A2.

PD 14-JUN-2001.

PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.

Query Match 4.9%; Score 42.8; DB 4; Length 456;

Best Local Similarity 86.8%; Pred. No. 0.31;

RESULT 736

ID ACN55539 standard; cDNA; 526 BP.

DE Cotton androecium tissue EST Clone ID: LIB3828-025-Q6-N6-B7, SEQ:10320.

PN US2004123340-A1.

PD 24-JUN-2004.

PA (DEIK/) DEIKMAN J.

PA (FENG/) FENG P C C.

PA (FINC/) FINCHER K L.

PA (ZIEG/) ZIEGLER T E.

Query Match 4.9%; Score 42.4; DB 13; Length 526;

Best Local Similarity 49.5%; Pred. No. 0.43;

RESULT 737

ID ADA71938 standard; DNA; 2000 BP.

DE Rice gene, SEQ ID 5263.

PN WO2003000898-A1.

PD 03-JAN-2003.

PA (SYGN) SYNGENTA PARTICIPATIONS AG.

Query Match 4.8%; Score 42; DB 8; Length 2000;

Best Local Similarity 9.2%; Pred. No. 1;

RESULT 738

ID ACN91732 standard; DNA; 631 BP.

DE Breast cancer related marker, seq id 2882.

PN US2003099974-A1.

PD 29-MAY-2003.

PA (MILL-) MILLENNIUM PHARM INC.

Query Match 4.8%; Score 41.8; DB 11; Length 631;

Best Local Similarity 41.4%; Pred. No. 0.69;

RESULT 739

ID ABQ74348 standard; DNA; 27359 BP.

DE Human transporter protein encoding gene SEQ ID NO:3.

PN US2004123340-A1.

PD 24-JUN-2004.

PA (DEIK/) DEIKMAN J.

PA (FENG/) FENG P C C.

PA (FINC/) FINCHER K L.

PA (ZIEG/) ZIEGLER T E.

Query Match 4.8%; Score 41.6; DB 13; Length 428;

Best Local Similarity 48.3%; Pred. No. 0.65;

RESULT 741

ID ADR63959 standard; cDNA; 574 BP.

DE Cotton cDNA sequence, SEQ ID 4740.

PN US2004181830-A1.

PD 16-SEP-2004.

PA (KOVA/) KOVALIC D K.

PA (ZHOU/) ZHOU Y.

PA (CAOY/) CAO Y.

Query Match 4.8%; Score 41.6; DB 13; Length 574;

Best Local Similarity 62.5%; Pred. No. 0.75;

RESULT 742

ID AD169792 standard; DNA; 384 BP.

DE Human ovarian cancer DNA marker #2534.

PN WO200170979-A2.

PD 27-SEP-2001.

PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.

Query Match 4.8%; Score 41.4; DB 5; Length 384;

Best Local Similarity 43.8%; Pred. No. 0.71;

RESULT 743

ID AD176128 standard; DNA; 384 BP.

DE Human ovarian cancer DNA marker #8870.

PN WO200170979-A2.

PD 27-SEP-2001.

PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.

Query Match 4.8%; Score 41.4; DB 5; Length 384;

Best Local Similarity 43.8%; Pred. No. 0.71;

RESULT 744

ID ACN53688 standard; cDNA; 421 BP.

DE Cotton androecium tissue EST Clone ID: LIB3828-010-Q1-K6-E3, SEQ:8469.

PN US2004123340-A1.

PD 24-JUN-2004.

PA (DEIK/) DEIKMAN J.

PA (FENG/) FENG P C C.

PA (FINC/) FINCHER K L.

PA (ZIEG/) ZIEGLER T E.

Query Match 4.7%; Score 40.8; DB 13; Length 421;

Best Local Similarity 48.3%; Pred. No. 1.1;

RESULT 745

ID ACN55836 standard; cDNA; 509 BP.

DE Cotton androecium tissue EST Clone ID: LIB3828-029-Q6-N6-B5, SEQ:10617.

PN US2004123340-A1.

PD 24-JUN-2004.

PA (DEIK/) DEIKMAN J.

PA (FENG/) FENG P C C.

PA (FINC/) FINCHER K L.

PA (ZIEG/) ZIEGLER T E.

Query Match 4.7%; Score 40.8; DB 13; Length 509;

Best Local Similarity 49.1%; Pred. No. 1.2;

RESULT 746

ID ACN58719 standard; cDNA; 534 BP.

DE Cotton gynoecium tissue EST Clone ID: LIB3829-011-Q6-N6-B7, SEQ:13500.

PN US2004123340-A1.

PD 24-JUN-2004.

PA (DEIK/) DEIKMAN J.

PA (FENG/) FENG P C C.

PA (FINC/) FINCHER K L.

PA (ZIEG/) ZIEGLER T E.

Query Match 4.7%; Score 40.6; DB 13; Length 534;

Best Local Similarity 48.9%; Pred. No. 1.4;

RESULT 747

ID ADL62362 standard; DNA; 1588 BP.

DE Human ovarian cancer DNA marker #20574.

PN WO200170979-A2.

PD 27-SEP-2001.

PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.

Query Match 4.7%; Score 40.6; DB 5; Length 1588;

Best Local Similarity 58.8%; Pred. No. 2.2;

RESULT 748

ID ACN89723 standard; DNA; 2436 BP.

DE Breast cancer related marker, seq id 10873.

PN US2003099974-A1.
 PD 29-MAY-2003.
 PA (MILL-) MILLENNIUM PHARM INC.
 Query Match 4.7%; Score 40.6; DB 11; Length 2436;
 Best Local Similarity 58.8%; Pred. No. 2.7;
 RESULT 749
 ID ADF82105 standard; DNA; 2619 BP.
 DE Leukaemia-related DNA sequence #2661.
 PN WO2003039443-A2.
 PD 15-MAY-2003.
 PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
 PA (UYLU-) UNIV LUDWIG MAXIMILIANS.
 PA (HAFE/) HAFERLACH T.
 PA (SCHO/) SCHOCH C.
 PA (KERN/) KERN W.
 Query Match 4.7%; Score 40.6; DB 10; Length 2619;
 Best Local Similarity 58.8%; Pred. No. 2.8;
 RESULT 750
 ID AED14464 standard; DNA; 2619 BP.
 DE Human cumulus cell differentially expressed gene.
 PN WO2005094306-A2.
 PD 13-OCT-2005.
 PA (UNMS) UNIV MICHIGAN STATE.
 Query Match 4.7%; Score 40.6; DB 14; Length 2619;
 Best Local Similarity 58.8%; Pred. No. 2.8;
 RESULT 751
 ID ABL33011 standard; DNA; 6171 BP.
 DE Human immune system associated gene SEQ ID NO: 984.
 PN WO200200928-A2.
 PD 03-JAN-2002.
 PA (EPIG-) EPIGENOMICS AG.
 Query Match 4.6%; Score 40.4; DB 6; Length 6171;
 Best Local Similarity 46.2%; Pred. No. 4.7;
 RESULT 752
 ID ACN58276 standard; cDNA; 508 BP.
 DE Cotton gynoecium tissue EST Clone ID: LIB3829-008-Q6-N6-D10, SEQ:13057.
 PN US2004123340-A1.
 PD 24-JUN-2004.
 PA (DEIK/) DEIKMAN J.
 PA (FENG/) FENG P C C.
 PA (FINC/) FINCHER K L.
 PA (ZIEG/) ZIEGLER T E.
 Query Match 4.6%; Score 40.2; DB 13; Length 508;
 Best Local Similarity 49.8%; Pred. No. 1.7;
 RESULT 753
 ID ABT42211 standard; DNA; 1186 BP.
 DE Toxicity modelling related rat gene SEQ ID No 1913.
 PN WO200295000-A2.
 PD 28-NOV-2002.
 PA (GENE-) GENE LOGIC INC.
 Query Match 4.6%; Score 39.6; DB 10; Length 1186;
 Best Local Similarity 58.5%; Pred. No. 3.7;
 RESULT 754
 ID ADP72715 standard; DNA; 1186 BP.
 DE Renal toxin progression gene marker #1304.
 PN WO2004048598-A2.
 PD 10-JUN-2004.
 PA (GENE-) GENE LOGIC INC.
 Query Match 4.6%; Score 39.6; DB 12; Length 1186;
 Best Local Similarity 58.5%; Pred. No. 3.7;
 RESULT 755
 ID ABV55803 standard; cDNA; 428 BP.
 DE Human prostate expression marker cDNA 55794.
 PN WO200160860-A2.
 PD 23-AUG-2001.
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 Query Match 4.5%; Score 39.4; DB 5; Length 428;
 Best Local Similarity 67.9%; Pred. No. 2.6;
 RESULT 756
 ID ABV51376 standard; cDNA; 488 BP.
 DE Human prostate expression marker cDNA 51367.
 PN WO200160860-A2.
 PD 23-AUG-2001.

PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 Query Match 4.5%; Score 39.4; DB 5; Length 488;
 Best Local Similarity 59.3%; Pred. No. 2.8;
 RESULT 757
 ID ABV44994 standard; cDNA; 309 BP.
 DE Human prostate expression marker cDNA 44985.
 PN WO200160860-A2.
 PD 23-AUG-2001.
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 Query Match 4.5%; Score 39.2; DB 5; Length 309;
 Best Local Similarity 48.8%; Pred. No. 2.6;
 RESULT 758
 ID ACN52334 standard; cDNA; 571 BP.
 DE Cotton androecium tissue EST Clone ID: LIB3828-014-Q1-N6-E11, SEQ:7115.
 PN US2004123340-A1.
 PD 24-JUN-2004.
 PA (DEIK/) DEIKMAN J.
 PA (FENG/) FENG P C C.
 PA (FINC/) FINCHER K L.
 PA (ZIEG/) ZIEGLER T E.
 Query Match 4.5%; Score 39.2; DB 13; Length 571;
 Best Local Similarity 49.5%; Pred. No. 3.4;
 RESULT 759
 ID ACN60732 standard; cDNA; 587 BP.
 DE Cotton gynoecium tissue EST Clone ID: LIB3829-027-Q6-K6-B6, SEQ:15513.
 PN US2004123340-A1.
 PD 24-JUN-2004.
 PA (DEIK/) DEIKMAN J.
 PA (FENG/) FENG P C C.
 PA (FINC/) FINCHER K L.
 PA (ZIEG/) ZIEGLER T E.
 Query Match 4.5%; Score 39.2; DB 13; Length 587;
 Best Local Similarity 49.1%; Pred. No. 3.5;
 RESULT 760
 ID ADQ23418 standard; DNA; 1873 BP.
 DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 6238.
 PN WO2004048938-A2.
 PD 10-JUN-2004.
 PA (PROT-) PROTEIN DESIGN LABS INC.
 Query Match 4.5%; Score 39.2; DB 12; Length 1873;
 Best Local Similarity 58.6%; Pred. No. 5.9;
 RESULT 761
 ID ADV34961 standard; cDNA; 1873 BP.
 DE Human cDNA differentially expressed in the presence of valproate SeqID37.
 PN US2003096264-A1.
 PD 22-MAY-2003.
 PA (PSYC-) PSYCHIATRIC GENOMICS INC.
 Query Match 4.5%; Score 39.2; DB 13; Length 1873;
 Best Local Similarity 58.6%; Pred. No. 5.9;
 RESULT 762
 ID ABK39934 standard; DNA; 5321 BP.
 DE Human chemically pretreated gene sequence #8 strand 1.
 PN WO200202806-A2.
 PD 10-JAN-2002.
 PA (EPIG-) EPIGENOMICS AG.
 Query Match 4.5%; Score 39.2; DB 6; Length 5321;
 Best Local Similarity 64.1%; Pred. No. 9.4;
 RESULT 763
 ID ABL92194 standard; DNA; 5321 BP.
 DE Chemically treated DNA repair gene fragment#2.
 PN WO200181622-A2.
 PD 01-NOV-2001.
 PA (EPIG-) EPIGENOMICS AG.
 Query Match 4.5%; Score 39.2; DB 6; Length 5321;
 Best Local Similarity 64.1%; Pred. No. 9.4;
 RESULT 764
 ID AAK71873 standard; DNA; 775 BP.
 DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:26685.
 PN WO200157182-A2.
 PD 09-AUG-2001.
 PA (HUWA-) HUMAN GENOME SCI INC.
 Query Match 4.5%; Score 39; DB 4; Length 775;
 Best Local Similarity 58.0%; Pred. No. 4.5;

RESULT 765
ID AAK71874 standard; DNA; 775 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:26686.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 58.0%; Score 39; DB 4; Length 775;
RESULT 766
ID ABV78103 standard; DNA; 1790 BP.
DE Hypoxia-regulated protein coding sequence #123.
PN WO200246465-A2.
PD 13-JUN-2002.
PA (OXFO-) OXFORD BIOMEDICA UK LTD.
Query Match
Best Local Similarity 4.5%; Score 39; DB 6; Length 1790;
Best Local Similarity 68.4%; Pred. No. 6.5;
RESULT 767
ID ADQ23564 standard; DNA; 2249 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 6384.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match
Best Local Similarity 4.5%; Score 39; DB 12; Length 2249;
Best Local Similarity 59.5%; Pred. No. 7.2;
RESULT 768
ID ACH30440 standard; cDNA; 413 BP.
DE Human testis cDNA #826.
PN US2003073623-A1.
PD 17-APR-2003.
PA (DRNA/) DRMANAC R T.
PA (LABA/) LABAT I.
PA (STAC/) STACHE-CRAIN B.
PA (DICK/) DICKSON M C.
PA (JONE/) JONES L W.
Query Match
Best Local Similarity 4.5%; Score 38.8; DB 9; Length 413;
Best Local Similarity 62.2%; Pred. No. 3.8;
RESULT 769
ID ACN49737 standard; cDNA; 546 BP.
DE Cotton primed seed EST Clone ID: LIB3825-026-Q6-N6-B2, SEQ:4518.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match
Best Local Similarity 4.5%; Score 38.8; DB 13; Length 546;
Best Local Similarity 48.6%; Pred. No. 4.3;
RESULT 770
ID ABQ54479 standard; cDNA; 862 BP.
DE Human ovarian antigen RHORE03 cDNA, SEQ ID NO:359.
PN WO200200677-A1.
PD 03-JAN-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 4.5%; Score 38.8; DB 6; Length 862;
Best Local Similarity 55.1%; Pred. No. 5.3;
RESULT 771
ID ADN05367 standard; cDNA; 1913 BP.
DE Antipsoriatic cDNA sequence #906.
PN WO2004028479-A2.
PD 08-APR-2004.
PA (GETH-) GENENTECH INC.
Query Match
Best Local Similarity 4.5%; Score 38.8; DB 12; Length 1913;
Best Local Similarity 58.8%; Pred. No. 7.6;
RESULT 772
ID ABN79984 standard; DNA; 16633 BP.
DE Human chemically modified disease associated gene SEQ ID NO 1.
PN WO200200927-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match
Best Local Similarity 4.5%; Score 38.8; DB 6; Length 16633;
Best Local Similarity 67.1%; Pred. No. 20;
RESULT 773
ID ADQ17536 standard; DNA; 332 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 353.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match
Best Local Similarity 4.4%; Score 38.6; DB 12; Length 332;
Best Local Similarity 55.6%; Pred. No. 3.9;
RESULT 774
ID AAK58069 standard; cDNA; 356 BP.
DE Human immune/haematopoietic antigen encoding cDNA SEQ ID NO:3129.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 4.4%; Score 38.6; DB 4; Length 356;
Best Local Similarity 57.1%; Pred. No. 4;
RESULT 775
ID ADQ22236 standard; DNA; 1083 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 5056.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match
Best Local Similarity 4.4%; Score 38.6; DB 12; Length 1083;
Best Local Similarity 55.6%; Pred. No. 6.7;
RESULT 776
ID ABN95915 standard; DNA; 2125 BP.
DE Gene #2413 used to diagnose liver cancer.
PN WO200229103-A2.
PD 11-APR-2002.
PA (GENE-) GENE LOGIC INC.
Query Match
Best Local Similarity 4.4%; Score 38.6; DB 6; Length 2125;
Best Local Similarity 63.4%; Pred. No. 9.1;
RESULT 777
ID AAL57274 standard; DNA; 2125 BP.
DE IGFALS 'human modifier of p53 pathway' DNA.
PN WO2003035833-A2.
PD 01-MAY-2003.
PA (EXEL-) EXELIXIS INC.
Query Match
Best Local Similarity 4.4%; Score 38.6; DB 8; Length 2125;
Best Local Similarity 63.4%; Pred. No. 9.1;
RESULT 778
ID ABL33883 standard; DNA; 6609 BP.
DE Human immune system associated gene SEQ ID NO: 1856.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match
Best Local Similarity 4.4%; Score 38.6; DB 6; Length 6609;
Best Local Similarity 54.0%; Pred. No. 15;
RESULT 779
ID ABN80247 standard; DNA; 6609 BP.
DE Human chemically modified disease associated gene SEQ ID NO 264.
PN WO200200927-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match
Best Local Similarity 4.4%; Score 38.6; DB 6; Length 6609;
Best Local Similarity 54.0%; Pred. No. 15;
RESULT 780
ID AAL11578 standard; cDNA; 337 BP.
DE Human breast cancer expressed polynucleotide 4035.
PN WO200151628-A2.
PD 19-JUL-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match
Best Local Similarity 4.4%; Score 38.4; DB 4; Length 337;
Best Local Similarity 42.1%; Pred. No. 4.5;
RESULT 781
ID ACN81779 standard; DNA; 424 BP.
DE Breast cancer related marker, seq id 2929.
PN US2003099974-A1.
PD 29-MAY-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match
Best Local Similarity 4.4%; Score 38.4; DB 11; Length 424;
Best Local Similarity 42.1%; Pred. No. 5;
RESULT 782
ID ACN46935 standard; cDNA; 499 BP.
DE Cotton primed seed EST Clone ID: LIB3825-005-Q1-N6-D10, SEQ:1716.

PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIRMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 4.4%; Score 38.4; DB 13; Length 499;
Best Local Similarity 47.8%; Pred. No. 5.3;
RESULT 783
ID ACD07397 standard; cDNA; 1072 BP.
DE Bread wheat Myb-related transcription factor #2 cDNA.
PN US2003024007-A1.
PD 30-JAN-2003.
PA (CAHO/) CAHOON R E.
PA (ODEL/) ODELL J T.
Query Match 4.4%; Score 38.4; DB 8; Length 1072;
Best Local Similarity 57.5%; Pred. No. 7.6;
RESULT 784
ID ADJ77758 standard; cDNA; 1072 BP.
DE cDNA encoding wheat Myb-related transcription factor #2.
PN US2004040057-A1.
PD 26-FEB-2004.
PA (CAHO/) CAHOON R E.
PA (FANG/) FANG Y.
PA (ODEL/) ODELL J T.
PA (WENG/) WENG Z.
Query Match 4.4%; Score 38.4; DB 12; Length 1072;
Best Local Similarity 57.5%; Pred. No. 7.6;
RESULT 785
ID ADF82072 standard; DNA; 1815 BP.
DE Leukemia-related DNA sequence #2628.
PN WO2003039443-A2.
PD 15-MAY-2003.
PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
PA (UYLU-) UNIV LUDWIG MAXIMILIANS.
PA (HAFE/) HAFERLACH T.
PA (SCHO/) SCHOCH C.
PA (KERN/) KERN W.
Query Match 4.4%; Score 38.4; DB 10; Length 1815;
Best Local Similarity 58.9%; Pred. No. 9.6;
RESULT 786
ID ADQ24756 standard; DNA; 1954 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 7576.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 4.4%; Score 38.4; DB 12; Length 1954;
Best Local Similarity 58.9%; Pred. No. 9.9;
RESULT 787
ID ACC79092 standard; cDNA; 2490 BP.
DE Human secreted protein SSCP-67 encoding cDNA SEQ ID NO:147.
PN WO2003016506-A2.
PD 27-FEB-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 4.4%; Score 38.4; DB 10; Length 2490;
Best Local Similarity 49.0%; Pred. No. 11;
RESULT 788
ID ABL33597 standard; DNA; 5195 BP.
DE Human immune system associated gene SEQ ID NO: 1570.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.4%; Score 38.4; DB 6; Length 5195;
Best Local Similarity 60.6%; Pred. No. 15;
RESULT 789
ID ABK28395 standard; DNA; 15743 BP.
DE DNA transcription associated genomic DNA #135.
PN WO200192565-A2.
PD 08-DEC-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.4%; Score 38.4; DB 6; Length 15743;
Best Local Similarity 56.2%; Pred. No. 26;
RESULT 790

ID AAL34680 standard; cDNA; 277 BP.
DE Human musculoskeletal system related polynucleotide SEQ ID NO 22.
PN WO200155367-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.4%; Score 38.2; DB 4; Length 277;
Best Local Similarity 56.6%; Pred. No. 4.7;
RESULT 791
ID ABX57668 standard; cDNA; 277 BP.
DE cDNA encoding novel human musculoskeletal system antigen #12.
PN US2002147140-A1.
PD 10-OCT-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 4.4%; Score 38.2; DB 8; Length 277;
Best Local Similarity 56.8%; Pred. No. 4.7;
RESULT 792
ID ADJ27395 standard; DNA; 277 BP.
DE Human musculoskeletal system-associated contig DNA - SEQ ID 22.
PN US2004009488-A1.
PD 15-JAN-2004.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.4%; Score 38.2; DB 12; Length 277;
Best Local Similarity 56.6%; Pred. No. 4.7;
RESULT 793
ID ABV55135 standard; cDNA; 279 BP.
DE Human prostate expression marker cDNA 55126.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.4%; Score 38.2; DB 5; Length 279;
Best Local Similarity 55.7%; Pred. No. 4.7;
RESULT 794
ID AAV80671 standard; cDNA; 1557 BP.
DE Partial human DNAX toll-like receptor DTLR7 encoding cDNA.
PN WO9850547-A2.
PD 12-NOV-1998.
PA (SCHE-) SCHERING CORP.
Query Match 4.4%; Score 38.2; DB 2; Length 1557;
Best Local Similarity 61.6%; Pred. No. 10;
RESULT 795
ID AAD26303 standard; cDNA; 1557 BP.
DE Human DNAX Toll like receptor (DTLR) 7 cDNA #2, alternative form.
PN WO200190151-A2.
PD 29-NOV-2001.
PA (SCHE-) SCHERING CORP.
Query Match 4.4%; Score 38.2; DB 6; Length 1557;
Best Local Similarity 61.6%; Pred. No. 10;
RESULT 796
ID RAD26288 standard; cDNA; 1557 BP.
DE Human DNAX Toll like receptor (DTLR) 7 cDNA #2.
PN WO200190151-A2.
PD 29-NOV-2001.
PA (SCHE-) SCHERING CORP.
Query Match 4.4%; Score 38.2; DB 6; Length 1557;
Best Local Similarity 61.6%; Pred. No. 10;
RESULT 797
ID RAD02321 standard; cDNA; 1939 BP.
DE Human serine protease #2, encoding HMGBM65 cDNA clone.
PN WO200068247-A2.
PD 16-NOV-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.4%; Score 38.2; DB 3; Length 1939;
Best Local Similarity 50.6%; Pred. No. 11;
RESULT 798
ID ABK90492 standard; cDNA; 1939 BP.
DE Human serine protease cDNA #1.
PN US2002119925-A1.
PD 29-AUG-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.4%; Score 38.2; DB 6; Length 1939;
Best Local Similarity 50.6%; Pred. No. 11;

RESULT 799
ID AAD28647 standard; cDNA; 1939 BP.
DE Human serine protease encoding gene 1 cDNA clone HMG6M5.
PN WO200198476-A1.
PD 27-DEC-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.4%; Score 38.2; DB 6; Length 1939;
Best Local Similarity 50.6%; Pred. No. 11;
RESULT 800
ID AAC98572 standard; cDNA; 260 BP.
DE Human colon cancer antigen nucleotide sequence SEQ ID NO:582.
PN WO200055351-A1.
PD 21-SEP-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.4%; Score 38; DB 3; Length 260;
Best Local Similarity 60.8%; Pred. No. 5.1;
RESULT 801
ID ACN55408 standard; cDNA; 499 BP.
DE Cotton androecium tissue EST Clone ID: LIB3828-023-Q6-N6-C10, SEQ:10189.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 4.4%; Score 38; DB 13; Length 499;
Best Local Similarity 48.2%; Pred. No. 6.9;
RESULT 802
ID AAD02118 standard; cDNA; 1474 BP.
DE Maize RAD51 orthologue #1 cDNA.
PN WO200058370-A2.
PD 16-NOV-2000.
PA (PTON-) PIONEER HI-BRED INT INC.
Query Match 4.4%; Score 38; DB 4; Length 1474;
Best Local Similarity 54.2%; Pred. No. 11;
RESULT 803
ID ADQ25148 standard; DNA; 1533 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 7968.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 4.4%; Score 38; DB 12; Length 1533;
Best Local Similarity 55.2%; Pred. No. 11;
RESULT 804
ID ABQ67122 standard; DNA; 5164 BP.
DE Human angiogenesis associated polynucleotide SEQ ID NO 152.
PN WO200246454-A2.
PD 13-JUN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.4%; Score 38; DB 6; Length 5164;
Best Local Similarity 59.1%; Pred. No. 20;
RESULT 805
ID ABL33642 standard; DNA; 6319 BP.
DE Human immune system associated gene SEQ ID NO: 1615.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.4%; Score 38; DB 6; Length 6319;
Best Local Similarity 56.3%; Pred. No. 22;
RESULT 806
ID AEA61217 standard; DNA; 294575 BP.
DE Human STK39 gene genomic sequence SEQ ID NO:127.
PN US2005130172-A1.
PD 16-JUN-2005.
PA (FARB-) BAYER CORP.
Query Match 4.4%; Score 38; DB 14; Length 294575;
Best Local Similarity 46.0%; Pred. No. 1.2e+02;
RESULT 807
ID ABD33100 standard; DNA; 313287 BP.
DE Human cancer-associated (CA) gene HD07-008.
PN WO2004058146-A2.
PD 15-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.

Query Match 4.4%; Score 38; DB 13; Length 313287;
Best Local Similarity 46.0%; Pred. No. 1.3e+02;
RESULT 808
ID AAL01787 standard; cDNA; 344 BP.
DE Human reproductive system related antigen cDNA SEQ ID NO: 1788.
PN WO200155320-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.3%; Score 37.8; DB 4; Length 344;
Best Local Similarity 52.3%; Pred. No. 6.6;
RESULT 809
ID ABL97080 standard; cDNA; 344 BP.
DE Human testicular antigen encoding cDNA SEQ ID NO: 748.
PN WO200155317-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.3%; Score 37.8; DB 4; Length 344;
Best Local Similarity 52.3%; Pred. No. 6.6;
RESULT 810
ID AAI82206 standard; cDNA; 480 BP.
DE Human polynucleotide SEQ ID NO 2266.
PN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 4.3%; Score 37.8; DB 4; Length 480;
Best Local Similarity 49.7%; Pred. No. 7.7;
RESULT 811
ID ABV56463 standard; cDNA; 332 BP.
DE Human prostate expression marker cDNA 56454.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.3%; Score 37.6; DB 5; Length 332;
Best Local Similarity 65.5%; Pred. No. 7.4;
RESULT 812
ID ACN49835 standard; cDNA; 450 BP.
DE Cotton primed seed EST Clone ID: LIB3825-031-Q6-N6-E4, SEQ:4616.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 4.3%; Score 37.6; DB 13; Length 450;
Best Local Similarity 48.2%; Pred. No. 8.5;
RESULT 813
ID ACN48235 standard; cDNA; 560 BP.
DE Cotton primed seed EST Clone ID: LIB3825-021-Q1-N6-B5, SEQ:3016.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 4.3%; Score 37.6; DB 13; Length 560;
Best Local Similarity 48.2%; Pred. No. 9.4;
RESULT 814
ID ACN51616 standard; cDNA; 579 BP.
DE Cotton androecium tissue EST Clone ID: LIB3828-005-Q1-N6-D1, SEQ:6397.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 4.3%; Score 37.6; DB 13; Length 579;
Best Local Similarity 48.2%; Pred. No. 9.5;
RESULT 815
ID AEC06158 standard; DNA; 3151 BP.
DE Mouse Smad1 DNA SEQ ID NO 12.
PN WO2005077403-A1.
PD 25-AUG-2005.
PA (STYC-) STRYKER CORP.

Query Match 4.3%; Score 37.6; DB 14; Length 3151;
 Best Local Similarity 48.2%; Pred. No. 20;
 RESULT 816
 ID AAS46329 standard; DNA; 8649 BP.
 DE Tumour suppressor gene derived chemically modified sequence #51.
 PN WO200169912-A2.
 PD 20-SEP-2001.
 PA (EPIG-) EPIGENOMICS AG.
 Query Match 4.3%; Score 37.6; DB 4; Length 8649;
 Best Local Similarity 68.4%; Pred. No. 32;
 RESULT 817
 ID ABK31246 standard; DNA; 8649 BP.
 DE Signal transduction associated gene modified DNA #45.
 PN WO200200926-A2.
 PD 03-JAN-2002.
 PA (EPIG-) EPIGENOMICS AG.
 Query Match 4.3%; Score 37.6; DB 6; Length 8649;
 Best Local Similarity 68.4%; Pred. No. 32;
 RESULT 818
 ID ABL70201 standard; DNA; 8649 BP.
 DE Chemically treated cell signalling DNA sequence#46.
 PN WO200202807-A2.
 PD 10-JAN-2002.
 PA (EPIG-) EPIGENOMICS AG.
 Query Match 4.3%; Score 37.6; DB 6; Length 8649;
 Best Local Similarity 68.4%; Pred. No. 32;
 RESULT 819
 ID AAS61159 standard; DNA; 8649 BP.
 DE Human gene regulation-associated gene oligonucleotide #114.
 PN WO200177375-A2.
 PD 18-OCT-2001.
 PA (EPIG-) EPIGENOMICS AG.
 Query Match 4.3%; Score 37.6; DB 6; Length 8649;
 Best Local Similarity 68.4%; Pred. No. 32;
 RESULT 820
 ID AAS58467 standard; cDNA; 16132 BP.
 DE Mouse peroxisomal acetylpolymine oxidase (mPAO) genomic DNA.
 PN WO2003068167-A2.
 PD 21-AUG-2003.
 PA (REGC) UNIV CALIFORNIA.
 Query Match 4.3%; Score 37.6; DB 9; Length 16132;
 Best Local Similarity 56.5%; Pred. No. 43;
 RESULT 821
 ID AAS23328 standard; cDNA; 158 BP.
 DE Human prostate cancer marker #50.
 PN WO200153836-A2.
 PD 26-JUL-2001.
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 Query Match 4.3%; Score 37.4; DB 5; Length 158;
 Best Local Similarity 57.1%; Pred. No. 6;
 RESULT 822
 ID ADE59443 standard; DNA; 305 BP.
 DE Human gene AAS21144, SEQ ID NO 5338.
 PN WO2003016475-A2.
 PD 27-FEB-2003.
 PA (GEHO) GEN HOSPITAL CORP.
 PA (FARB) BAYER AG.
 Query Match 4.3%; Score 37.4; DB 10; Length 305;
 Best Local Similarity 67.1%; Pred. No. 8.1;
 RESULT 823
 ID AAI91834 standard; cDNA; 411 BP.
 DE Human polynucleotide SEQ ID NO 11894.
 PN WO200164835-A2.
 PD 07-SEP-2001.
 PA (HYSE-) HYSEQ INC.
 Query Match 4.3%; Score 37.4; DB 4; Length 411;
 Best Local Similarity 57.1%; Pred. No. 9.2;
 RESULT 824
 ID ACH30697 standard; cDNA; 416 BP.
 DE Human testis cDNA #1083.
 PN US2003073623-A1.
 PD 17-APR-2003.
 PA (DRMA/) DRMANAC R T.

PA (LABA/) LABAT I.
 PA (STAC/) STACHE-CRAIN B.
 PA (DICK/) DICKSON M C.
 PA (JONE/) JONES L W.
 Query Match 4.3%; Score 37.4; DB 9; Length 416;
 Best Local Similarity 58.0%; Pred. No. 9.3;
 RESULT 825
 ID AAI86835 standard; cDNA; 435 BP.
 DE Human polynucleotide SEQ ID NO 6895.
 PN WO200164835-A2.
 PD 07-SEP-2001.
 PA (HYSE-) HYSEQ INC.
 Query Match 4.3%; Score 37.4; DB 4; Length 435;
 Best Local Similarity 57.1%; Pred. No. 9.5;
 RESULT 826
 ID AAL01335 standard; cDNA; 439 BP.
 DE Human reproductive system related antigen cDNA SEQ ID NO: 1336.
 PN WO200155320-A2.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 4.3%; Score 37.4; DB 4; Length 439;
 Best Local Similarity 48.8%; Pred. No. 9.5;
 RESULT 827
 ID ABL96789 standard; cDNA; 439 BP.
 DE Human testicular antigen encoding cDNA SEQ ID NO: 457.
 PN WO200155317-A2.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 4.3%; Score 37.4; DB 4; Length 439;
 Best Local Similarity 48.8%; Pred. No. 9.5;
 RESULT 828
 ID AAS34169 standard; cDNA; 1035 BP.
 DE Human cDNA encoding a novel foetal antigen, SEQ ID No 693.
 PN WO200155312-A2.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 4.3%; Score 37.4; DB 5; Length 1035;
 Best Local Similarity 67.1%; Pred. No. 14;
 RESULT 829
 ID ABZ68674 standard; cDNA; 2398 BP.
 DE Nucleotide sequence of a membrane steroid receptor.
 PN WO2002101016-A2.
 PD 19-DEC-2002.
 PA (TEXA) UNIV TEXAS SYSTEM.
 Query Match 4.3%; Score 37.4; DB 8; Length 2398;
 Best Local Similarity 57.1%; Pred. No. 21;
 RESULT 830
 ID ADP25184 standard; cDNA; 2398 BP.
 DE PRO polypeptide encoding cDNA SEQ ID NO:2362.
 PN WO2004041170-A2.
 PD 21-MAY-2004.
 PA (GETH) GENENTECH INC.
 Query Match 4.3%; Score 37.4; DB 13; Length 2398;
 Best Local Similarity 57.1%; Pred. No. 21;
 RESULT 831
 ID AEB48498 standard; DNA; 2398 BP.
 DE DNA encoding human steroid progesterin receptor gamma (mSR-gamma).
 PN WO2005068999-A1.
 PD 28-JUL-2005.
 PA (FARB) BAYER HEALTHCARE AG.
 Query Match 4.3%; Score 37.4; DB 14; Length 2398;
 Best Local Similarity 57.1%; Pred. No. 21;
 RESULT 832
 ID ABN80324 standard; DNA; 8047 BP.
 DE Human chemically modified disease associated gene SEQ ID NO 341.
 PN WO200200927-A2.
 PD 03-JAN-2002.
 PA (EPIG-) EPIGENOMICS AG.
 Query Match 4.3%; Score 37.4; DB 6; Length 8047;
 Best Local Similarity 50.7%; Pred. No. 36;
 RESULT 833
 ID ABK33999 standard; DNA; 8111 BP.
 DE Human DNA for staging of Astrocytomas #43.

PN WO200202808-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.3%; Score 37.4; DB 6; Length 8111;
Best Local Similarity 67.1%; Pred. No. 36;
RESULT 834
ID ADA20390 standard; DNA; 8111 BP.
DE Prostate tumour related genomic DNA sample #28.
PN WO2002103042-A2.
PD 27-DEC-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.3%; Score 37.4; DB 8; Length 8111;
Best Local Similarity 67.1%; Pred. No. 36;
RESULT 835
ID ADA84197 standard; DNA; 8111 BP.
DE Human renal/prostate carcinoma associated DNA SEQ ID NO:55.
PN WO2002103041-A2.
PD 27-DEC-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.3%; Score 37.4; DB 8; Length 8111;
Best Local Similarity 67.1%; Pred. No. 36;
RESULT 836
ID ABL33257 standard; DNA; 14950 BP.
DE Human immune system associated gene SEQ ID NO: 1230.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.3%; Score 37.4; DB 6; Length 14950;
Best Local Similarity 55.9%; Pred. No. 47;
RESULT 837
ID ABL18650 standard; DNA; 80226 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 7423.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NV.
Query Match 4.3%; Score 37.4; DB 4; Length 80226;
Best Local Similarity 53.0%; Pred. No. 1e+02;
RESULT 838
ID ABD33102 standard; DNA; 111836 BP.
DE Murine cancer-associated (CA) gene MD07-009.
PN WO2004058146-A2.
PD 15-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 4.3%; Score 37.4; DB 13; Length 111836;
Best Local Similarity 57.1%; Pred. No. 1.2e+02;
RESULT 839
ID ABX48652 standard; cDNA; 426 BP.
DE Bovine EST associated with lactation/muscle/fat deposition #13817.
PN US2002137139-A1.
PD 26-SEP-2002.
PA (BYAT/) BYATT J C.
PA (MATH/) MATHIALAGAN N.
PA (TAON/) TAO N.
PA (WARR/) WARREN W C.
Query Match 4.3%; Score 37.2; DB 8; Length 426;
Best Local Similarity 54.3%; Pred. No. 11;
RESULT 840
ID ACN56344 standard; cDNA; 565 BP.
DE Cotton androecium tissue EST Clone ID: LTB3828-034-Q6-N6-B10, SEQ:11125.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 4.3%; Score 37.2; DB 13; Length 565;
Best Local Similarity 48.2%; Pred. No. 12;
RESULT 841
ID AAS26890 standard; cDNA; 2549 BP.
DE Human cDNA encoding a novel secreted protein, SEQ ID 82.
PN WO200155441-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.

Query Match 4.3%; Score 37.2; DB 4; Length 2549;
Best Local Similarity 57.9%; Pred. No. 24;
RESULT 842
ID ADR41347 standard; cDNA; 2644 BP.
DE Human CD-like molecule HDTEJ03 cDNA, SEQ ID NO:146.
PN WO200226930-A2.
PD 04-APR-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.3%; Score 37.2; DB 7; Length 2644;
Best Local Similarity 57.9%; Pred. No. 24;
RESULT 843
ID ABO54403 standard; cDNA; 2911 BP.
DE Human ovarian antigen HAOE30 cDNA, SEQ ID NO:283.
PN WO200200677-A1.
PD 03-JAN-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.3%; Score 37.2; DB 6; Length 2911;
Best Local Similarity 51.9%; Pred. No. 25;
RESULT 844
ID ABL33356 standard; DNA; 6577 BP.
DE Human immune system associated gene SEQ ID NO: 1329.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.3%; Score 37.2; DB 6; Length 6577;
Best Local Similarity 56.6%; Pred. No. 37;
RESULT 845
ID ABL70561 standard; DNA; 6577 BP.
DE Chemically treated cell signalling DNA sequence#226.
PN WO200202807-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.3%; Score 37.2; DB 6; Length 6577;
Best Local Similarity 56.6%; Pred. No. 37;
RESULT 846
ID AAS61221 standard; DNA; 6577 BP.
DE Human gene regulation-associated gene oligonucleotide #176.
PN WO200177375-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.3%; Score 37.2; DB 6; Length 6577;
Best Local Similarity 56.6%; Pred. No. 37;
RESULT 847
ID ADS17402 standard; DNA; 78064 BP.
DE Nucleotide sequence of zebrafish MAP2K6.
PN WO2004078713-A2.
PD 16-SEP-2004.
PA (EXEL-) EXELIXIS INC.
Query Match 4.3%; Score 37.2; DB 13; Length 78064;
Best Local Similarity 65.9%; Pred. No. 1.1e+02;
RESULT 848
ID ADD69391 standard; DNA; 240823 BP.
DE Human PG-3 DNA - SEQ ID 127.
PN WO2003048185-A2.
PD 12-JUN-2003.
PA (GENV-) GENVEC INC.
Query Match 4.3%; Score 37.2; DB 10; Length 240823;
Best Local Similarity 44.9%; Pred. No. 1.9e+02;
RESULT 849
ID AAF24497 standard; cDNA; 240825 BP.
DE Human PG-3 gene.
Query Match 4.3%; Score 37.2; DB 4; Length 240825;
Best Local Similarity 44.9%; Pred. No. 1.9e+02;
RESULT 850
ID ABO81802 standard; DNA; 240825 BP.
DE Human PG-3 gene SEQ ID NO:1.
Query Match 4.3%; Score 37.2; DB 6; Length 240825;
Best Local Similarity 44.9%; Pred. No. 1.9e+02;
RESULT 851
ID ADJ76070 standard; DNA; 127 BP.
DE Marker gene SEQ ID NO:1322.
PN EPI394274-A2.
PD 03-MAR-2004.

PA (GENO-) GENOX RES INC.
Query Match 4.3%; Score 37; DB 12; Length 127;
Best Local Similarity 62.4%; Pred. No. 7;
RESULT 852
ID ADL11530 standard; cDNA; 291 BP.
DE Cat flea hindgut and malpighian tubule (HMT) protein cDNA #1935.
PN US2004067516-A1.
PD 08-APR-2004.
PA (BRAN/) BRANDT K S.
PA (GAIN/) GAINES P J.
PA (STIN/) STINCHCOMB D T.
PA (WISN/) WISNEWSKI N.
Query Match 4.3%; Score 37; DB 12; Length 291;
Best Local Similarity 60.4%; Pred. No. 10;
RESULT 853
ID ACH49203 standard; cDNA; 409 BP.
DE Human leukocyte cDNA #797.
PN US2003073623-A1.
PD 17-APR-2003.
PA (DRMA/) DRMANAC R T.
PA (LABA/) LABAT I.
PA (STAC/) STACHE-CRAIN B.
PA (DICK/) DICKSON M C.
PA (JONE/) JONES L W.
Query Match 4.3%; Score 37; DB 9; Length 409;
Best Local Similarity 53.1%; Pred. No. 12;
RESULT 854
ID AAI98819 standard; cDNA; 444 BP.
DE Human excretory related polynucleotide SEQ ID NO 263.
PN WO200155313-A2.
PD 02-AUG-2001.
PA (HUNA-) HUMAN GENOME SCI INC.
Query Match 4.3%; Score 37; DB 4; Length 444;
Best Local Similarity 63.2%; Pred. No. 12;
RESULT 855
ID AAI63215 standard; cDNA; 444 BP.
DE Human kidney related polynucleotide SEQ ID NO 255.
PN WO200155323-A2.
PD 02-AUG-2001.
PA (HUNA-) HUMAN GENOME SCI INC.
Query Match 4.3%; Score 37; DB 5; Length 444;
Best Local Similarity 63.2%; Pred. No. 12;
RESULT 856
ID ACN62215 standard; cDNA; 516 BP.
DE Cotton gymnocium tissue EST Clone ID: LIB3829-026-Q6-N6-F3, SEQ:16996.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 4.3%; Score 37; DB 13; Length 516;
Best Local Similarity 48.8%; Pred. No. 13;
RESULT 857
ID ABL32171 standard; DNA; 3973 BP.
DE Human immune system associated gene SEQ ID NO: 144.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.3%; Score 37; DB 6; Length 3973;
Best Local Similarity 62.4%; Pred. No. 33;
RESULT 858
ID ABL34205 standard; DNA; 5397 BP.
DE Human immune system associated gene SEQ ID NO: 2178.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.3%; Score 37; DB 6; Length 5397;
Best Local Similarity 67.5%; Pred. No. 38;
RESULT 859
ID ABK40041 standard; DNA; 6136 BP.
DE Human chemically pretreated gene sequence #62 strand 1.
PN WO200202806-A2.

PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.3%; Score 37; DB 6; Length 6136;
Best Local Similarity 57.3%; Pred. No. 41;
RESULT 860
ID ABL33649 standard; DNA; 8234 BP.
DE Human immune system associated gene SEQ ID NO: 1622.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.3%; Score 37; DB 6; Length 8234;
Best Local Similarity 62.4%; Pred. No. 46;
RESULT 861
ID ABL34042 standard; DNA; 10039 BP.
DE Human immune system associated gene SEQ ID NO: 2015.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.3%; Score 37; DB 6; Length 10039;
Best Local Similarity 57.3%; Pred. No. 51;
RESULT 862
ID ABV47775 standard; cDNA; 282 BP.
DE Human prostate expression marker cDNA 47766.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.2%; Score 36.8; DB 5; Length 282;
Best Local Similarity 63.6%; Pred. No. 11;
RESULT 863
ID ABV59054 standard; cDNA; 360 BP.
DE Human prostate expression marker cDNA 59045.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.2%; Score 36.8; DB 5; Length 360;
Best Local Similarity 51.9%; Pred. No. 13;
RESULT 864
ID ABV07958 standard; cDNA; 370 BP.
DE Human prostate expression marker cDNA 7949.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.2%; Score 36.8; DB 5; Length 370;
Best Local Similarity 54.0%; Pred. No. 13;
RESULT 865
ID ADQ20928 standard; DNA; 391 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 3748.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 4.2%; Score 36.8; DB 12; Length 391;
Best Local Similarity 66.2%; Pred. No. 13;
RESULT 866
ID ADL43518 standard; DNA; 445 BP.
DE Human ovarian cancer DNA marker #17408.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.2%; Score 36.8; DB 5; Length 445;
Best Local Similarity 58.0%; Pred. No. 14;
RESULT 867
ID ACN58685 standard; cDNA; 483 BP.
DE Cotton gymnocium tissue EST Clone ID: LIB3829-011-Q6-K6-C8, SEQ:13466.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 4.2%; Score 36.8; DB 13; Length 483;
Best Local Similarity 47.4%; Pred. No. 15;
RESULT 868
ID ABQ25138 standard; DNA; 631 BP.

DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 11729.
PN WO200218632-A2.
PD 07-MAR-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.2%; Score 36.8; DB 6; Length 631;
Best Local Similarity 66.2%; Pred. No. 16;
RESULT 869
ID ABQ25139 standard; DNA; 631 BP.
DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 11730.
PN WO200218632-A2.
PD 07-MAR-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.2%; Score 36.8; DB 6; Length 631;
Best Local Similarity 66.2%; Pred. No. 16;
RESULT 870
ID AAD57083 standard; DNA; 1290 BP.
DE Human aldo-keto reductase IC, AKRIC2 DNA #1.
PN WO2003051182-A2.
PD 26-JUN-2003.
PA (META-) METABOLEX INC.
Query Match 4.2%; Score 36.8; DB 9; Length 1290;
Best Local Similarity 58.0%; Pred. No. 23;
RESULT 871
ID ADP24450 standard; cDNA; 1290 BP.
DE PRO polypeptide encoding cDNA SEQ ID NO:1628.
PN WO2004041170-A2.
PD 21-MAY-2004.
PA (GETH) GENENTECH INC.
Query Match 4.2%; Score 36.8; DB 13; Length 1290;
Best Local Similarity 58.0%; Pred. No. 23;
RESULT 872
ID ADU05984 standard; DNA; 1290 BP.
DE Novel bronchial cancer-associated human gene SeqID206.
PN DE10316701-A1.
PD 04-NOV-2004.
PA (HINZ/) HINZMANN B.
PA (HERM/) HERMANN K.
PA (CAST/) HEIDEN CASTANOS-VELEZ E.
Query Match 4.2%; Score 36.8; DB 13; Length 1290;
Best Local Similarity 58.0%; Pred. No. 23;
RESULT 873
ID ABA93750 standard; cDNA; 1316 BP.
DE Human cell structure and motility cDNA clone tes3_16b5.
PN WO200198454-A2.
PD 27-DEC-2001.
PA (GEHU-) GERMAN HUMAN GENOME PROJECT.
Query Match 4.2%; Score 36.8; DB 6; Length 1316;
Best Local Similarity 55.5%; Pred. No. 23;
RESULT 874
ID AAV07665 standard; cDNA; 1508 BP.
DE Maize Bx1 cDNA (DIMBOA biosynthetic gene).
PN WO9840505-A1.
PD 17-SEP-1998.
PA (DEKA-) DEKALB GENETICS CORP.
Query Match 4.2%; Score 36.8; DB 2; Length 1508;
Best Local Similarity 58.0%; Pred. No. 24;
RESULT 875
ID AAF29898 standard; DNA; 1697 BP.
DE Human h15590 DNA.
PN WO200100879-A1.
PD 04-JAN-2001.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 4.2%; Score 36.8; DB 5; Length 1697;
Best Local Similarity 61.5%; Pred. No. 26;
RESULT 876
ID ADJ77843 standard; cDNA; 1725 BP.
DE Corn lipase cDNA #3.
PN US6673988-B1.
PD 06-JAN-2004.
PA (DUPO) DU PONT DE NEMOURS & CO E I.
Query Match 4.2%; Score 36.8; DB 12; Length 1725;
Best Local Similarity 53.5%; Pred. No. 26;
RESULT 877

ID AAT79634 standard; DNA; 1898 BP.
DE DNA encoding human ubiquitous nuclear receptor polypeptide.
PN US5639616-A.
PD 17-JUN-1997.
PA (ARCH-) ARCH DEV CORP.
Query Match 4.2%; Score 36.8; DB 2; Length 1898;
Best Local Similarity 63.6%; Pred. No. 27;
RESULT 878
ID AAC76167 standard; cDNA; 2070 BP.
DE Human ORFX ORF1722 polynucleotide sequence SEQ ID NO:3443.
PN WO200058473-A2.
PD 05-OCT-2000.
PA (CURA-) CURAGEN CORP.
Query Match 4.2%; Score 36.8; DB 3; Length 2070;
Best Local Similarity 53.5%; Pred. No. 28;
RESULT 879
ID ADR99088 standard; DNA; 2100 BP.
DE Tudor repeat associator with PCTAIRE 2, PCTAIRE2BP, DNA SEQ ID 94.
PN WO2004078035-A2.
PD 16-SEP-2004.
PA (FARB) BAYER PHARM CORP.
Query Match 4.2%; Score 36.8; DB 13; Length 2100;
Best Local Similarity 53.5%; Pred. No. 28;
RESULT 880
ID ACN92771 standard; DNA; 2111 BP.
DE Breast cancer related marker, seq id 13921.
PN US2003099974-A1.
PD 29-MAY-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 4.2%; Score 36.8; DB 11; Length 2111;
Best Local Similarity 61.5%; Pred. No. 28;
RESULT 881
ID AEF55813 standard; DNA; 2182 BP.
DE Human genomic DNA #420.
PN WO2006008128-A2.
PD 26-JAN-2006.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.2%; Score 36.8; DB 15; Length 2182;
Best Local Similarity 59.6%; Pred. No. 29;
RESULT 882
ID ABL33871 standard; DNA; 5511 BP.
DE Human immune system associated gene SEQ ID NO: 1844.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.2%; Score 36.8; DB 6; Length 5511;
Best Local Similarity 53.5%; Pred. No. 44;
RESULT 883
ID ABL70480 standard; DNA; 9742 BP.
DE Chemically treated cell signalling DNA sequence complementary to#185.
PN WO200202807-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.2%; Score 36.8; DB 6; Length 9742;
Best Local Similarity 53.5%; Pred. No. 57;
RESULT 884
ID AAS46478 standard; DNA; 14112 BP.
DE Tumour suppressor gene derived chemically modified sequence #200.
PN WO200168912-A2.
PD 20-SEP-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.2%; Score 36.8; DB 4; Length 14112;
Best Local Similarity 63.6%; Pred. No. 67;
RESULT 885
ID ABL33443 standard; DNA; 14112 BP.
DE Human immune system associated gene SEQ ID NO: 1416.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.2%; Score 36.8; DB 6; Length 14112;
Best Local Similarity 63.6%; Pred. No. 67;
RESULT 886
ID ABK31333 standard; DNA; 14112 BP.

DE Signal transduction associated gene modified complementary DNA #88.
PN WO200200926-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.2%; Score 36.8; DB 6; Length 14112;
Best Local Similarity 63.8%; Pred. No. 67;
RESULT 887
ID ABO66980 standard; DNA; 14112 BP.
DE Human angiogenesis associated polynucleotide SEQ ID NO 10.
PN WO200246454-A2.
PD 13-JUN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.2%; Score 36.8; DB 6; Length 14112;
Best Local Similarity 63.6%; Pred. No. 67;
RESULT 888
ID ADQ97025 standard; DNA; 57889 BP.
DE Mouse cancer associated sequence MD10-002, SEQ ID 1.
PN WO2004060304-A2.
PD 22-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 4.2%; Score 36.8; DB 12; Length 57889;
Best Local Similarity 69.4%; Pred. No. 1.3e+02;
RESULT 889
ID ADQ97557 standard; DNA; 254396 BP.
DE Human cancer associated sequence HD09-013, SEQ ID 534.
PN WO2004060304-A2.
PD 22-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 4.2%; Score 36.8; DB 12; Length 254396;
Best Local Similarity 55.5%; Pred. No. 2.5e+02;
RESULT 890
ID ABV48821 standard; cDNA; 265 BP.
DE Human prostate expression marker cDNA 48812.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.2%; Score 36.6; DB 5; Length 265;
Best Local Similarity 63.5%; Pred. No. 13;
RESULT 891
ID AAH70126 standard; cDNA; 545 BP.
DE Human cervical cancer marker nucleic acid 1400.
PN WO200142467-A2.
PD 14-JUN-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.2%; Score 36.6; DB 4; Length 545;
Best Local Similarity 42.7%; Pred. No. 17;
RESULT 892
ID ADT17571 standard; cDNA; 1054 BP.
DE Plant cDNA, Seq ID 2897.
PN US2004216190-A1.
PD 28-OCT-2004.
PA (KOVA/) KOVALIC D K.
Query Match 4.2%; Score 36.6; DB 13; Length 1054;
Best Local Similarity 62.6%; Pred. No. 24;
RESULT 893
ID AAV28734 standard; cDNA; 1102 BP.
DE Murine smooth muscle cell specific SM22 alpha gene cDNA.
PN WO9815575-A1.
PD 16-APR-1998.
PA (ARCH-) ARCH DEV CORP.
Query Match 4.2%; Score 36.6; DB 2; Length 1102;
Best Local Similarity 71.6%; Pred. No. 24;
RESULT 894
ID AAH26685 standard; cDNA; 1102 BP.
DE Mouse smooth muscle 22 alpha (SM22-alpha) cDNA.
PN US284743-B1.
PD 04-SEP-2001.
PA (ARCH-) ARCH DEV CORP.
Query Match 4.2%; Score 36.6; DB 4; Length 1102;
Best Local Similarity 71.6%; Pred. No. 24;
RESULT 895
ID AAD20564 standard; cDNA; 1102 BP.
DE Murine SM22alpha cDNA.

PN US6291211-B1.
PD 18-SEP-2001.
PA (ARCH-) ARCH DEV CORP.
Query Match 4.2%; Score 36.6; DB 4; Length 1102;
Best Local Similarity 71.6%; Pred. No. 24;
RESULT 896
ID AAD21105 standard; cDNA; 1102 BP.
DE Murine SM22 alpha cDNA.
PN US6297221-B1.
PD 02-OCT-2001.
PA (ARCH-) ARCH DEV CORP.
Query Match 4.2%; Score 36.6; DB 4; Length 1102;
Best Local Similarity 71.6%; Pred. No. 24;
RESULT 897
ID ABK33330 standard; cDNA; 1102 BP.
DE Mouse cDNA encoding SM22alpha.
PN US6331527-B1.
PD 18-DEC-2001.
PA (ARCH-) ARCH DEV CORP.
Query Match 4.2%; Score 36.6; DB 6; Length 1102;
Best Local Similarity 71.6%; Pred. No. 24;
RESULT 898
ID ADN04573 standard; cDNA; 1342 BP.
DE Antipsoriatic cDNA sequence #492.
PN WO2004028479-A2.
PD 08-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 4.2%; Score 36.6; DB 12; Length 1342;
Best Local Similarity 68.0%; Pred. No. 26;
RESULT 899
ID ADU06264 standard; DNA; 1342 BP.
DE Novel bronchial cancer-associated human gene SeqID488.
PN DE10316701-A1.
PD 04-NOV-2004.
PA (HINZ/) HINZMANN B.
PA (HERM/) HERMANN K.
PA (CAST/) HEIDEN CASTANOS-VELEZ E.
Query Match 4.2%; Score 36.6; DB 13; Length 1342;
Best Local Similarity 68.0%; Pred. No. 26;
RESULT 900
ID ABE83780 standard; cDNA; 3623 BP.
DE Human cDNA differentially expressed in asthma, SEQ ID NO:188.
PN WO2005118403-A2.
PD 15-DEC-2005.
PA (LINK-) LINKAGENE LTD.
Query Match 4.2%; Score 36.6; DB 15; Length 3623;
Best Local Similarity 56.1%; Pred. No. 41;
RESULT 901
ID ABL33169 standard; DNA; 7781 BP.
DE Human immune system associated gene SEQ ID NO: 1142.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.2%; Score 36.6; DB 6; Length 7781;
Best Local Similarity 62.6%; Pred. No. 58;
RESULT 902
ID ABL32887 standard; DNA; 16439 BP.
DE Human immune system associated gene SEQ ID NO: 860.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.2%; Score 36.6; DB 6; Length 16439;
Best Local Similarity 68.0%; Pred. No. 82;
RESULT 903
ID AAF22297 standard; DNA; 96583 BP.
DE BAC containing repeats from centromeres 1-4 #20.
PN WO20055325-A2.
PD 21-SEP-2000.
PA (UYCH-) UNIV CHICAGO.
Query Match 4.2%; Score 36.6; DB 3; Length 96583;
Best Local Similarity 54.0%; Pred. No. 1.8e+02;
RESULT 904
ID AAL08212 standard; cDNA; 220 BP.

DE Human breast cancer expressed polynucleotide 669.
PN WO200151628-A2.
PD 19-JUL-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.2%; Score 36.4; DB 4; Length 220;
Best Local Similarity 58.2%; Pred. No. 13;
RESULT 905
ID AAL25957 standard; cDNA; 313 BP.
DE Human breast cancer expressed polynucleotide 18414.
PN WO200151628-A2.
PD 19-JUL-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.2%; Score 36.4; DB 4; Length 313;
Best Local Similarity 58.2%; Pred. No. 15;
RESULT 906
ID AAI82408 standard; cDNA; 391 BP.
DE Human polynucleotide SEQ ID NO 2468.
PN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 4.2%; Score 36.4; DB 4; Length 391;
Best Local Similarity 61.7%; Pred. No. 17;
RESULT 907
ID ADI69469 standard; DNA; 424 BP.
DE Human ovarian cancer DNA marker #2211.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.2%; Score 36.4; DB 5; Length 424;
Best Local Similarity 47.3%; Pred. No. 18;
RESULT 908
ID ADI75809 standard; DNA; 424 BP.
DE Human ovarian cancer DNA marker #8551.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.2%; Score 36.4; DB 5; Length 424;
Best Local Similarity 47.3%; Pred. No. 18;
RESULT 909
ID AAL19122 standard; cDNA; 472 BP.
DE Human breast cancer expressed polynucleotide 11579.
PN WO200151628-A2.
PD 19-JUL-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.2%; Score 36.4; DB 4; Length 472;
Best Local Similarity 58.2%; Pred. No. 19;
RESULT 910
ID AAC79470 standard; cDNA; 578 BP.
DE CDNA sequence of human breast tumour clone B511S.
PN WO200061756-A2.
PD 19-OCT-2000.
PA (CORI-) CORIXA CORP.
Query Match 4.2%; Score 36.4; DB 3; Length 578;
Best Local Similarity 49.0%; Pred. No. 20;
RESULT 911
ID AAI67224 standard; cDNA; 578 BP.
DE B511S CDNA sequence.
PN WO200175171-A2.
PD 11-OCT-2001.
PA (CORI-) CORIXA CORP.
Query Match 4.2%; Score 36.4; DB 4; Length 578;
Best Local Similarity 49.0%; Pred. No. 20;
RESULT 912
ID ABK29014 standard; cDNA; 578 BP.
DE Human breast tumour polypeptide full length cDNA clone #1.
PN WO200198339-A2.
PD 27-DEC-2001.
PA (CORI-) CORIXA CORP.
Query Match 4.2%; Score 36.4; DB 6; Length 578;
Best Local Similarity 49.0%; Pred. No. 20;
RESULT 913
ID ADT94972 standard; cDNA; 624 BP.
DE Colon cancer associated human cDNA sequence #491.
PN US2003087818-A1.
PD 08-MAY-2003.
PA (CORI-) CORIXA CORP.
Query Match 4.2%; Score 36.4; DB 11; Length 624;
Best Local Similarity 57.1%; Pred. No. 21;
RESULT 914
ID ADX41454 standard; cDNA; 624 BP.
DE Human CDNA encoding colon cancer protein SEQ ID NO 491.
PN WO200274156-A2.
PD 26-SEP-2002.
PA (CORI-) CORIXA CORP.
Query Match 4.2%; Score 36.4; DB 11; Length 624;
Best Local Similarity 57.1%; Pred. No. 21;
RESULT 915
ID ACN87147 standard; DNA; 627 BP.
DE Breast cancer related marker, seq id 8297.
PN US200309974-A1.
PD 29-MAY-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 4.2%; Score 36.4; DB 11; Length 627;
Best Local Similarity 58.2%; Pred. No. 21;
RESULT 916
ID AAF72823 standard; DNA; 826 BP.
DE Secreted protein gene #25.
PN WO200107459-A1.
PD 01-FEB-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.2%; Score 36.4; DB 4; Length 826;
Best Local Similarity 49.5%; Pred. No. 24;
RESULT 917
ID ABL90008 standard; cDNA; 1350 BP.
DE Human polynucleotide SEQ ID NO 570.
PN WO200190304-A2.
PD 29-NOV-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.2%; Score 36.4; DB 6; Length 1350;
Best Local Similarity 49.5%; Pred. No. 30;
RESULT 918
ID ADD47667 standard; DNA; 1450 BP.
DE Human gene BC004560, SEQ ID NO 13363.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 4.2%; Score 36.4; DB 10; Length 1450;
Best Local Similarity 50.0%; Pred. No. 31;
RESULT 919
ID AEA26104 standard; DNA; 1640 BP.
DE Human renal cell carcinoma-related LSAMP gene SeqID124.
PN WO2005047519-A2.
PD 26-MAY-2005.
PA (VAND-) VAN ANDEL RES INST.
Query Match 4.2%; Score 36.4; DB 14; Length 1640;
Best Local Similarity 59.8%; Pred. No. 33;
RESULT 920
ID ACN92828 standard; DNA; 2304 BP.
DE Breast cancer related marker, seq id 13978.
PN US200309974-A1.
PD 29-MAY-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 4.2%; Score 36.4; DB 11; Length 2304;
Best Local Similarity 54.5%; Pred. No. 38;
RESULT 921
ID ACA92424 standard; DNA; 2463 BP.
DE DNA encoding human PMMW-9.
PN WO2003031939-A2.
PD 17-APR-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 4.2%; Score 36.4; DB 10; Length 2463;
Best Local Similarity 52.7%; Pred. No. 39;
RESULT 922
ID ADR73483 standard; DNA; 2479 BP.
DE Human Lutheran blood group, LU, gene.

PN WO2004076682-A2.
 PD 10-SEP-2004.
 PA (SURR-) SURROMED INC. 4.2%; Score 36.4; DB 13; Length 2479;
 Query Match 50.8%; Pred. No. 39;
 Best Local Similarity
 RESULT 923
 ID ADV97196 standard; cDNA; 2479 BP.
 DE Human Lutheran blood group glycoprotein (LU) cDNA, SEQ:51.
 PN US2005003390-A1.
 PD 06-JAN-2005.
 PA (AXEN/) AXENOVICH S A.
 PA (STUL/) STULL R.
 PA (GELM/) GELMAN M.
 PA (CHUI/) CHUI K.
 PA (NGDD/) NG D.
 Query Match 4.2%; Score 36.4; DB 14; Length 2479;
 Best Local Similarity 50.8%; Pred. No. 39;
 RESULT 924
 ID AD226456 standard; cDNA; 2479 BP.
 DE Human Lutheran blood group antigen cDNA.
 PN WO2005030999-A1.
 PD 07-APR-2005.
 PA (DAND) DANA FARBER CANCER INST INC.
 Query Match 4.2%; Score 36.4; DB 14; Length 2479;
 Best Local Similarity 50.6%; Pred. No. 39;
 RESULT 925
 ID AEE60841 standard; DNA; 2479 BP.
 DE Human pathological responsiveness gene SEQ ID NO:50.
 PN US2005266420-A1.
 PD 01-DEC-2005.
 PA (TEXA) UNIV TEXAS SYSTEM.
 PA (MILL-) MILLENIUM PHARM INC.
 Query Match 4.2%; Score 36.4; DB 15; Length 2479;
 Best Local Similarity 50.6%; Pred. No. 39;
 RESULT 926
 ID AAS46320 standard; DNA; 2865 BP.
 DE Tumour suppressor gene derived chemically modified sequence #42.
 PN WO200168912-A2.
 PD 20-SEP-2001.
 PA (EPIG-) EPIGENOMICS AG. 4.2%; Score 36.4; DB 4; Length 2865;
 Query Match 4.2%; Score 36.4; DB 4; Length 2865;
 Best Local Similarity 59.8%; Pred. No. 42;
 RESULT 927
 ID ABN80051 standard; DNA; 2865 BP.
 DE Human chemically modified disease associated gene SEQ ID NO 68.
 PN WO20020927-A2.
 PD 03-JAN-2002.
 PA (EPIG-) EPIGENOMICS AG. 4.2%; Score 36.4; DB 6; Length 2865;
 Query Match 4.2%; Score 36.4; DB 6; Length 2865;
 Best Local Similarity 59.8%; Pred. No. 42;
 RESULT 928
 ID ABN80022 standard; DNA; 636 BP.
 DE Human chemically modified disease associated gene SEQ ID NO 39.
 PN WO20020927-A2.
 PD 03-JAN-2002.
 PA (EPIG-) EPIGENOMICS AG. 4.2%; Score 36.4; DB 6; Length 636;
 Query Match 4.2%; Score 36.4; DB 6; Length 636;
 Best Local Similarity 55.8%; Pred. No. 61;
 RESULT 929
 ID ABL33568 standard; DNA; 8305 BP.
 DE Human immune system associated gene SEQ ID NO: 1541.
 PN WO20020928-A2.
 PD 03-JAN-2002.
 PA (EPIG-) EPIGENOMICS AG. 4.2%; Score 36.4; DB 6; Length 8305;
 Query Match 4.2%; Score 36.4; DB 6; Length 8305;
 Best Local Similarity 55.6%; Pred. No. 68;
 RESULT 930
 ID ADQ22695 standard; DNA; 12010 BP.
 DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 5515.
 PN WO2004048938-A2.
 PD 10-JUN-2004.
 PA (PROT-) PROTEIN DESIGN LABS INC. 4.2%; Score 36.4; DB 12; Length 12010;
 Query Match 4.2%; Score 36.4; DB 12; Length 12010;

Best Local Similarity 61.7%; Pred. No. 80;
 RESULT 931
 ID ADQ22739 standard; DNA; 12010 BP.
 DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 5559.
 PN WO2004048938-A2.
 PD 10-JUN-2004.
 PA (PROT-) PROTEIN DESIGN LABS INC. 4.2%; Score 36.4; DB 12; Length 12010;
 Query Match 4.2%; Score 36.4; DB 12; Length 12010;
 Best Local Similarity 61.7%; Pred. No. 80;
 RESULT 932
 ID ADQ97056 standard; DNA; 169865 BP.
 DE Human cancer associated sequence HD11-007, SEQ ID 32.
 PN WO2004060304-A2.
 PD 22-JUL-2004.
 PA (SAGR-) SAGRES DISCOVERY INC. 4.2%; Score 36.4; DB 12; Length 169865;
 Query Match 4.2%; Score 36.4; DB 12; Length 169865;
 Best Local Similarity 49.5%; Pred. No. 2.7e+02;
 RESULT 933
 ID AAS63092 standard; cDNA; 139 BP.
 DE Cell death protective sequence CNT-00728, ORF #24.
 PN WO200176532-A2.
 PD 18-OCT-2001.
 PA (COGE-) COGENT NEUROSCIENCE INC. 4.2%; Score 36.2; DB 6; Length 139;
 Query Match 4.2%; Score 36.2; DB 6; Length 139;
 Best Local Similarity 65.4%; Pred. No. 12;
 RESULT 934
 ID ABV60296 standard; cDNA; 238 BP.
 DE Human prostate expression marker cDNA 60287.
 PN WO200160860-A2.
 PD 23-AUG-2001.
 PA (MILL-) MILLENIUM PREDICTIVE MEDICINE INC. 4.2%; Score 36.2; DB 5; Length 238;
 Query Match 4.2%; Score 36.2; DB 5; Length 238;
 Best Local Similarity 68.5%; Pred. No. 15;
 RESULT 935
 ID ACN59994 standard; cDNA; 282 BP.
 DE Cotton gynoecium tissue EST Clone ID: L1B3829-036-Q1-N6-D2, SEQ:14775.
 PN US2004123340-A1.
 PD 24-JUN-2004.
 PA (DEIK/) DEIKMAN J. 4.2%; Score 36.2; DB 13; Length 282;
 PA (FENG/) FENG P C C. 4.2%; Score 36.2; DB 13; Length 282;
 PA (FINC/) FINCHER K L. 4.2%; Score 36.2; DB 13; Length 282;
 PA (ZIEG/) ZIEGLER T E. 4.2%; Score 36.2; DB 13; Length 282;
 Query Match 4.2%; Score 36.2; DB 13; Length 282;
 Best Local Similarity 47.9%; Pred. No. 17;
 RESULT 936
 ID ACN33051 standard; cDNA; 328 BP.
 DE Cotton androecium tissue EST Clone ID: L1B3828-021-Q1-N6-C4, SEQ:7832.
 PN US2004123340-A1.
 PD 24-JUN-2004.
 PA (DEIK/) DEIKMAN J. 4.2%; Score 36.2; DB 13; Length 328;
 PA (FENG/) FENG P C C. 4.2%; Score 36.2; DB 13; Length 328;
 PA (FINC/) FINCHER K L. 4.2%; Score 36.2; DB 13; Length 328;
 PA (ZIEG/) ZIEGLER T E. 4.2%; Score 36.2; DB 13; Length 328;
 Query Match 4.2%; Score 36.2; DB 13; Length 328;
 Best Local Similarity 47.9%; Pred. No. 18;
 RESULT 937
 ID ABX40394 standard; cDNA; 358 BP.
 DE Bovine EST associated with lactation/muscle/fat deposition #5559.
 PN US2002137139-A1.
 PD 26-SEP-2002.
 PA (BYAT/) BYATT J C. 4.2%; Score 36.2; DB 8; Length 358;
 PA (MATH/) MATHIALAGAN N. 4.2%; Score 36.2; DB 8; Length 358;
 PA (TAON/) TAO N. 4.2%; Score 36.2; DB 8; Length 358;
 PA (WARR/) WARREN W C. 4.2%; Score 36.2; DB 8; Length 358;
 Query Match 4.2%; Score 36.2; DB 8; Length 358;
 Best Local Similarity 59.0%; Pred. No. 19;
 RESULT 938
 ID AAI30868 standard; cDNA; 369 BP.
 DE Human polynucleotide SEQ ID NO 10928.
 PN WO200164835-A2.
 PD 07-SEP-2001.
 PA (HYSE-) HYSEQ INC. 4.2%; Score 36.2; DB 4; Length 369;
 Query Match 4.2%; Score 36.2; DB 4; Length 369;

Best Local Similarity 65.4%; Pred. No. 19;
RESULT 939
ID ADQ04292 standard; DNA; 439 BP.
DE Maize transcription factor seqid 1138.
PN US2004123339-A1.
PD 24-JUN-2004.
PA (CONN/) CONNER T W.
PA (HECK/) HECK G R.
PA (LIUJ/) LIU J.
Query Match
Best Local Similarity 4.2%; Score 36.2; DB 12; Length 439;
RESULT 940
ID AD261999 standard; DNA; 673 BP.
DE Murine Tscap91a gene, SEQ ID 1723.
PN US2005084872-A1.
PD 21-APR-2005.
PA (LUMP/) LUM P Y.
PA (TANY/) TAN Y.
PA (DAIH/) DAI H.
PA (MUIS/) MUISE E S.
PA (BERG/) BERGER J P.
PA (THOM/) THOMPSON J R.
Query Match
Best Local Similarity 4.2%; Score 36.2; DB 14; Length 673;
RESULT 941
ID AAC59830 standard; DNA; 1176 BP.
DE Human secreted protein encoding DNA clone vq9 1.
PN WO200055375-A1.
PD 21-SEP-2000.
PA (ALPH-) ALPHAGENE INC.
Query Match
Best Local Similarity 4.2%; Score 36.2; DB 3; Length 1176;
RESULT 942
ID AAG63068 standard; cDNA; 1466 BP.
DE Cell death protective sequence CNI-00728.
PN WO200176532-A2.
PD 18-OCT-2001.
PA (COGE-) COGENT NEUROSCIENCE INC.
Query Match
Best Local Similarity 4.2%; Score 36.2; DB 6; Length 1466;
RESULT 943
ID ADP04700 standard; cDNA; 2275 BP.
DE Sea squirt cDNA with tissue specific expression in development Seq 295.
PN JP2004057129-A.
PD 26-FEB-2004.
PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
Query Match
Best Local Similarity 52.2%; Pred. No. 43;
RESULT 944
ID ADG75808 standard; DNA; 2534 BP.
DE Human protein modification and maintenance molecule DNA SeqID132.
PN WO2003083084-A2.
PD 09-OCT-2003.
PA (INCY-) INCYTE CORP.
Query Match
Best Local Similarity 4.2%; Score 36.2; DB 10; Length 2534;
RESULT 945
ID AD249479 standard; DNA; 2867 BP.
DE Insulin signaling pathway related gene, SEQ ID 808.
PN US2005085436-A1.
PD 21-APR-2005.
PA (LIHH/) LI H.
PA (MAJJ/) MA J.
Query Match
Best Local Similarity 4.2%; Score 36.2; DB 14; Length 2867;
RESULT 946
ID ABB69145 standard; DNA; 2867 BP.
DE Human modulator of IGF1R pathway polynucleotide #22.
PN WO2005073723-A1.
PD 11-AUG-2005.
PA (EXEL-) EXELIXIS INC.
PA (NICO/) NICOLL M.
Query Match

Best Local Similarity 59.0%; Pred. No. 48;
RESULT 947
ID AAF15852 standard; cDNA; 2873 BP.
DE Human prostate cancer antigen nucleotide sequence SEQ ID NO:287.
PN WO200055174-A1.
PD 21-SEP-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
PA (ROSE/) ROSEN C A.
Query Match
Best Local Similarity 4.2%; Score 36.2; DB 3; Length 2873;
RESULT 948
ID ABO67152 standard; DNA; 5867 BP.
DE Human angiogenesis associated polynucleotide SEQ ID NO 182.
PN WO200246454-A2.
PD 13-JUN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match
Best Local Similarity 4.2%; Score 36.2; DB 6; Length 5867;
RESULT 949
ID ABR39967 standard; DNA; 8943 BP.
DE Human chemically pretreated gene sequence #24 strand 2.
PN WO200202806-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match
Best Local Similarity 4.2%; Score 36.2; DB 6; Length 8943;
RESULT 950
ID ABL33501 standard; DNA; 9157 BP.
DE Human immune system associated gene SEQ ID NO: 1474.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match
Best Local Similarity 4.2%; Score 36.2; DB 6; Length 9157;
RESULT 951
ID ABL34178 standard; DNA; 13084 BP.
DE Human immune system associated gene SEQ ID NO: 2151.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match
Best Local Similarity 4.2%; Score 36.2; DB 6; Length 13084;
RESULT 952
ID ABV44994 standard; cDNA; 309 BP.
DE Human prostate expression marker cDNA 44985.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match
Best Local Similarity 4.1%; Score 36; DB 5; Length 309;
RESULT 953
ID AAL19599 standard; cDNA; 405 BP.
DE Human breast cancer expressed polynucleotide 12056.
PN WO200151628-A2.
PD 19-JUL-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match
Best Local Similarity 4.1%; Score 36; DB 4; Length 405;
RESULT 954
ID ABV23693 standard; cDNA; 489 BP.
DE Human prostate expression marker cDNA 23684.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match
Best Local Similarity 4.1%; Score 36; DB 5; Length 489;
RESULT 955
ID ABV29562 standard; cDNA; 489 BP.
DE Human prostate expression marker cDNA 29553.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match

Best Local Similarity 52.7%; Pred. No. 24;
RESULT 956
ID ACN55766 standard; cDNA; 513 BP.
DE Cotton androecium tissue EST Clone ID: LIB3828-028-Q6-N6-C2, SEQ:10547.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 4.1%; Score 36; DB 13; Length 513;
Best Local Similarity 47.7%; Pred. No. 25;
RESULT 957
ID ACN62215 standard; cDNA; 516 BP.
DE Cotton gynoecium tissue EST Clone ID: LIB3829-026-Q6-N6-F3, SEQ:16996.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 4.1%; Score 36; DB 13; Length 516;
Best Local Similarity 47.7%; Pred. No. 25;
RESULT 958
ID ACN53350 standard; cDNA; 528 BP.
DE Cotton androecium tissue EST Clone ID: LIB3828-006-Q1-N6-F8, SEQ:8131.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 4.1%; Score 36; DB 13; Length 528;
Best Local Similarity 47.7%; Pred. No. 25;
RESULT 959
ID ACN45364 standard; cDNA; 533 BP.
DE Cotton primed seed EST Clone ID: LIB3825-001-Q1-N6-A8, SEQ:145.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 4.1%; Score 36; DB 13; Length 533;
Best Local Similarity 64.3%; Pred. No. 25;
RESULT 960
ID ACN53339 standard; cDNA; 537 BP.
DE Cotton androecium tissue EST Clone ID: LIB3828-006-Q1-N6-D9, SEQ:8120.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 4.1%; Score 36; DB 13; Length 537;
Best Local Similarity 47.7%; Pred. No. 25;
RESULT 961
ID ACN51258 standard; cDNA; 554 BP.
DE Cotton androecium tissue EST Clone ID: LIB3828-013-Q1-N6-B2, SEQ:6039.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 4.1%; Score 36; DB 13; Length 554;
Best Local Similarity 47.7%; Pred. No. 26;
RESULT 962
ID ACN46001 standard; cDNA; 559 BP.
DE Cotton primed seed EST Clone ID: LIB3825-012-Q1-N6-F6, SEQ:782.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.

PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 4.1%; Score 36; DB 13; Length 559;
Best Local Similarity 49.0%; Pred. No. 26;
RESULT 963
ID ACN52090 standard; cDNA; 571 BP.
DE Cotton androecium tissue EST Clone ID: LIB3828-011-Q1-N6-B9, SEQ:6871.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 4.1%; Score 36; DB 13; Length 571;
Best Local Similarity 47.7%; Pred. No. 26;
RESULT 964
ID ACN52875 standard; cDNA; 576 BP.
DE Cotton androecium tissue EST Clone ID: LIB3828-018-Q1-N6-H5, SEQ:7656.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 4.1%; Score 36; DB 13; Length 576;
Best Local Similarity 47.7%; Pred. No. 26;
RESULT 965
ID ACN51619 standard; cDNA; 579 BP.
DE Cotton androecium tissue EST Clone ID: LIB3828-005-Q1-N6-D4, SEQ:6400.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 4.1%; Score 36; DB 13; Length 579;
Best Local Similarity 47.4%; Pred. No. 26;
RESULT 966
ID ACN50136 standard; cDNA; 636 BP.
DE Cotton non-primed seed EST Clone ID: LIB3826-001-Q1-K6-F4, SEQ:4917.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 4.1%; Score 36; DB 13; Length 636;
Best Local Similarity 67.1%; Pred. No. 27;
RESULT 967
ID AAQ86744 standard; cDNA; 1285 BP.
DE TIMP-3 metalloproteinase inhibitor coding sequence.
PN WO9509913-A1.
PD 13-APR-1995.
PA (INCY-) INCYTE PHARM INC.
Query Match 4.1%; Score 36; DB 2; Length 1285;
Best Local Similarity 58.3%; Pred. No. 38;
RESULT 968
ID AAD07709 standard; cDNA; 1328 BP.
DE Human secreted protein-encoding gene 5 cDNA clone HPMGR66, SEQ ID NO:15.
PN WO200134800-A1.
PD 17-MAY-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.1%; Score 36; DB 5; Length 1328;
Best Local Similarity 54.5%; Pred. No. 38;
RESULT 969
ID AAD08331 standard; cDNA; 1355 BP.
DE Human secreted protein-encoding gene 20 cDNA clone HMEJL08, SEQ ID NO:59.
PN WO200136440-A1.
PD 25-MAY-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.1%; Score 36; DB 4; Length 1355;
Best Local Similarity 54.5%; Pred. No. 39;

RESULT 970
ID AAD07732 standard; cDNA; 1355 BP.
DE Human secreted protein-encoding Gene 5 cDNA clone HPMGR66, SEQ ID NO:38.
PN WO200134800-A1.
PD 17-MAY-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.1%; Score 36; DB 5; Length 1355;
Best Local Similarity 54.5%; Pred. No. 39;
RESULT 971
ID ADD71195 standard; cDNA; 2200 BP.
DE Human intracellular signalling molecule INTSIG-32 cDNA SEQ ID NO:84.
PN WO2003039348-A2.
PD 15-MAY-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 4.1%; Score 36; DB 10; Length 2200;
Best Local Similarity 58.3%; Pred. No. 48;
RESULT 972
ID ADB62738 standard; cDNA; 2390 BP.
DE Human cDNA encoding clone NT2NE20069580.
PN EP1308459-A2.
PD 07-MAY-2003.
PA (HELI-) RES ASSOC BIOTECHNOLOGY.
Query Match 4.1%; Score 36; DB 10; Length 2390;
Best Local Similarity 45.7%; Pred. No. 50;
RESULT 973
ID AEF65450 standard; cDNA; 3332 BP.
DE Mouse G protein-coupled receptor kinase 2 (GRK2) homolog gene sequence.
PN WO2006009890-A2.
PD 26-JAN-2006.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 4.1%; Score 36; DB 10; Length 3332;
Best Local Similarity 50.0%; Pred. No. 58;
RESULT 974
ID ABL06562 standard; cDNA; 4453 BP.
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 14168.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 4.1%; Score 36; DB 4; Length 4453;
Best Local Similarity 55.6%; Pred. No. 66;
RESULT 975
ID ABQ67069 standard; cDNA; 5611 BP.
DE Human angiogenesis associated polynucleotide SEQ ID NO 99.
PN WO200246454-A2.
PD 13-JUN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.1%; Score 36; DB 6; Length 5611;
Best Local Similarity 62.0%; Pred. No. 73;
RESULT 976
ID ABL34078 standard; cDNA; 6062 BP.
DE Human immune system associated gene SEQ ID NO: 2051.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.1%; Score 36; DB 6; Length 6062;
Best Local Similarity 67.1%; Pred. No. 76;
RESULT 977
ID ABQ67048 standard; cDNA; 14362 BP.
DE Human angiogenesis associated polynucleotide SEQ ID NO 78.
PN WO200246454-A2.
PD 13-JUN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.1%; Score 36; DB 6; Length 14362;
Best Local Similarity 54.5%; Pred. No. 1.1e+02;
RESULT 978
ID AAS45514 standard; cDNA; 14708 BP.
DE Chemically pretreated genomic DNA associated with cell cycle #110.
PN WO200168911-A2.
PD 20-SEP-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.1%; Score 36; DB 4; Length 14708;
Best Local Similarity 54.5%; Pred. No. 1.1e+02;

RESULT 979
ID ABL34245 standard; cDNA; 14708 BP.
DE Human immune system associated gene SEQ ID NO: 2218.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.1%; Score 36; DB 6; Length 14708;
Best Local Similarity 54.5%; Pred. No. 1.1e+02;
RESULT 980
ID ABU92325 standard; cDNA; 14708 BP.
DE Chemically treated DNA repair gene fragment complementary to #67.
PN WO200181622-A2.
PD 01-NOV-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.1%; Score 36; DB 6; Length 14708;
Best Local Similarity 54.5%; Pred. No. 1.1e+02;
RESULT 981
ID ABK28450 standard; cDNA; 14708 BP.
DE DNA transcription associated complementary genomic DNA #162.
PN WO200192565-A2.
PD 06-DEC-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.1%; Score 36; DB 6; Length 14708;
Best Local Similarity 54.5%; Pred. No. 1.1e+02;
RESULT 982
ID ABL32654 standard; cDNA; 17211 BP.
DE Human immune system associated gene SEQ ID NO: 627.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.1%; Score 36; DB 6; Length 17211;
Best Local Similarity 49.2%; Pred. No. 1.2e+02;
RESULT 983
ID ABL32767 standard; cDNA; 19659 BP.
DE Human immune system associated gene SEQ ID NO: 740.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.1%; Score 36; DB 6; Length 19659;
Best Local Similarity 67.1%; Pred. No. 1.3e+02;
RESULT 984
ID AAK90436 standard; cDNA; 21860 BP.
DE Human digestive system antigen genomic sequence SEQ ID NO: 4012.
PN WO200155314-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.1%; Score 36; DB 4; Length 21860;
Best Local Similarity 67.1%; Pred. No. 1.4e+02;
RESULT 985
ID AAK7599 standard; cDNA; 21860 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:32411.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.1%; Score 36; DB 4; Length 21860;
Best Local Similarity 67.1%; Pred. No. 1.4e+02;
RESULT 986
ID AAL37438 standard; cDNA; 21860 BP.
DE Human musculoskeletal system related polynucleotide SEQ ID NO 3803.
PN WO200155367-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.1%; Score 36; DB 4; Length 21860;
Best Local Similarity 67.1%; Pred. No. 1.4e+02;
RESULT 987
ID AAD16680 standard; cDNA; 21860 BP.
DE Human pancreatic related protein-encoding genomic DNA, SEQ ID NO:44.
PN WO200155327-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.1%; Score 36; DB 5; Length 21860;
Best Local Similarity 67.1%; Pred. No. 1.4e+02;
RESULT 988
ID ABX60426 standard; cDNA; 21860 BP.

DE cDNA encoding novel human musculoskeletal system antigen #2770.
PN US2002147140-A1.
PD 10-OCT-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 4.1%; Score 36; DB 8; Length 21860;
Best Local Similarity 67.1%; Pred. No. 1.4e+02;
RESULT 989
ID ADJ31176 standard; DNA; 21860 BP.
DE Human musculoskeletal system-associated genomic DNA - SEQ ID 3803.
PN US2004009488-A1.
PD 15-JAN-2004.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.1%; Score 36; DB 12; Length 21860;
Best Local Similarity 67.1%; Pred. No. 1.4e+02;
RESULT 990
ID ABL07108 standard; cDNA; 48452 BP.
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 15806.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 4.1%; Score 36; DB 4; Length 48452;
Best Local Similarity 60.0%; Pred. No. 1.9e+02;
RESULT 991
ID AAL28691 standard; DNA; 41 BP.
DE Human SNP oligonucleotide #1899.
PN WO200147944-A2.
PD 05-JUL-2001.
PA (CURA-) CURAGEN CORP.
Query Match 4.1%; Score 35.8; DB 4; Length 41;
Best Local Similarity 94.9%; Pred. No. 9;
RESULT 992
ID AAA08355 standard; DNA; 47 BP.
DE Human TGC-440 secretory protein PCR primer SEQ ID NO:16.
PN WO200014226-A1.
PD 16-MAR-2000.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 4.1%; Score 35.8; DB 3; Length 47;
Best Local Similarity 85.1%; Pred. No. 9.6;
RESULT 993
ID ABX44678 standard; cDNA; 368 BP.
DE Bovine EST associated with lactation/muscle/fat deposition #9843.
PN US2002137139-A1.
PD 26-SEP-2002.
PA (BYAT/) BYATT J C.
PA (MATH/) MATHIALAGAN N.
PA (TAON/) TAO N.
PA (WARR/) WARREN W C.
Query Match 4.1%; Score 35.8; DB 8; Length 368;
Best Local Similarity 65.8%; Pred. No. 24;
RESULT 994
ID AAI86808 standard; cDNA; 377 BP.
DE Human polynucleotide SEQ ID NO 6868.
PN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 4.1%; Score 35.8; DB 4; Length 377;
Best Local Similarity 61.1%; Pred. No. 25;
RESULT 995
ID AAI88641 standard; cDNA; 384 BP.
DE Human polynucleotide SEQ ID NO 8701.
PN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 4.1%; Score 35.8; DB 4; Length 384;
Best Local Similarity 61.1%; Pred. No. 25;
RESULT 996
ID ABV59190 standard; cDNA; 460 BP.
DE Human prostate expression marker cDNA 59181.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.

Query Match 4.1%; Score 35.8; DB 5; Length 460;
Best Local Similarity 63.2%; Pred. No. 27;
RESULT 997
ID ACN51760 standard; cDNA; 467 BP.
DE Cotton androecium tissue EST Clone ID: LIB3828-007-Q1-N6-P9, SEQ.6541.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 4.1%; Score 35.8; DB 13; Length 467;
Best Local Similarity 48.7%; Pred. No. 27;
RESULT 998
ID ABK5238 standard; cDNA; 486 BP.
DE Human colon cancer-associated cDNA, SEQ ID NO 708.
PN WO200212280-A2.
PD 14-FEB-2002.
PA (CORI-) CORIXA CORP.
Query Match 4.1%; Score 35.8; DB 6; Length 486;
Best Local Similarity 57.1%; Pred. No. 28;
RESULT 999
ID ADT94877 standard; cDNA; 563 BP.
DE Colon cancer associated human cDNA sequence #396.
PN US2003087818-A1.
PD 08-MAY-2003.
PA (CORI-) CORIXA CORP.
Query Match 4.1%; Score 35.8; DB 11; Length 563;
Best Local Similarity 57.1%; Pred. No. 29;
RESULT 1000
ID ADX41359 standard; cDNA; 563 BP.
DE Human cDNA encoding colon cancer protein SEQ ID NO 396.
PN WO200274156-A2.
PD 26-SEP-2002.
PA (CORI-) CORIXA CORP.
Query Match 4.1%; Score 35.8; DB 11; Length 563;
Best Local Similarity 57.1%; Pred. No. 29;
RESULT 1001
ID ADT95504 standard; cDNA; 587 BP.
DE Colon cancer associated human cDNA sequence #1023.
PN US2003087818-A1.
PD 08-MAY-2003.
PA (CORI-) CORIXA CORP.
Query Match 4.1%; Score 35.8; DB 11; Length 587;
Best Local Similarity 57.1%; Pred. No. 30;
RESULT 1002
ID ADX41986 standard; cDNA; 587 BP.
DE Human cDNA encoding colon cancer protein SEQ ID NO 1023.
PN WO200274156-A2.
PD 26-SEP-2002.
PA (CORI-) CORIXA CORP.
Query Match 4.1%; Score 35.8; DB 11; Length 587;
Best Local Similarity 57.1%; Pred. No. 30;
RESULT 1003
ID AAV58362 standard; cDNA; 618 BP.
DE Coding sequence for secreted protein of clone DO19_1.
PN WO9837094-A2.
PD 27-AUG-1998.
PA (GEMY) GENETICS INST INC.
Query Match 4.1%; Score 35.8; DB 2; Length 618;
Best Local Similarity 61.1%; Pred. No. 31;
RESULT 1004
ID ADT95765 standard; cDNA; 644 BP.
DE Colon cancer associated human cDNA sequence #1284.
PN US2003087818-A1.
PD 08-MAY-2003.
PA (CORI-) CORIXA CORP.
Query Match 4.1%; Score 35.8; DB 11; Length 644;
Best Local Similarity 57.1%; Pred. No. 31;
RESULT 1005
ID ADX42247 standard; cDNA; 644 BP.
DE Human cDNA encoding colon cancer protein SEQ ID NO 1284.
PN WO200274156-A2.

PD 26-SEP-2002.
PA (CORI-) CORIXA CORP.
Query Match 4.1%; Score 35.8; DB 11; Length 644;
Best Local Similarity 57.1%; Pred. No. 31;
RESULT 1006
ID ADP76748 standard; cDNA; 963 BP.
DE Novel human secreted and transmembrane protein cDNA SeqID 423.
PN WO2003072035-A2.
PD 04-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 4.1%; Score 35.8; DB 10; Length 963;
Best Local Similarity 65.8%; Pred. No. 38;
RESULT 1007
ID AAD05534 standard; cDNA; 1011 BP.
DE Human secreted protein-encoding gene 7 cDNA clone HOFMQ33, SEQ ID NO:53.
PN WO200134767-A2.
PD 17-MAY-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.1%; Score 35.8; DB 4; Length 1011;
Best Local Similarity 65.8%; Pred. No. 38;
RESULT 1008
ID ADA40429 standard; cDNA; 1011 BP.
DE Human secreted protein encoding cDNA.
PN WO2002102993-A2.
PD 27-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.1%; Score 35.8; DB 8; Length 1011;
Best Local Similarity 65.8%; Pred. No. 38;
RESULT 1009
ID ACC50793 standard; cDNA; 1011 BP.
DE Human secreted protein coding sequence, SEQ ID 460.
PN WO200295010-A2.
PD 28-NOV-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.1%; Score 35.8; DB 8; Length 1011;
Best Local Similarity 65.8%; Pred. No. 38;
RESULT 1010
ID ABZ71437 standard; cDNA; 1011 BP.
DE Secreted protein-encoding gene 129 cDNA clone HOFMQ33, SEQ ID NO:258.
PN WO200276488-A1.
PD 03-OCT-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.1%; Score 35.8; DB 8; Length 1011;
Best Local Similarity 65.8%; Pred. No. 38;
RESULT 1011
ID ADB91395 standard; cDNA; 1011 BP.
DE Human secreted protein cDNA #SEQ ID 341.
PN WO2003004622-A2.
PD 16-JAN-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.1%; Score 35.8; DB 9; Length 1011;
Best Local Similarity 65.8%; Pred. No. 38;
RESULT 1012
ID ADC73895 standard; cDNA; 1011 BP.
DE Human secreted protein-related DNA - SEQ ID 528.
PN WO2003038063-A2.
PD 08-MAY-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.1%; Score 35.8; DB 10; Length 1011;
Best Local Similarity 65.8%; Pred. No. 38;
RESULT 1013
ID ADA56594 standard; cDNA; 1011 BP.
DE Gene encoding human secreted protein #404.
PN WO2002102994-A2.
PD 27-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.1%; Score 35.8; DB 10; Length 1011;
Best Local Similarity 65.8%; Pred. No. 38;
RESULT 1014
ID ABQ54241 standard; cDNA; 1106 BP.
DE Human ovarian antigen HRACW30 cDNA, SEQ ID NO:121.
PN WO200200677-A1.
PD 03-JAN-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.1%; Score 35.8; DB 6; Length 1106;
Best Local Similarity 52.0%; Pred. No. 40;
RESULT 1015
ID ADD78282 standard; DNA; 1612 BP.
DE Human CGDD-24 coding sequence.
PN WO2003077875-A2.
PD 25-SEP-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 4.1%; Score 35.8; DB 10; Length 1612;
Best Local Similarity 63.2%; Pred. No. 47;
RESULT 1016
ID ABK43722 standard; cDNA; 1887 BP.
DE DNA encoding novel central nervous system protein #302.
PN WO200155318-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.1%; Score 35.8; DB 4; Length 1887;
Best Local Similarity 61.1%; Pred. No. 51;
RESULT 1017
ID ADI54109 standard; cDNA; 1887 BP.
DE cDNA encoding novel human protein seq id 312.
PN US2004018969-A1.
PD 29-JAN-2004.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 4.1%; Score 35.8; DB 12; Length 1887;
Best Local Similarity 61.1%; Pred. No. 51;
RESULT 1018
ID ADI32345 standard; DNA; 1944 BP.
DE Mouse OAS1b DNA.
PN US2003235575-A1.
PD 25-DEC-2003.
PA (AMHP) WYETH.
PA (BAYU) BAYLOR COLLEGE MEDICINE.
Query Match 4.1%; Score 35.8; DB 12; Length 1944;
Best Local Similarity 51.6%; Pred. No. 52;
RESULT 1019
ID AAT59700 standard; DNA; 2001 BP.
DE PTH-like peptide DNA clone HHM-8.
PN US5605815-A.
PD 25-FEB-1997.
PA (UYVA) UNIV YALE.
Query Match 4.1%; Score 35.8; DB 2; Length 2001;
Best Local Similarity 59.2%; Pred. No. 52;
RESULT 1020
ID AAC79959 standard; cDNA; 2329 BP.
DE Human secreted protein encoding cDNA for gene 12.
PN WO200058357-A1.
PD 05-OCT-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.1%; Score 35.8; DB 3; Length 2329;
Best Local Similarity 57.7%; Pred. No. 56;
RESULT 1021
ID AAZ51555 standard; cDNA; 3535 BP.
DE Human hypoxia response regulating gene, 95 cDNA.
PN WO200012525-A1.
PD 09-MAR-2000.
PA (QUAR-) QUARK BIOTECH INC.
PA (KOHN/) KOHN K.
Query Match 4.1%; Score 35.8; DB 3; Length 3535;
Best Local Similarity 54.1%; Pred. No. 68;
RESULT 1022
ID ADQ22432 standard; DNA; 3982 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 5252.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 4.1%; Score 35.8; DB 12; Length 3982;
Best Local Similarity 52.3%; Pred. No. 71;
RESULT 1023
ID ACN88609 standard; DNA; 4296 BP.

DE Breast cancer related marker, seq id 9759.
PN US200309974-A1.
PD 29-MAY-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 4.1%; Score 35.8; DB 11; Length 4296;
Best Local Similarity 51.8%; Pred. No. 74;
RESULT 1024
ID ACN90377 standard; DNA; 4552 BP.
DE Breast cancer related marker, seq id 11527.
PN US200309974-A1.
PD 29-MAY-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 4.1%; Score 35.8; DB 11; Length 4552;
Best Local Similarity 65.8%; Pred. No. 76;
RESULT 1025
ID AAS60872 standard; cDNA; 4877 BP.
DE Human cancer agent-resistance marker #531.
PN WO200179556-A2.
PD 25-OCT-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.1%; Score 35.8; DB 4; Length 4877;
Best Local Similarity 63.2%; Pred. No. 78;
RESULT 1026
ID AAS60871 standard; cDNA; 4877 BP.
DE Human cancer agent-resistance marker #530.
PN WO200179556-A2.
PD 25-OCT-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.1%; Score 35.8; DB 4; Length 4877;
Best Local Similarity 63.2%; Pred. No. 78;
RESULT 1027
ID AAS60883 standard; cDNA; 4877 BP.
DE Human cancer agent-resistance marker #542.
PN WO200179556-A2.
PD 25-OCT-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.1%; Score 35.8; DB 4; Length 4877;
Best Local Similarity 63.2%; Pred. No. 78;
RESULT 1028
ID ABN80020 standard; DNA; 6561 BP.
DE Human chemically modified disease associated gene SEQ ID NO 37.
PN WO200200927-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.1%; Score 35.8; DB 6; Length 6561;
Best Local Similarity 52.3%; Pred. No. 89;
RESULT 1029
ID ABL32638 standard; DNA; 6650 BP.
DE Human immune system associated gene SEQ ID NO: 611.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.1%; Score 35.8; DB 6; Length 6650;
Best Local Similarity 65.8%; Pred. No. 90;
RESULT 1030
ID AAS46727 standard; DNA; 7244 BP.
DE Tumour suppressor gene derived chemically modified sequence #450.
PN WO200168912-A2.
PD 20-SEP-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.1%; Score 35.8; DB 4; Length 7244;
Best Local Similarity 55.1%; Pred. No. 94;
RESULT 1031
ID ABL92323 standard; DNA; 10762 BP.
DE Chemically treated DNA repair gene fragment complementary to #66.
PN WO200181622-A2.
PD 01-NOV-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.1%; Score 35.8; DB 6; Length 10762;
Best Local Similarity 65.8%; Pred. No. 1.1e+02;
RESULT 1032
ID ABL33451 standard; DNA; 19787 BP.
DE Human immune system associated gene SEQ ID NO: 1424.

PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.1%; Score 35.8; DB 6; Length 19787;
Best Local Similarity 44.2%; Pred. No. 1.5e+02;
RESULT 1033
ID ABD33498 standard; DNA; 23503 BP.
DE Murine cancer-associated (CA) gene MD07-097.
PN WO2004058146-A2.
PD 15-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 4.1%; Score 35.8; DB 13; Length 23503;
Best Local Similarity 56.3%; Pred. No. 1.6e+02;
RESULT 1034
ID AAS46787 standard; DNA; 61020 BP.
DE Tumour suppressor gene derived chemically modified sequence #513.
PN WO200168912-A2.
PD 20-SEP-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.1%; Score 35.8; DB 4; Length 61020;
Best Local Similarity 65.8%; Pred. No. 2.5e+02;
RESULT 1035
ID AAF22293 standard; DNA; 101786 BP.
DE BAC containing repeats from centromeres 1-4 #16.
PN WO200055325-A2.
PD 21-SEP-2000.
PA (UYCH-) UNIV CHICAGO.
Query Match 4.1%; Score 35.8; DB 3; Length 101786;
Best Local Similarity 65.8%; Pred. No. 3.1e+02;
RESULT 1036
ID ADI76910 standard; DNA; 250 BP.
DE Human ovarian cancer DNA marker #9652.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.1%; Score 35.6; DB 5; Length 250;
Best Local Similarity 39.4%; Pred. No. 23;
RESULT 1037
ID ADI70589 standard; DNA; 250 BP.
DE Human ovarian cancer DNA marker #3331.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.1%; Score 35.6; DB 5; Length 250;
Best Local Similarity 39.4%; Pred. No. 23;
RESULT 1038
ID ABV19977 standard; cDNA; 295 BP.
DE Human prostate expression marker cDNA i9968.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.1%; Score 35.6; DB 5; Length 295;
Best Local Similarity 62.2%; Pred. No. 25;
RESULT 1039
ID ABV49738 standard; cDNA; 303 BP.
DE Human prostate expression marker cDNA 49729.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.1%; Score 35.6; DB 5; Length 303;
Best Local Similarity 62.2%; Pred. No. 25;
RESULT 1040
ID ADM16713 standard; DNA; 346 BP.
DE PRM-P5-H4 encoding sequence.
PN WO2004027041-A2.
PD 01-APR-2004.
PA (MERI-) MERIAL LTD.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
Query Match 4.1%; Score 35.6; DB 12; Length 346;
Best Local Similarity 58.5%; Pred. No. 27;
RESULT 1041
ID ABV54410 standard; cDNA; 462 BP.
DE Human prostate expression marker cDNA 54401.

PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.1%; Score 35.6; DB 5; Length 462;
Best Local Similarity 62.2%; Pred. No. 31;
RESULT 1042
ID AA193637 standard; cDNA; 478 BP.
DE Human polynucleotide SEQ ID NO 13697.
PN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 4.1%; Score 35.6; DB 4; Length 478;
Best Local Similarity 47.7%; Pred. No. 31;
RESULT 1043
ID AA187737 standard; cDNA; 481 BP.
DE Human polynucleotide SEQ ID NO 7797.
PN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 4.1%; Score 35.6; DB 4; Length 481;
Best Local Similarity 53.6%; Pred. No. 31;
RESULT 1044
ID ACH38616 standard; cDNA; 481 BP.
DE Human endothelial cell cDNA #6749.
PN US2003073623-A1.
PD 17-APR-2003.
PA (DRMA/) DRMANAC R T.
PA (LABA/) LABAT I.
PA (STAC/) STACHE-CRAIN B.
PA (DICK/) DICKSON M C.
PA (JONE/) JONES L W.
Query Match 4.1%; Score 35.6; DB 9; Length 481;
Best Local Similarity 53.6%; Pred. No. 31;
RESULT 1045
ID ACN48060 standard; cDNA; 487 BP.
DE Cotton primed seed EST Clone ID: LIB3825-018-Q1-N6-F4, SEQ:2841.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 4.1%; Score 35.6; DB 13; Length 487;
Best Local Similarity 47.3%; Pred. No. 31;
RESULT 1046
ID AAK57064 standard; cDNA; 532 BP.
DE Human immune/haematopoietic antigen encoding cDNA SEQ ID NO:2124.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUNA-) HUMAN GENOME SCI INC.
Query Match 4.1%; Score 35.6; DB 4; Length 532;
Best Local Similarity 57.4%; Pred. No. 33;
RESULT 1047
ID ACN62126 standard; cDNA; 533 BP.
DE Cotton gynoecium tissue EST Clone ID: LIB3829-025-Q6-N6-E11, SEQ:16907.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 4.1%; Score 35.6; DB 13; Length 533;
Best Local Similarity 47.9%; Pred. No. 33;
RESULT 1048
ID ABV14236 standard; cDNA; 545 BP.
DE Human prostate expression marker cDNA 14227.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.1%; Score 35.6; DB 5; Length 545;
Best Local Similarity 53.6%; Pred. No. 33;
RESULT 1049
ID AAH31453 standard; cDNA; 632 BP.

DE Human olfactory receptor polynucleotide, SEQ ID NO: 25.
PN WO200127158-A2.
PD 19-APR-2001.
PA (DIGI-) DIGISCENTS.
PA (YEDA) YEDA RES & DEV CO LTD.
Query Match 4.1%; Score 35.6; DB 4; Length 632;
Best Local Similarity 49.5%; Pred. No. 35;
RESULT 1050
ID ADE29043 standard; DNA; 683 BP.
DE Human selected interacting domain DNA - SEQ ID 29.
PN WO2003046176-A2.
PD 05-JUN-2003.
PA (HYBR-) HYBRIGENICS.
Query Match 4.1%; Score 35.6; DB 10; Length 683;
Best Local Similarity 60.2%; Pred. No. 36;
RESULT 1051
ID ABN98603 standard; DNA; 936 BP.
DE Arabidopsis thaliana expressed polynucleotide SEQ ID NO 371.
PN US2002023281-A1.
PD 21-FEB-2002.
PA (GORL/) GORLACH J.
PA (ANY/) AN Y.
PA (HAMI/) HAMILTON C M.
PA (PRIC/) PRICE J L.
PA (RAIN/) RAINES T M.
PA (YUY/) YU Y.
PA (RAME/) RAMEAKA J G.
PA (PAGE/) PAGE A.
PA (MATH/) MATHW A V.
PA (LEDF/) LEDFORD B L.
PA (WOES/) WOESSNER J P.
PA (HAAS/) HAAS W D.
PA (GARC/) GARCIA C A.
PA (KRIC/) KRICKER M.
PA (SLAT/) SLATER T.
PA (DAVI/) DAVIS K R.
PA (ALLE/) ALLEN K.
PA (HOFF/) HOFFMAN N.
PA (HURB/) HURBAN P.
Query Match 4.1%; Score 35.6; DB 6; Length 936;
Best Local Similarity 62.5%; Pred. No. 42;
RESULT 1052
ID ADF82222 standard; DNA; 1084 BP.
DE Leukaemia-related DNA sequence #2778.
PN WO2003039443-A2.
PD 15-MAY-2003.
PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
PA (UYLU-) UNIV LUDWIG MAXIMILIANS.
PA (HAPE/) HAFERLACH T.
PA (SCHO/) SCHOCH C.
PA (KERN/) KERN W.
Query Match 4.1%; Score 35.6; DB 10; Length 1084;
Best Local Similarity 64.6%; Pred. No. 45;
RESULT 1053
ID ADJ80201 standard; cDNA; 1103 BP.
DE Novel human nucleic acid-associated protein coding sequence #19.
PN WO2003038052-A2.
PD 08-MAY-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 4.1%; Score 35.6; DB 10; Length 1103;
Best Local Similarity 62.2%; Pred. No. 45;
RESULT 1054
ID AEC20303 standard; DNA; 1103 BP.
DE Human nucleic acid-associated protein (NAAP) coding sequence - SEQ ID 77.
PN US2005186569-A1.
PD 25-AUG-2005.
PA (BSCH/) BSCHA S D.
PA (BORO/) BOROWSKY M L.
PA (BURF/) BURFORD N.
PA (CHAW/) CHAWLA N K.
PA (ELLI/) ELLIOTT V S.
PA (EMER/) EMERLING B M.
PA (FORS/) FORSYTHE I J.

PA (GIET/) GIETZEN K J.
PA (GORV/) GORVAD A E.
PA (GRIF/) GRIFFIN J A.
PA (HAPA/) HAPALIA A J A.
PA (ISON/) ISON C H.
PA (LALP/) LAL P.
PA (LEES/) LEE E A.
PA (LEES/) LEE S.
PA (LEES/) LEE S Y.
PA (MARQ/) MARQUIS J P.
PA (RAMK/) RAMKOMAR J.
PA (SPRA/) SPRAGUE W W.
PA (SWAR/) SWARNAKAR A.
PA (TANG/) TANG Y T.
PA (WARR/) WARREN B A.
PA (YANG/) YANG J.
PA (YUEH/) YUE H.
PA (ZEBAR/) ZEBARJADIAN Y.
Query Match 4.1%; Score 35.6; DB 14; Length 1103;
Best Local Similarity 62.2%; Pred. No. 45;
RESULT 1055
ID AAC59836 standard; DNA; 1204 BP.
DE Human secreted protein encoding DNA clone vq21 1.
PN WO200055375-A1.
PD 21-SEP-2000.
PA (ALPH-) ALPHAGENE INC.
Query Match 4.1%; Score 35.6; DB 3; Length 1204;
Best Local Similarity 58.5%; Pred. No. 47;
RESULT 1056
ID ADT99265 standard; DNA; 1233 BP.
DE Mouse parkin protein encoding DNA.
PN US2004214763-A1.
PD 28-OCT-2004.
PA (AVET) AVENTIS PHARMA SA.
PA (INRM) INST NAT SANTE & RECH MEDICALE.
Query Match 4.1%; Score 35.6; DB 13; Length 1233;
Best Local Similarity 58.5%; Pred. No. 48;
RESULT 1057
ID ADP55498 standard; cDNA; 1284 BP.
DE Human PRO cDNA sequence SEQ ID NO:1474.
PN WO2004039956-A2.
PD 13-MAY-2004.
PA (GETH) GENENTECH INC.
Query Match 4.1%; Score 35.6; DB 13; Length 1284;
Best Local Similarity 60.2%; Pred. No. 49;
RESULT 1058
ID ABE83638 standard; cDNA; 1284 BP.
DE Human cDNA differentially expressed in asthma, SEQ ID NO:46.
PN WO2005118403-A2.
PD 15-DEC-2005.
PA (LINK-) LINKAGENE LTD.
Query Match 4.1%; Score 35.6; DB 15; Length 1284;
Best Local Similarity 60.2%; Pred. No. 49;
RESULT 1059
ID AAS26060 standard; cDNA; 1801 BP.
DE Human cDNA encoding a novel secreted protein, Seq ID 239.
PN WO200155322-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.1%; Score 35.6; DB 4; Length 1801;
Best Local Similarity 58.5%; Pred. No. 57;
RESULT 1060
ID ABX73401 standard; DNA; 1801 BP.
DE Human novel polynucleotide #229.
PN US2002132753-A1.
PD 19-SEP-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 4.1%; Score 35.6; DB 8; Length 1801;
Best Local Similarity 58.5%; Pred. No. 57;
RESULT 1061
ID AAL45822 standard; cDNA; 2185 BP.

DE Human secreted protein coding sequence SEQ ID NO: 27.
PN WO200228877-A1.
PD 11-APR-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.1%; Score 35.6; DB 6; Length 2185;
Best Local Similarity 60.2%; Pred. No. 62;
RESULT 1062
ID AAQ05055 standard; DNA; 2400 BP.
DE Placenta-specific protein Pp11 encoding DNA.
PN EP374909-A.
PD 27-JUN-1990.
PA (BEHW) BEHRINGERWERKE AG.
Query Match 4.1%; Score 35.6; DB 2; Length 2400;
Best Local Similarity 58.5%; Pred. No. 64;
RESULT 1063
ID AEF55950 standard; DNA; 2500 BP.
DE Human genomic DNA #557.
PN WO2006008128-A2.
PD 26-JAN-2006.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.1%; Score 35.6; DB 15; Length 2500;
Best Local Similarity 55.7%; Pred. No. 66;
RESULT 1064
ID AEF55714 standard; DNA; 2500 BP.
DE Human genomic DNA #321.
PN WO2006008128-A2.
PD 26-JAN-2006.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.1%; Score 35.6; DB 15; Length 2500;
Best Local Similarity 55.7%; Pred. No. 66;
RESULT 1065
ID AEF55557 standard; DNA; 2646 BP.
DE Human genomic DNA #164.
PN WO2006008128-A2.
PD 26-JAN-2006.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.1%; Score 35.6; DB 15; Length 2646;
Best Local Similarity 54.6%; Pred. No. 67;
RESULT 1066
ID ADE29042 standard; DNA; 2890 BP.
DE Human AIM1 selected interacting domain DNA - SEQ ID 28.
PN WO2003046176-A2.
PD 05-JUN-2003.
PA (HYBR-) HYBRIGENICS.
Query Match 4.1%; Score 35.6; DB 10; Length 2890;
Best Local Similarity 60.2%; Pred. No. 70;
RESULT 1067
ID ADA53524 standard; cDNA; 3266 BP.
DE Human coding sequence, SEQ ID 1092.
PN EP1293569-A2.
PD 19-MAR-2003.
PA (HELI-) HELIX RES INST.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 4.1%; Score 35.6; DB 10; Length 3266;
Best Local Similarity 60.2%; Pred. No. 74;
RESULT 1068
ID AAX87412 standard; cDNA; 3607 BP.
DE Hepatocellular carcinoma marker Gene L4 cDNA.
PN WO9939200-A1.
PD 05-AUG-1999.
PA (UYJE-) UNIV JEFFERSON THOMAS.
Query Match 4.1%; Score 35.6; DB 2; Length 3607;
Best Local Similarity 58.5%; Pred. No. 77;
RESULT 1069
ID ACN91230 standard; DNA; 3811 BP.
DE Breast cancer related marker, seq id 12380.
PN US200309974-A1.
PD 29-MAY-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 4.1%; Score 35.6; DB 11; Length 3811;
Best Local Similarity 64.6%; Pred. No. 79;
RESULT 1070
ID ADQ63590 standard; cDNA; 4092 BP.

DE Novel human cDNA sequence #751.
PN EPI440981-A2.
PD 28-JUL-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 4.1%; Score 35.6; DB 12; Length 4092;
Best Local Similarity 60.2%; Pred. No. 83;
RESULT 1071
ID AAZ34304 standard; cDNA; 4199 BP.
DE Human PRO286 nucleotide sequence.
PN WO9946281-A2.
PD 16-SEP-1999.
PA (GETH) GENENTECH INC.
Query Match 4.1%; Score 35.6; DB 2; Length 4199;
Best Local Similarity 60.2%; Pred. No. 83;
RESULT 1072
ID AAX58296 standard; cDNA; 4199 BP.
DE Human Toll protein PRO286 cDNA.
PN WO9920756-A2.
PD 29-APR-1999.
PA (GETH) GENENTECH INC.
Query Match 4.1%; Score 35.6; DB 2; Length 4199;
Best Local Similarity 60.2%; Pred. No. 83;
RESULT 1073
ID AAC78584 standard; cDNA; 4199 BP.
DE Human PRO286 nucleotide sequence SEQ ID NO:497.
PN WO200053756-A2.
PD 14-SEP-2000.
PA (GETH) GENENTECH INC.
Query Match 4.1%; Score 35.6; DB 3; Length 4199;
Best Local Similarity 60.2%; Pred. No. 83;
RESULT 1074
ID ACA63872 standard; cDNA; 4199 BP.
DE Novel human secreted and transmembrane protein PRO286 cDNA.
PN US2002192706-A1.
PD 19-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 4.1%; Score 35.6; DB 8; Length 4199;
Best Local Similarity 60.2%; Pred. No. 83;
RESULT 1075
ID ACA72036 standard; cDNA; 4199 BP.
DE Human secreted and transmembrane PRO polypeptide #32 cDNA.
PN US2002177553-A1.
PD 28-NOV-2002.
PA (GETH) GENENTECH INC.
Query Match 4.1%; Score 35.6; DB 8; Length 4199;
Best Local Similarity 60.2%; Pred. No. 83;
RESULT 1076
ID ABX92676 standard; cDNA; 4199 BP.
DE cDNA encoding human PRO286 polypeptide.
PN US2002169284-A1.
PD 14-NOV-2002.
PA (GETH) GENENTECH INC.
Query Match 4.1%; Score 35.6; DB 8; Length 4199;
Best Local Similarity 60.2%; Pred. No. 83;
RESULT 1077
ID ACA66417 standard; cDNA; 4199 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO286.
PN US2003004102-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 4.1%; Score 35.6; DB 8; Length 4199;
Best Local Similarity 60.2%; Pred. No. 83;
RESULT 1078
ID ACAG2618 standard; cDNA; 4199 BP.
DE Human cDNA encoding Toll protein PRO286.
PN US2003027260-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 4.1%; Score 35.6; DB 8; Length 4199;
Best Local Similarity 60.2%; Pred. No. 83;
RESULT 1079
ID ADA25036 standard; cDNA; 4199 BP.
DE Novel human secreted and transmembrane protein PRO286 cDNA.
PN US2003050241-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.1%; Score 35.6; DB 9; Length 4199;
Best Local Similarity 60.2%; Pred. No. 83;
RESULT 1080
ID ACJ30018 standard; cDNA; 4199 BP.
DE Novel human secreted and transmembrane protein PRO286 cDNA.
PN US2003050240-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.1%; Score 35.6; DB 9; Length 4199;
Best Local Similarity 60.2%; Pred. No. 83;
RESULT 1081
ID ADA12697 standard; cDNA; 4199 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO586.
PN US2003055216-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.1%; Score 35.6; DB 9; Length 4199;
Best Local Similarity 60.2%; Pred. No. 83;
RESULT 1082
ID ACD29433 standard; cDNA; 4199 BP.
DE Novel human secreted and transmembrane polypeptide cDNA #127.
PN US2003049633-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.1%; Score 35.6; DB 9; Length 4199;
Best Local Similarity 60.2%; Pred. No. 83;
RESULT 1083
ID AD874003 standard; cDNA; 4199 BP.
DE Human PRO polynucleotide sequence #127.
PN US2003045462-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.1%; Score 35.6; DB 10; Length 4199;
Best Local Similarity 60.2%; Pred. No. 83;
RESULT 1084
ID ADB76719 standard; cDNA; 4199 BP.
DE Human PRO polynucleotide sequence #127.
PN US2003083248-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 4.1%; Score 35.6; DB 10; Length 4199;
Best Local Similarity 60.2%; Pred. No. 83;
RESULT 1085
ID ADC44145 standard; cDNA; 4199 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO286.
PN US2003054986-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.1%; Score 35.6; DB 10; Length 4199;
Best Local Similarity 60.2%; Pred. No. 83;
RESULT 1086
ID ADC61905 standard; cDNA; 4199 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO286.
PN US2003049684-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.1%; Score 35.6; DB 10; Length 4199;
Best Local Similarity 60.2%; Pred. No. 83;
RESULT 1087
ID ADC63869 standard; cDNA; 4199 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO286.
PN US2003054405-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.1%; Score 35.6; DB 10; Length 4199;
Best Local Similarity 60.2%; Pred. No. 83;
RESULT 1088
ID ADC66969 standard; cDNA; 4199 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO286.
PN US2003060406-A1.
PD 27-MAR-2003.

PA (GETH) GENENTECH INC.
Query Match 4.1%; Score 35.6; DB 10; Length 4199;
Best Local Similarity 60.2%; Pred. No. 83;
RESULT 1099
ID ADC659093 standard; cDNA; 4199 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO286.
PN US2003064407-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.1%; Score 35.6; DB 10; Length 4199;
Best Local Similarity 60.2%; Pred. No. 83;
RESULT 1090
ID ADC63153 standard; cDNA; 4199 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO286.
PN US2003068648-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.1%; Score 35.6; DB 10; Length 4199;
Best Local Similarity 60.2%; Pred. No. 83;
RESULT 1091
ID ADC68218 standard; cDNA; 4199 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO286.
PN US2003069178-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.1%; Score 35.6; DB 10; Length 4199;
Best Local Similarity 60.2%; Pred. No. 83;
RESULT 1092
ID ADC41538 standard; cDNA; 4199 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO286.
PN US2003072745-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.1%; Score 35.6; DB 10; Length 4199;
Best Local Similarity 60.2%; Pred. No. 83;
RESULT 1093
ID ADC67593 standard; cDNA; 4199 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO286.
PN US2003073131-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.1%; Score 35.6; DB 10; Length 4199;
Best Local Similarity 60.2%; Pred. No. 83;
RESULT 1094
ID ADC62529 standard; cDNA; 4199 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO286.
PN US2003073624-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.1%; Score 35.6; DB 10; Length 4199;
Best Local Similarity 60.2%; Pred. No. 83;
RESULT 1095
ID ADC42162 standard; cDNA; 4199 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO286.
PN US2003104998-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 4.1%; Score 35.6; DB 10; Length 4199;
Best Local Similarity 60.2%; Pred. No. 83;
RESULT 1096
ID ADE49531 standard; cDNA; 4199 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO286.
PN US2003096744-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 4.1%; Score 35.6; DB 10; Length 4199;
Best Local Similarity 60.2%; Pred. No. 83;
RESULT 1097
ID ADE35585 standard; cDNA; 4199 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO286.
PN US2003203434-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.

Query Match 4.1%; Score 35.6; DB 10; Length 4199;
Best Local Similarity 60.2%; Pred. No. 83;
RESULT 1098
ID ADE16699 standard; cDNA; 4199 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO286.
PN US2003203435-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 4.1%; Score 35.6; DB 10; Length 4199;
Best Local Similarity 60.2%; Pred. No. 83;
RESULT 1099
ID ADD73314 standard; cDNA; 4199 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO286.
PN US2003203436-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 4.1%; Score 35.6; DB 10; Length 4199;
Best Local Similarity 60.2%; Pred. No. 83;
RESULT 1100
ID ADD72672 standard; cDNA; 4199 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO286.
PN US2003194781-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 4.1%; Score 35.6; DB 10; Length 4199;
Best Local Similarity 60.2%; Pred. No. 83;
RESULT 1101
ID ADE17323 standard; cDNA; 4199 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO286.
PN US2003203433-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 4.1%; Score 35.6; DB 10; Length 4199;
Best Local Similarity 60.2%; Pred. No. 83;
RESULT 1102
ID ADF47337 standard; cDNA; 4199 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO286.
PN US2003195333-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 4.1%; Score 35.6; DB 10; Length 4199;
Best Local Similarity 60.2%; Pred. No. 83;
RESULT 1103
ID ADG53094 standard; cDNA; 4199 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO286.
PN US2003216561-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 4.1%; Score 35.6; DB 10; Length 4199;
Best Local Similarity 60.2%; Pred. No. 83;
RESULT 1104
ID ADG60414 standard; cDNA; 4199 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO286.
PN US2003206915-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 4.1%; Score 35.6; DB 10; Length 4199;
Best Local Similarity 60.2%; Pred. No. 83;
RESULT 1105
ID ADI61174 standard; cDNA; 4199 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO286.
PN US2003077700-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.1%; Score 35.6; DB 10; Length 4199;
Best Local Similarity 60.2%; Pred. No. 83;
RESULT 1106
ID ADC42837 standard; cDNA; 4199 BP.
DE Novel human secreted and transmembrane protein PRO286 cDNA.
PN US2003050239-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.1%; Score 35.6; DB 10; Length 4199;


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Best Local Similarity 60.2%; Pred. No. 83;
RESULT 1107
ID ADE48831 standard; cDNA; 4199 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO286.
PN US2003104536-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 4.1%; Score 35.6; DB 12; Length 4199;
Best Local Similarity 60.2%; Pred. No. 83;
RESULT 1108
ID ADE89932 standard; cDNA; 4199 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO286.
PN US2003130181-A1.
PD 10-JUL-2003.
PA (ASHK/) ASHKENAZI A J.
PA (BAKE/) BAKER K P.
PA (BOTS/) BOTSTEIN D.
PA (DESN/) DESNOYERS L.
PA (EATO/) EATON D L.
PA (FERR/) FERRARA N.
PA (FILV/) FILVAROFF E.
PA (FONG/) FONG S.
PA (GAOM/) GAO W.
PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M B.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GIRM/) GIRMALDI J C.
PA (GUEN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (KLJA/) KLJAVIN I J.
PA (KUOS/) KUO S S.
PA (NAPI/) NAPIER M A.
PA (PANJ/) PAN J.
PA (PAON/) PAONI N F.
PA (ROIM/) ROY M A.
PA (SHEL/) SHELTON D L.
PA (STEW/) STEWART T A.
PA (TUNA/) TUNAS D.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 4.1%; Score 35.6; DB 12; Length 4199;
Best Local Similarity 60.2%; Pred. No. 83;
RESULT 1109
ID ADF61572 standard; cDNA; 4199 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO286.
PN US2003195345-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 4.1%; Score 35.6; DB 12; Length 4199;
Best Local Similarity 60.2%; Pred. No. 83;
RESULT 1110
ID ADF40264 standard; cDNA; 4199 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO286.
PN US2003198994-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 4.1%; Score 35.6; DB 12; Length 4199;
Best Local Similarity 60.2%; Pred. No. 83;
RESULT 1111
ID ADF46060 standard; cDNA; 4199 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO286.
PN US2003195148-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 4.1%; Score 35.6; DB 12; Length 4199;
Best Local Similarity 60.2%; Pred. No. 83;
RESULT 1112
ID ADF24456 standard; cDNA; 4199 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO286.
PN US2003204055-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.

Query Match 4.1%; Score 35.6; DB 12; Length 4199;
Best Local Similarity 60.2%; Pred. No. 83;
RESULT 1113
ID ADF40888 standard; cDNA; 4199 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO286.
PN US2003199021-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 4.1%; Score 35.6; DB 12; Length 4199;
Best Local Similarity 60.2%; Pred. No. 83;
RESULT 1114
ID ADF23832 standard; cDNA; 4199 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO286.
PN US2003203402-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 4.1%; Score 35.6; DB 12; Length 4199;
Best Local Similarity 60.2%; Pred. No. 83;
RESULT 1115
ID ADF33815 standard; cDNA; 4199 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO286.
PN US2003194780-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 4.1%; Score 35.6; DB 12; Length 4199;
Best Local Similarity 60.2%; Pred. No. 83;
RESULT 1116
ID ADF2782 standard; cDNA; 4199 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO286.
PN US2003199436-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 4.1%; Score 35.6; DB 12; Length 4199;
Best Local Similarity 60.2%; Pred. No. 83;
RESULT 1117
ID ADF27918 standard; cDNA; 4199 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO286.
PN US2003199437-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 4.1%; Score 35.6; DB 12; Length 4199;
Best Local Similarity 60.2%; Pred. No. 83;
RESULT 1118
ID ADF41512 standard; cDNA; 4199 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO286.
PN US2003199435-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 4.1%; Score 35.6; DB 12; Length 4199;
Best Local Similarity 60.2%; Pred. No. 83;
RESULT 1119
ID ADF33191 standard; cDNA; 4199 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO286.
PN US2003211091-A1.
PD 13-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 4.1%; Score 35.6; DB 12; Length 4199;
Best Local Similarity 60.2%; Pred. No. 83;
RESULT 1120
ID ADF25557 standard; cDNA; 4199 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO286.
PN US2003211092-A1.
PD 13-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 4.1%; Score 35.6; DB 12; Length 4199;
Best Local Similarity 60.2%; Pred. No. 83;
RESULT 1121
ID ADF26658 standard; cDNA; 4199 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO286.
PN US2003199674-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 4.1%; Score 35.6; DB 12; Length 4199;
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Best Local Similarity 60.2%; Pred. No. 83;
RESULT 1122
ID ADF34447 standard; cDNA; 4199 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO286.
PN US2003194410-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 4.1%; Score 35.6; DB 12; Length 4199;
Best Local Similarity 60.2%; Pred. No. 83;
RESULT 1123
ID ADF46684 standard; cDNA; 4199 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO286.
PN US2003195344-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 4.1%; Score 35.6; DB 12; Length 4199;
Best Local Similarity 60.2%; Pred. No. 83;
RESULT 1124
ID ADG50670 standard; cDNA; 4199 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO286.
PN US2003207803-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 4.1%; Score 35.6; DB 12; Length 4199;
Best Local Similarity 60.2%; Pred. No. 83;
RESULT 1125
ID ADG50046 standard; cDNA; 4199 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO286.
PN US2003215905-A1.
PD 20-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 4.1%; Score 35.6; DB 12; Length 4199;
Best Local Similarity 60.2%; Pred. No. 83;
RESULT 1126
ID ADG51918 standard; cDNA; 4199 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO286.
PN US2003215908-A1.
PD 20-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 4.1%; Score 35.6; DB 12; Length 4199;
Best Local Similarity 60.2%; Pred. No. 83;
RESULT 1127
ID ADG49422 standard; cDNA; 4199 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO286.
PN US2003216305-A1.
PD 20-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 4.1%; Score 35.6; DB 12; Length 4199;
Best Local Similarity 60.2%; Pred. No. 83;
RESULT 1128
ID ADG48798 standard; cDNA; 4199 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO286.
PN US2003216560-A1.
PD 20-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 4.1%; Score 35.6; DB 12; Length 4199;
Best Local Similarity 60.2%; Pred. No. 83;
RESULT 1129
ID ADG51294 standard; cDNA; 4199 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO286.
PN US2004005312-A1.
PD 08-JAN-2004.
PA (GETH ) GENENTECH INC.
Query Match 4.1%; Score 35.6; DB 12; Length 4199;
Best Local Similarity 60.2%; Pred. No. 83;
RESULT 1130
ID ADG59238 standard; cDNA; 4199 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO286.
PN US2004005657-A1.
PD 08-JAN-2004.
PA (GETH ) GENENTECH INC.
Query Match 4.1%; Score 35.6; DB 12; Length 4199;
Best Local Similarity 60.2%; Pred. No. 83;
RESULT 1131
ID ADG62694 standard; cDNA; 4199 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO286.
PN US2004006219-A1.
PD 08-JAN-2004.
PA (GETH ) GENENTECH INC.
Query Match 4.1%; Score 35.6; DB 12; Length 4199;
Best Local Similarity 60.2%; Pred. No. 83;
RESULT 1132
ID ADH25719 standard; cDNA; 4199 BP.
DE Human neurotrophin homologue related nucleotide sequence SEQ ID NO:497.
PN EP1386931-A1.
PD 04-FEB-2004.
PA (GETH ) GENENTECH INC.
Query Match 4.1%; Score 35.6; DB 12; Length 4199;
Best Local Similarity 60.2%; Pred. No. 83;
RESULT 1133
ID ADH17496 standard; cDNA; 4199 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO286.
PN US2004048332-A1.
PD 11-MAR-2004.
PA (GETH ) GENENTECH INC.
Query Match 4.1%; Score 35.6; DB 12; Length 4199;
Best Local Similarity 60.2%; Pred. No. 83;
RESULT 1134
ID ADL07330 standard; cDNA; 4199 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO286.
PN US2004063921-A1.
PD 01-APR-2004.
PA (GETH ) GENENTECH INC.
Query Match 4.1%; Score 35.6; DB 12; Length 4199;
Best Local Similarity 60.2%; Pred. No. 83;
RESULT 1135
ID ADU50452 standard; cDNA; 4199 BP.
DE PRO286 coding sequence, SEQ ID 497.
PN US2004223964-A1.
PD 11-NOV-2004.
PA (GETH ) GENENTECH INC.
Query Match 4.1%; Score 35.6; DB 13; Length 4199;
Best Local Similarity 60.2%; Pred. No. 83;
RESULT 1136
ID ADM49731 standard; cDNA; 4199 BP.
DE PRO286 cDNA, SEQ ID 497.
PN US2005014226-A1.
PD 20-JAN-2005.
PA (ASHK/) ASHENAZI A J.
PA (BAKE/) BAKER K P.
PA (BOTS/) BOTSTEIN D.
PA (DESN/) DESNOYERS L.
PA (EATO/) EATON D L.
PA (FERE/) FERRARA N.
PA (FILV/) FILVAROFF E.
PA (FONG/) FONG S.
PA (GAOW/) GAO W.
PA (GERE/) GERBER H.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GRIM/) GRIMALDI J C.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (KLJA/) KLJAVIN I J.
PA (KUOS/) KUO S S.
PA (NAPI/) NAPIER M A.
PA (PANJ/) PAN J.
PA (PAON/) PAONI N F.
PA (ROYM/) ROY M A.
PA (SHEL/) SHELTON D L.
PA (STEW/) STEWART T A.
PA (TUMA/) TUMAS D.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 4.1%; Score 35.6; DB 14; Length 4199;
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Best Local Similarity 60.2%; Pred. No. 83;
RESULT 1137
ID AD523392 standard; cDNA; 4199 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO286.
PN US2005084935-A1.
PD 21-APR-2005.
PA (ASHK/) ASHKENAZI A J.
PA (BAKE/) BAKER K P.
PA (BOTS/) BOTSTEIN D.
PA (DESN/) DESNOYERS L.
PA (EATO/) EATON D L.
PA (FERR/) FERRARA N.
PA (FILV/) FILVAROFF E.
PA (FONG/) FONG S.
PA (GAOM/) GAO W.
PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODONSKI P J.
PA (GRIM/) GRIMALDI J C.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (KLJA/) KLJAVIN I J.
PA (KUOS/) KUO S S.
PA (NAPI/) NAPIER M A.
PA (PANJ/) PAN J.
PA (PAON/) PAONI N F.
PA (ROYM/) ROY M A.
PA (SHEL/) SHELTON D L.
PA (STEW/) STEWART T A.
PA (TUNA/) TUNAS D. P M.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match
Best Local Similarity 4.1%; Score 35.6; DB 14; Length 4199;
Pred. No. 83;
RESULT 1138
ID AED48220 standard; cDNA; 4199 BP.
DE Human PRO286 cDNA, clone DNA426631154.
PN US2005227342-A1.
PD 13-OCT-2005.
PA (GETH/) GENENTECH INC.
Query Match
Best Local Similarity 4.1%; Score 35.6; DB 14; Length 4199;
Pred. No. 83;
RESULT 1139
ID ADU23156 standard; cDNA; 4211 BP.
DE Human Toll-like receptor 8 (TLR8) cDNA sequence - SEQ ID 48.
PN WO2004094671-A2.
PD 04-NOV-2004.
PA (COLE-) COLEY PHARM GMBH.
PA (COLE-) COLEY PHARM GROUP INC.
Query Match
Best Local Similarity 4.1%; Score 35.6; DB 13; Length 4211;
Pred. No. 83;
RESULT 1140
ID AEF77703 standard; cDNA; 4211 BP.
DE Human toll-like receptor 8 (TLR8) variant 2 cDNA.
PN WO20060171-A2.
PD 16-FEB-2006.
PA (META-) METABOLEX INC.
Query Match
Best Local Similarity 4.1%; Score 35.6; DB 15; Length 4211;
Pred. No. 83;
RESULT 1141
ID ABLJ34030 standard; DNA; 6048 BP.
DE Human immune system associated gene SEQ ID NO: 2003.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match
Best Local Similarity 4.1%; Score 35.6; DB 6; Length 6048;
Pred. No. 98;
RESULT 1142
ID AAG63352 standard; DNA; 6048 BP.
DE Chemically pretreated metabolism associated gene #47.
PN WO200176451-A2.
PD 18-OCT-2001.

PA (EPIG-) EPIGENOMICS AG.
Query Match
Best Local Similarity 4.1%; Score 35.6; DB 6; Length 6048;
Pred. No. 98;
RESULT 1143
ID AAG46338 standard; DNA; 6063 BP.
DE Tumour suppressor gene derived chemically modified sequence #60.
PN WO200168912-A2.
PD 20-SEP-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match
Best Local Similarity 4.1%; Score 35.6; DB 4; Length 6063;
Pred. No. 98;
RESULT 1144
ID AAK52133 standard; cDNA; 6792 BP.
DE Human polynucleotide SEQ ID NO 678.
PN WO200157190-A2.
PD 09-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 4.1%; Score 35.6; DB 4; Length 6792;
Pred. No. 1e+02;
RESULT 1145
ID AED73524 standard; cDNA; 6802 BP.
DE Human placental protein encoding cDNA SEQ ID NO:352.
PN US2005255114-A1.
PD 17-NOV-2005.
PA (NUVE-) NUVELO INC.
Query Match
Best Local Similarity 4.1%; Score 35.6; DB 14; Length 6802;
Pred. No. 1e+02;
RESULT 1146
ID AAH90035 standard; cDNA; 6815 BP.
DE Human bone marrow cDNA, SEQ ID NO: 279.
PN WO200153453-A2.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 4.1%; Score 35.6; DB 5; Length 6815;
Pred. No. 1e+02;
RESULT 1147
ID ABZ35054 standard; cDNA; 6817 BP.
DE Human gene expression profile polynucleotide SEQ ID NO 166.
PN WO200274979-A2.
PD 26-SEP-2002.
PA (ORTH) ORTHO CLINICAL DIAGNOSTICS INC.
Query Match
Best Local Similarity 4.1%; Score 35.6; DB 6; Length 6817;
Pred. No. 1e+02;
RESULT 1148
ID ABR84449 standard; cDNA; 6817 BP.
DE Human cDNA differentially expressed in granulocytic cells #1020.
PN WO200228999-A2.
PD 11-APR-2002.
PA (GENE-) GENE LOGIC INC.
Query Match
Best Local Similarity 4.1%; Score 35.6; DB 6; Length 6817;
Pred. No. 1e+02;
RESULT 1149
ID ADE85674 standard; DNA; 6817 BP.
DE Farnesyl transferase inhibitor modulated leukemia associated gene #893.
PN WO2003038129-A2.
PD 08-MAY-2003.
PA (ORTH) ORTHO CLINICAL DIAGNOSTICS INC.
Query Match
Best Local Similarity 4.1%; Score 35.6; DB 10; Length 6817;
Pred. No. 1e+02;
RESULT 1150
ID ADR26031 standard; DNA; 6817 BP.
DE Breast cancer prognosis marker #1892.
PN WO2004065545-A2.
PD 05-AUG-2004.
PA (ROSE-) ROSETTA INPHARMATICS LLC.
PA (NECA-) NETHERLANDS CANCER INST.
Query Match
Best Local Similarity 4.1%; Score 35.6; DB 13; Length 6817;
Pred. No. 1e+02;
RESULT 1151
ID AEC82974 standard; cDNA; 6817 BP.
DE Breast cancer associated cDNA SEQ ID NO 542.
PN WO2005083429-A2.
PD 09-SEP-2005.


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PA (VERI-) VERIDEX LLC.
Query Match 4.1%; Score 35.6; DB 14; Length 6817;
Best Local Similarity 60.2%; Pred. No. 1e+02;
RESULT 1152
ID AAH89922 standard; cDNA; 7317 BP.
DE Human bone marrow cDNA, SEQ ID NO: 53.
PN WO200153453-A2.
PD 26-JUL-2001.
PA (HYSB-) HYSBQ INC.
Query Match 4.1%; Score 35.6; DB 5; Length 7317;
Best Local Similarity 60.2%; Pred. No. 1.1e+02;
RESULT 1153
ID ABQ77419 standard; cDNA; 7364 BP.
DE Human CGDD cDNA 3075937CB1 SEQ ID 33.
PN WO2003014322-A2.
PD 20-FEB-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 4.1%; Score 35.6; DB 8; Length 7364;
Best Local Similarity 60.2%; Pred. No. 1.1e+02;
RESULT 1154
ID ABK28343 standard; DNA; 10138 BP.
DE DNA transcription associated genomic DNA #109.
PN WO200192565-A2.
PD 06-DEC-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.1%; Score 35.6; DB 6; Length 10138;
Best Local Similarity 60.2%; Pred. No. 1.2e+02;
RESULT 1155
ID ABL33900 standard; DNA; 11662 BP.
DE Human immune system associated gene SEQ ID NO: 1873.
PN WO20020928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.1%; Score 35.6; DB 6; Length 11662;
Best Local Similarity 64.6%; Pred. No. 1.3e+02;
RESULT 1156
ID ABQ67059 standard; DNA; 34688 BP.
DE Human angiogenesis associated polynucleotide SEQ ID NO 89.
PN WO200246454-A2.
PD 13-JUN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.1%; Score 35.6; DB 6; Length 34688;
Best Local Similarity 64.6%; Pred. No. 2.2e+02;
RESULT 1157
ID AAK78813 standard; DNA; 51469 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:33625.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.1%; Score 35.6; DB 4; Length 51469;
Best Local Similarity 54.8%; Pred. No. 2.6e+02;
RESULT 1158
ID RAK70270 standard; DNA; 51469 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:25082.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.1%; Score 35.6; DB 4; Length 51469;
Best Local Similarity 54.6%; Pred. No. 2.6e+02;
RESULT 1159
ID RAK69322 standard; DNA; 51469 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:24134.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.1%; Score 35.6; DB 4; Length 51469;
Best Local Similarity 54.6%; Pred. No. 2.6e+02;
RESULT 1160
ID ADQ97873 standard; DNA; 114454 BP.
DE Mouse cancer associated sequence MD11-016, SEQ ID 850.
PN WO2004060304-A2.
PD 22-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.

Query Match 4.1%; Score 35.6; DB 12; Length 114454;
Best Local Similarity 48.1%; Pred. No. 3.7e+02;
RESULT 1161
ID AEF74795 standard; DNA; 178863 BP.
DE Human polynucleotide #309.
PN WO2006013561-A2.
PD 09-FEB-2006.
PA (VISS-) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.
PA (HADA-) HADASIT MEDICAL RES SERVICES & DEV LTD.
Query Match 4.1%; Score 35.6; DB 15; Length 178863;
Best Local Similarity 53.6%; Pred. No. 4.5e+02;
RESULT 1162
ID ABD33364 standard; DNA; 203132 BP.
DE Murine cancer-associated (CA) gene MD07-067.
PN WO2004058146-A2.
PD 15-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 4.1%; Score 35.6; DB 13; Length 203132;
Best Local Similarity 48.5%; Pred. No. 4.8e+02;
RESULT 1163
ID ADZ13443 standard; DNA; 203132 BP.
DE Murine cancer-associated genomic DNA #84.
PN WO2005031001-A2.
PD 07-APR-2005.
PA (CHIR-) CHIRON CORP.
Query Match 4.1%; Score 35.6; DB 14; Length 203132;
Best Local Similarity 48.5%; Pred. No. 4.8e+02;
RESULT 1164
ID ABV19042 standard; cDNA; 252 BP.
DE Human prostate expression marker cDNA 19033.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.1%; Score 35.4; DB 5; Length 252;
Best Local Similarity 63.5%; Pred. No. 26;
RESULT 1165
ID ABV49607 standard; cDNA; 302 BP.
DE Human prostate expression marker cDNA 49598.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.1%; Score 35.4; DB 5; Length 302;
Best Local Similarity 69.6%; Pred. No. 29;
RESULT 1166
ID AAL00078 standard; cDNA; 324 BP.
DE Human reproductive system related antigen cDNA SEQ ID NO: 79.
PN WO200155320-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.1%; Score 35.4; DB 4; Length 324;
Best Local Similarity 62.8%; Pred. No. 30;
RESULT 1167
ID ABV48140 standard; cDNA; 350 BP.
DE Human prostate expression marker cDNA 48131.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.1%; Score 35.4; DB 5; Length 350;
Best Local Similarity 53.7%; Pred. No. 31;
RESULT 1168
ID ABX36333 standard; cDNA; 405 BP.
DE Bovine EST associated with lactation/muscle/fat deposition #1498.
PN US2002137139-A1.
PD 26-SEP-2002.
PA (BYAT-) BYATT J C.
PA (MATH-) MATHIALAGAN N.
PA (TAON-) TAO N.
PA (WARE-) WARREN W C.
Query Match 4.1%; Score 35.4; DB 8; Length 405;
Best Local Similarity 66.2%; Pred. No. 33;
RESULT 1169
ID ABV57623 standard; cDNA; 488 BP.
DE Human prostate expression marker cDNA 57614.
```


PN WO200150860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.1%; Score 35.4; DB 5; Length 488;
Best Local Similarity 59.4%; Pred. No. 36;
RESULT 1170
ID ACN46717 standard; cDNA; 522 BP.
DE Cotton primed seed EST Clone ID: LIB3825-003-Q1-N6-C8, SEQ:1498.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 4.1%; Score 35.4; DB 13; Length 522;
Best Local Similarity 48.3%; Pred. No. 37;
RESULT 1171
ID ACN47378 standard; cDNA; 574 BP.
DE Cotton primed seed EST Clone ID: LIB3825-010-Q1-N6-G2, SEQ:2159.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 4.1%; Score 35.4; DB 13; Length 574;
Best Local Similarity 48.3%; Pred. No. 38;
RESULT 1172
ID ABO22672 standard; DNA; 673 BP.
DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 9263.
PN WO200218632-A2.
PD 07-MAR-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.1%; Score 35.4; DB 6; Length 673;
Best Local Similarity 54.8%; Pred. No. 41;
RESULT 1173
ID ABO22673 standard; DNA; 673 BP.
DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 9264.
PN WO200218632-A2.
PD 07-MAR-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.1%; Score 35.4; DB 6; Length 673;
Best Local Similarity 54.8%; Pred. No. 41;
RESULT 1174
ID AAS29157 standard; cDNA; 792 BP.
DE cDNA encoding for human DNA-binding protein #128.
PN WO20015162-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.1%; Score 35.4; DB 5; Length 792;
Best Local Similarity 59.4%; Pred. No. 44;
RESULT 1175
ID ABS68297 standard; cDNA; 792 BP.
DE cDNA encoding human DNA-binding protein #128.
PN US2002102638-A1.
PD 01-AUG-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 4.1%; Score 35.4; DB 6; Length 792;
Best Local Similarity 59.4%; Pred. No. 44;
RESULT 1176
ID ADC25291 standard; cDNA; 792 BP.
DE Human cDNA from extracellular matrix gene 128.
PN US2003049650-A1.
PD 13-MAR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.1%; Score 35.4; DB 10; Length 792;
Best Local Similarity 59.4%; Pred. No. 44;
RESULT 1177
ID ABO54594 standard; cDNA; 1058 BP.
DE Human ovarian antigen HCOMW35 cDNA, SEQ ID NO:474.
PN WO200200677-A1.

PD 03-JAN-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.1%; Score 35.4; DB 6; Length 1058;
Best Local Similarity 56.4%; Pred. No. 50;
RESULT 1178
ID AAD08425 standard; cDNA; 1143 BP.
DE Human secreted protein-encoding gene 22 cDNA clone HARNB17, SEQ ID NO:32.
PN WO200134643-A1.
PD 17-MAY-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.1%; Score 35.4; DB 4; Length 1143;
Best Local Similarity 54.1%; Pred. No. 52;
RESULT 1179
ID ACC74280 standard; cDNA; 1233 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003027275-A1.
PD 06-FEB-2003.
Query Match 4.1%; Score 35.4; DB 8; Length 1233;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1180
ID AAS46043 standard; cDNA; 1234 BP.
DE Human DNA encoding PRO polypeptide sequence #119.
PN WO200168848-A2.
PD 20-SEP-2001.
PA (GETH-) GENENTECH INC.
Query Match 4.1%; Score 35.4; DB 4; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1181
ID AAF92089 standard; cDNA; 1234 BP.
DE Human PRO3566 cDNA.
PN WO200116318-A2.
PD 08-MAR-2001.
PA (GETH-) GENENTECH INC.
Query Match 4.1%; Score 35.4; DB 4; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1182
ID ABS74409 standard; cDNA; 1234 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO3566.
PN US2002119130-A1.
PD 29-AUG-2002.
PA (GETH-) GENENTECH INC.
Query Match 4.1%; Score 35.4; DB 6; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1183
ID ACA89493 standard; cDNA; 1234 BP.
DE cDNA encoding human PRO polypeptide #119.
PN US2003036146-A1.
PD 20-FEB-2003.
PA (GETH-) GENENTECH INC.
Query Match 4.1%; Score 35.4; DB 8; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1184
ID ACA73503 standard; cDNA; 1234 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #119.
PN US2003036146-A1.
PD 20-FEB-2003.
PA (GETH-) GENENTECH INC.
Query Match 4.1%; Score 35.4; DB 8; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1185
ID ACA05818 standard; cDNA; 1234 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #119.
PN US2003036162-A1.
PD 20-FEB-2003.
PA (GETH-) GENENTECH INC.
Query Match 4.1%; Score 35.4; DB 8; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1186
ID ACA66652 standard; cDNA; 1234 BP.
DE cDNA encoding human PRO protein #119.
PN US2003036137-A1.
PD 20-FEB-2003.
PA (GETH-) GENENTECH INC.
Query Match 4.1%; Score 35.4; DB 8; Length 1234;

Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1187
ID ACA91195 standard; cDNA; 1234 BP.
DE Novel human secreted and transmembrane protein PRO3566 cDNA.
PN US2003018173-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 4.1%; Score 35.4; DB 8; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1188
ID ACD81572 standard; cDNA; 1234 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO3566.
PN US2003009013-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 4.1%; Score 35.4; DB 8; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1189
ID ACF20227 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003040063-A1.
PD 27-FEB-2003.
Query Match 4.1%; Score 35.4; DB 8; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1190
ID ACF19613 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003040064-A1.
PD 27-FEB-2003.
Query Match 4.1%; Score 35.4; DB 8; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1191
ID ACD21901 standard; cDNA; 1234 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #119.
PN US2003027267-A1.
PD 06-FEB-2003.
Query Match 4.1%; Score 35.4; DB 8; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1192
ID ACF13066 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003036160-A1.
PD 20-FEB-2003.
Query Match 4.1%; Score 35.4; DB 8; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1193
ID ACD25169 standard; cDNA; 1234 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #119.
PN US2003044925-A1.
PD 06-MAR-2003.
Query Match 4.1%; Score 35.4; DB 8; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1194
ID ACF00218 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003054474-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.1%; Score 35.4; DB 8; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1195
ID ACA60394 standard; cDNA; 1234 BP.
DE Novel human secreted and transmembrane protein PRO3566 cDNA.
PN US2003018183-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 4.1%; Score 35.4; DB 8; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1196
ID ACA72275 standard; cDNA; 1234 BP.
DE Novel human secreted and transmembrane protein PRO3566 cDNA.
PN US2003032114-A1.
PD 13-FEB-2003.

Query Match 4.1%; Score 35.4; DB 8; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1197
ID ACD04799 standard; cDNA; 1234 BP.
DE Novel human secreted and transmembrane protein PRO3566 cDNA.
PN US2003032101-A1.
PD 13-FEB-2003.
Query Match 4.1%; Score 35.4; DB 8; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1198
ID ACD18260 standard; cDNA; 1234 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #119.
PN US2003036124-A1.
PD 20-FEB-2003.
Query Match 4.1%; Score 35.4; DB 8; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1199
ID ACD08267 standard; cDNA; 1234 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #119.
PN US2003040054-A1.
PD 27-FEB-2003.
Query Match 4.1%; Score 35.4; DB 8; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1200
ID ACA88701 standard; cDNA; 1234 BP.
DE Novel human secreted and transmembrane protein PRO3566 cDNA.
PN US2003036133-A1.
PD 20-FEB-2003.
Query Match 4.1%; Score 35.4; DB 8; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1201
ID ACA70143 standard; cDNA; 1234 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #119.
PN US2003036134-A1.
PD 20-FEB-2003.
Query Match 4.1%; Score 35.4; DB 8; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1202
ID ACD12365 standard; cDNA; 1234 BP.
DE Novel human secreted and transmembrane protein PRO3566 cDNA.
PN US2003022294-A1.
PD 30-JAN-2003.
Query Match 4.1%; Score 35.4; DB 8; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1203
ID ACD15908 standard; cDNA; 1234 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #119.
PN US2003027324-A1.
PD 06-FEB-2003.
Query Match 4.1%; Score 35.4; DB 8; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1204
ID ACD25476 standard; cDNA; 1234 BP.
DE Novel human secreted and transmembrane protein PRO3566 cDNA.
PN US2003036118-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 4.1%; Score 35.4; DB 8; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1205
ID ACD17953 standard; cDNA; 1234 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #119.
PN US2003036123-A1.
PD 20-FEB-2003.
Query Match 4.1%; Score 35.4; DB 8; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1206
ID ACC88240 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003036148-A1.
PD 20-FEB-2003.
Query Match 4.1%; Score 35.4; DB 8; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;

RESULT 1207
ID ACD21594 standard; cDNA; 1234 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #119.
PN US2003040060-A1.
PD 27-FEB-2003.
Query Match 4.1%; Score 35.4; DB 8; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1208
ID ACD18661 standard; cDNA; 1234 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #119.
PN US2003044916-A1.
PD 06-MAR-2003.
Query Match 4.1%; Score 35.4; DB 8; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1209
ID ACA58841 standard; cDNA; 1234 BP.
DE cDNA encoding human secreted polypeptide PRO3566.
PN US2003013855-A1.
PD 16-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 4.1%; Score 35.4; DB 8; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1210
ID ABX98271 standard; cDNA; 1234 BP.
DE Human cDNA encoding a secreted/transmembrane protein, SEQ ID 237.
PN US2003036156-A1.
PD 20-FEB-2003.
Query Match 4.1%; Score 35.4; DB 8; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1211
ID ACD14022 standard; cDNA; 1234 BP.
DE Human PRO polynucleotide #119.
PN US2003032117-A1.
PD 13-FEB-2003.
Query Match 4.1%; Score 35.4; DB 8; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1212
ID ACD09802 standard; cDNA; 1234 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #119.
PN US2003036128-A1.
PD 20-FEB-2003.
Query Match 4.1%; Score 35.4; DB 8; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1213
ID ACC88547 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003027266-A1.
PD 06-FEB-2003.
Query Match 4.1%; Score 35.4; DB 8; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1214
ID ACD21287 standard; cDNA; 1234 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #119.
PN US2003054483-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.1%; Score 35.4; DB 8; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1215
ID ABX75659 standard; cDNA; 1234 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO3566.
PN US2003022298-A1.
PD 30-JAN-2003.
Query Match 4.1%; Score 35.4; DB 8; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1216
ID ACA64017 standard; cDNA; 1234 BP.
DE cDNA encoding human PRO polypeptide #32.
PN US2002182638-A1.
PD 05-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 4.1%; Score 35.4; DB 8; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;

RESULT 1217
ID ABX97862 standard; cDNA; 1234 BP.
DE Human PRO polynucleotide #119.
PN US2003032102-A1.
PD 13-FEB-2003.
Query Match 4.1%; Score 35.4; DB 8; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1218
ID ACA97338 standard; cDNA; 1234 BP.
DE Novel human secreted and transmembrane protein PRO3566 cDNA.
PN US2003036117-A1.
PD 20-FEB-2003.
Query Match 4.1%; Score 35.4; DB 8; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1219
ID ACA57801 standard; cDNA; 1234 BP.
DE Human PRO3566 cDNA.
PN US2003036143-A1.
PD 20-FEB-2003.
Query Match 4.1%; Score 35.4; DB 8; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1220
ID ACD14329 standard; cDNA; 1234 BP.
DE Human PRO polynucleotide #119.
PN US2003032130-A1.
PD 13-FEB-2003.
Query Match 4.1%; Score 35.4; DB 8; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1221
ID ACC91112 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003032138-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 4.1%; Score 35.4; DB 8; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1222
ID ACC88854 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003036132-A1.
PD 20-FEB-2003.
Query Match 4.1%; Score 35.4; DB 8; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1223
ID ACD07051 standard; cDNA; 1234 BP.
DE Human PRO polynucleotide #119.
PN US2003008353-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 4.1%; Score 35.4; DB 8; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1224
ID ACA67502 standard; cDNA; 1234 BP.
DE Human PRO polynucleotide #119.
PN US2003017542-A1.
PD 23-JAN-2003.
Query Match 4.1%; Score 35.4; DB 8; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1225
ID ACC81557 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003032137-A1.
PD 13-FEB-2003.
Query Match 4.1%; Score 35.4; DB 8; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1226
ID ACA91281 standard; cDNA; 1234 BP.
DE cDNA encoding human PRO polypeptide #32.
PN US2003018168-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 4.1%; Score 35.4; DB 8; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;

RESULT 1227
ID ACC89161 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003027269-A1.
PD 06-FEB-2003.
Query Match 4.1%; Score 35.4; DB 8; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1228
ID ACC86517 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003027268-A1.
PD 06-FEB-2003.
Query Match 4.1%; Score 35.4; DB 8; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1229
ID ACC89775 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003027274-A1.
PD 06-FEB-2003.
Query Match 4.1%; Score 35.4; DB 8; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1230
ID ACC32954 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003032135-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 4.1%; Score 35.4; DB 8; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1231
ID ACAT2582 standard; cDNA; 1234 BP.
DE Human PRO polynucleotide #119.
PN US2003022285-A1.
PD 30-JAN-2003.
Query Match 4.1%; Score 35.4; DB 8; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1232
ID ACA99100 standard; cDNA; 1234 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #119.
PN US2003022297-A1.
PD 30-JAN-2003.
Query Match 4.1%; Score 35.4; DB 8; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1233
ID ACA9836 standard; cDNA; 1234 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #119.
PN US2003032105-A1.
PD 13-FEB-2003.
Query Match 4.1%; Score 35.4; DB 8; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1234
ID ACA96979 standard; cDNA; 1234 BP.
DE Novel human secreted and transmembrane protein PRO3566 cDNA.
PN US2003032123-A1.
PD 13-FEB-2003.
Query Match 4.1%; Score 35.4; DB 8; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1235
ID ACA90975 standard; cDNA; 1234 BP.
DE Novel human secreted and transmembrane protein PRO3566 cDNA.
PN US2003032108-A1.
PD 13-FEB-2003.
Query Match 4.1%; Score 35.4; DB 8; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1236
ID ACA70757 standard; cDNA; 1234 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #119.
PN US2003032111-A1.
PD 13-FEB-2003.
Query Match 4.1%; Score 35.4; DB 8; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1237
ID ACA95267 standard; cDNA; 1234 BP.

DE Novel human secreted and transmembrane protein PRO3566 cDNA.
PN US2003032119-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 4.1%; Score 35.4; DB 8; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1238
ID ACC86210 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003027263-A1.
PD 06-FEB-2003.
Query Match 4.1%; Score 35.4; DB 8; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1239
ID ACDA5180 standard; cDNA; 1234 BP.
DE Human secreted/transmembrane polypeptide PRO3566 cDNA.
PN US2003009012-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 4.1%; Score 35.4; DB 8; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1240
ID ACC90082 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003027271-A1.
PD 06-FEB-2003.
Query Match 4.1%; Score 35.4; DB 8; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1241
ID ACID12690 standard; cDNA; 1234 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #119.
PN US2003036125-A1.
PD 20-FEB-2003.
Query Match 4.1%; Score 35.4; DB 8; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1242
ID ACF19920 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003040068-A1.
PD 27-FEB-2003.
Query Match 4.1%; Score 35.4; DB 8; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1243
ID ABX76864 standard; cDNA; 1234 BP.
DE Human PRO polynucleotide #119.
PN US2003027280-A1.
PD 06-FEB-2003.
Query Match 4.1%; Score 35.4; DB 8; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1244
ID ACA73196 standard; cDNA; 1234 BP.
DE Novel human secreted and transmembrane protein PRO3566 cDNA.
PN US2003022300-A1.
PD 30-JAN-2003.
Query Match 4.1%; Score 35.4; DB 8; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1245
ID ACA86739 standard; cDNA; 1234 BP.
DE Novel human secreted and transmembrane protein PRO3566 cDNA.
PN US2003036136-A1.
PD 20-FEB-2003.
Query Match 4.1%; Score 35.4; DB 8; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1246
ID ACA74583 standard; cDNA; 1234 BP.
DE cDNA encoding human PRO polypeptide #119.
PN US2003036138-A1.
PD 20-FEB-2003.
Query Match 4.1%; Score 35.4; DB 8; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1247
ID ACA70450 standard; cDNA; 1234 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #119.

PN US2003032109-A1.
PD 13-FEB-2003.
Query Match 4.1%; Score 35.4; DB 8; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1248
ID ACID14636 standard; cDNA; 1234 BP.
DE Human PRO polynucleotide #119.
PN US2003040066-A1.
PD 27-FEB-2003.
Query Match 4.1%; Score 35.4; DB 8; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1249
ID ACA93728 standard; cDNA; 1234 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO3566.
PN US2003045684-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.1%; Score 35.4; DB 8; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1250
ID ACA68308 standard; cDNA; 1234 BP.
DE Novel human secreted and transmembrane protein PRO3566 cDNA.
PN US2003032104-A1.
PD 13-FEB-2003.
Query Match 4.1%; Score 35.4; DB 8; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1251
ID ABX98773 standard; cDNA; 1234 BP.
DE Novel human secreted and transmembrane protein PRO3566 cDNA.
PN US2003036157-A1.
PD 20-FEB-2003.
Query Match 4.1%; Score 35.4; DB 8; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1252
ID ACA67302 standard; cDNA; 1234 BP.
DE cDNA encoding human secreted polypeptide PRO3566.
PN US2003027212-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 4.1%; Score 35.4; DB 8; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1253
ID ACC81250 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003032120-A1.
PD 13-FEB-2003.
Query Match 4.1%; Score 35.4; DB 8; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1254
ID ACA95574 standard; cDNA; 1234 BP.
DE Novel human secreted and transmembrane protein PRO3566 cDNA.
PN US2003036155-A1.
PD 20-FEB-2003.
Query Match 4.1%; Score 35.4; DB 8; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1255
ID ACD04492 standard; cDNA; 1234 BP.
DE Novel human secreted and transmembrane protein PRO3566 cDNA.
PN US2003022296-A1.
PD 30-JAN-2003.
Query Match 4.1%; Score 35.4; DB 8; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1256
ID ACC87933 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003027281-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 4.1%; Score 35.4; DB 8; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1257
ID ACF12595 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.

PN US2003040058-A1.
PD 27-FEB-2003.
Query Match 4.1%; Score 35.4; DB 8; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1258
ID ACH66275 standard; cDNA; 1234 BP.
DE Novel human secreted and transmembrane protein PRO3566 cDNA.
PN US2003027986-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 4.1%; Score 35.4; DB 8; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1259
ID ACA96310 standard; cDNA; 1234 BP.
DE Human PRO polynucleotide #119.
PN US2003017540-A1.
PD 23-JAN-2003.
Query Match 4.1%; Score 35.4; DB 8; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1260
ID ACA65084 standard; cDNA; 1234 BP.
DE Human PRO polynucleotide #119.
PN US2003032106-A1.
PD 13-FEB-2003.
Query Match 4.1%; Score 35.4; DB 8; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1261
ID ACA73810 standard; cDNA; 1234 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #119.
PN US2003032129-A1.
PD 13-FEB-2003.
Query Match 4.1%; Score 35.4; DB 8; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1262
ID ACA74222 standard; cDNA; 1234 BP.
DE Novel human secreted and transmembrane protein PRO3566 cDNA.
PN US2003032131-A1.
PD 13-FEB-2003.
Query Match 4.1%; Score 35.4; DB 8; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1263
ID ACA96617 standard; cDNA; 1234 BP.
DE Human PRO polynucleotide #119.
PN US2003032103-A1.
PD 13-FEB-2003.
Query Match 4.1%; Score 35.4; DB 8; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1264
ID ACD10723 standard; cDNA; 1234 BP.
DE cDNA encoding human PRO polypeptide #119.
PN US2003032107-A1.
PD 13-FEB-2003.
Query Match 4.1%; Score 35.4; DB 8; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1265
ID ACC91419 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003032139-A1.
PD 13-FEB-2003.
Query Match 4.1%; Score 35.4; DB 8; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1266
ID ACD02754 standard; cDNA; 1234 BP.
DE cDNA encoding human PRO polypeptide #119.
PN US2003022301-A1.
PD 30-JAN-2003.
Query Match 4.1%; Score 35.4; DB 8; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1267
ID ACC87319 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003036165-A1.
PD 20-FEB-2003.

PA (GETH) GENENTECH INC.

Query Match 4.1%; Score 35.4; DB 8; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1268

ID ACC85903 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003027262-A1.
PD 06-FEB-2003.

Query Match 4.1%; Score 35.4; DB 8; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1269

ID ACA65391 standard; cDNA; 1234 BP.
DE Human PRO polynucleotide #119.
PN US2003032110-A1.
PD 13-FEB-2003.

Query Match 4.1%; Score 35.4; DB 8; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1270

ID ACA94208 standard; cDNA; 1234 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #119.
PN US2003036142-A1.
PD 20-FEB-2003.

Query Match 4.1%; Score 35.4; DB 8; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1271

ID ACA97952 standard; cDNA; 1234 BP.
DE Human PRO polynucleotide #119.
PN US2003036145-A1.
PD 20-FEB-2003.

Query Match 4.1%; Score 35.4; DB 8; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1272

ID ACA91454 standard; cDNA; 1234 BP.
DE Novel human secreted and transmembrane protein PRO3566 cDNA.
PN US2003036154-A1.
PD 20-FEB-2003.

Query Match 4.1%; Score 35.4; DB 8; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1273

ID ACA90668 standard; cDNA; 1234 BP.
DE Novel human secreted and transmembrane protein PRO3566 cDNA.
PN US2003036153-A1.
PD 20-FEB-2003.

Query Match 4.1%; Score 35.4; DB 8; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1274

ID ACD16215 standard; cDNA; 1234 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #119.
PN US2003044931-A1.
PD 06-MAR-2003.

Query Match 4.1%; Score 35.4; DB 8; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1275

ID ACD17376 standard; cDNA; 1234 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #119.
PN US2003036150-A1.
PD 20-FEB-2003.

Query Match 4.1%; Score 35.4; DB 8; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1276

ID ACC92033 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003040069-A1.
PD 27-FEB-2003.

Query Match 4.1%; Score 35.4; DB 8; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1277

ID ACD02329 standard; cDNA; 1234 BP.
DE Novel human secreted and transmembrane protein PRO3566 cDNA.
PN US2002183493-A1.
PD 05-DEC-2002.

Query Match 4.1%; Score 35.4; DB 8; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1278

ID ACD02329 standard; cDNA; 1234 BP.
DE Novel human secreted and transmembrane protein PRO3566 cDNA.
PN US2002183493-A1.
PD 05-DEC-2002.

PA (GETH) GENENTECH INC.

Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1278
ID ACA74890 standard; cDNA; 1234 BP.
DE cDNA encoding human PRO polypeptide #119.
PN US2003022293-A1.
PD 30-JAN-2003.
Query Match 4.1%; Score 35.4; DB 8; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1279
ID ACA91761 standard; cDNA; 1234 BP.
DE Human PRO polynucleotide #119.
PN US2003032128-A1.
PD 13-FEB-2003.
Query Match 4.1%; Score 35.4; DB 8; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1280
ID ACA89320 standard; cDNA; 1234 BP.
DE Novel human secreted and transmembrane protein PRO3566 cDNA.
PN US2003036634-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 4.1%; Score 35.4; DB 8; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1281
ID ACA71405 standard; cDNA; 1234 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #119.
PN US2003032116-A1.
PD 13-FEB-2003.
Query Match 4.1%; Score 35.4; DB 8; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1282
ID ACC90805 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003032122-A1.
PD 13-FEB-2003.
Query Match 4.1%; Score 35.4; DB 8; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1283
ID ACA65815 standard; cDNA; 1234 BP.
DE cDNA encoding human PRO protein #119.
PN US2003036139-A1.
PD 20-FEB-2003.
Query Match 4.1%; Score 35.4; DB 8; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1284
ID ACA68957 standard; cDNA; 1234 BP.
DE Novel human secreted and transmembrane protein PRO3566 cDNA.
PN US2002183494-A1.
PD 05-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 4.1%; Score 35.4; DB 8; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1285
ID ACA94960 standard; cDNA; 1234 BP.
DE cDNA encoding human PRO polypeptide #119.
PN US2003017541-A1.
PD 23-JAN-2003.
Query Match 4.1%; Score 35.4; DB 8; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1286
ID ACD16522 standard; cDNA; 1234 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #119.
PN US2003017543-A1.
PD 23-JAN-2003.
Query Match 4.1%; Score 35.4; DB 8; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1287
ID ACD15601 standard; cDNA; 1234 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #119.
PN US2003036152-A1.
PD 20-FEB-2003.
Query Match 4.1%; Score 35.4; DB 8; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;

RESULT 1288
ID ACA98479 standard; cDNA; 1234 BP.
DE Human PRO polynucleotide #32.
PN US2003027993-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 4.1%; Score 35.4; DB 8; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1289
ID ABX16704 standard; cDNA; 1234 BP.
DE Human cDNA encoding secreted/transmembrane protein #119.
PN US2002127584-A1.
PD 12-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 4.1%; Score 35.4; DB 8; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1290
ID ACA33404 standard; cDNA; 1234 BP.
DE cDNA encoding human PRO polypeptide #32.
PN US2003023042-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 4.1%; Score 35.4; DB 9; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1291
ID ACA97645 standard; cDNA; 1234 BP.
DE Human PRO polynucleotide #119.
PN US2003032115-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 4.1%; Score 35.4; DB 9; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1292
ID ACA99094 standard; cDNA; 1234 BP.
DE Novel human secreted and transmembrane protein PRO3566 cDNA.
PN US2003032140-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 4.1%; Score 35.4; DB 9; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1293
ID ACC91726 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003040076-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 4.1%; Score 35.4; DB 9; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1294
ID ACD11137 standard; cDNA; 1234 BP.
DE Novel human secreted and transmembrane protein PRO3566 cDNA.
PN US2003008352-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 4.1%; Score 35.4; DB 9; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1295
ID ACD14987 standard; cDNA; 1234 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #119.
PN US2003044922-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.1%; Score 35.4; DB 9; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1296
ID ACD11751 standard; cDNA; 1234 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #119.
PN US2003032118-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 4.1%; Score 35.4; DB 9; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1297
ID ACC95880 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003036135-A1.
PD 20-FEB-2003.

Query Match 4.1%; Score 35.4; DB 9; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1298
ID ACF16443 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003054455-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.1%; Score 35.4; DB 9; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1299
ID ACF02561 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003049741-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.1%; Score 35.4; DB 9; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1300
ID ACF02868 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003049743-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.1%; Score 35.4; DB 9; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1301
ID ACF21455 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003049769-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.1%; Score 35.4; DB 9; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1302
ID ACF10139 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003068743-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.1%; Score 35.4; DB 9; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1303
ID ACF78032 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003054479-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.1%; Score 35.4; DB 9; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1304
ID ACD46737 standard; cDNA; 1234 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #119.
PN US2003068685-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.1%; Score 35.4; DB 9; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1305
ID ACD49500 standard; cDNA; 1234 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #119.
PN US2003068725-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.1%; Score 35.4; DB 9; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1306
ID ACF28267 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003068752-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.1%; Score 35.4; DB 9; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;

Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1307
ID ACD89957 standard; cDNA; 1234 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #119.
PN US200308682-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.1%; Score 35.4; DB 9; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1308
ID ACD84352 standard; cDNA; 1234 BP.
DE Human PRO polynucleotide #119.
PN US2003068701-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.1%; Score 35.4; DB 9; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1309
ID ACD99126 standard; cDNA; 1234 BP.
DE cDNA encoding human PRO polypeptide #119.
PN US2003068755-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.1%; Score 35.4; DB 9; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1310
ID ADA77989 standard; cDNA; 1234 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #119.
PN US2003073180-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.1%; Score 35.4; DB 9; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1311
ID ACF4868 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003104539-A1.
PD 05-JUN-2003.
Query Match 4.1%; Score 35.4; DB 9; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1312
ID ACD09188 standard; cDNA; 1234 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #119.
PN US2003036131-A1.
PD 20-FEB-2003.
Query Match 4.1%; Score 35.4; DB 9; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1313
ID ACF11981 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003040075-A1.
PD 27-FEB-2003.
Query Match 4.1%; Score 35.4; DB 9; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1314
ID ACF41215 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003054459-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.1%; Score 35.4; DB 9; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1315
ID ACF15829 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003044930-A1.
PD 06-MAR-2003.
Query Match 4.1%; Score 35.4; DB 9; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1316
ID ACF16136 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003040071-A1.

PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 4.1%; Score 35.4; DB 9; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1317
ID ACD31963 standard; cDNA; 1234 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #119.
PN US2003054471-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.1%; Score 35.4; DB 9; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1318
ID ACF18771 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003064452-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.1%; Score 35.4; DB 9; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1319
ID ACF09218 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003068705-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.1%; Score 35.4; DB 9; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1320
ID ACF78339 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003054473-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.1%; Score 35.4; DB 9; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1321
ID ACF51938 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003064440-A1.
PD 03-APR-2003.
Query Match 4.1%; Score 35.4; DB 9; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1322
ID ACF26425 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003068704-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.1%; Score 35.4; DB 9; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1323
ID ACF24218 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003068722-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.1%; Score 35.4; DB 9; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1324
ID ACF63529 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003073183-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.1%; Score 35.4; DB 9; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1325
ID ACF50403 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003104549-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.

Query Match
Best Local Similarity 4.1%; Score 35.4; DB 9; Length 1234;
RESULT 1326
ID ACH07874 standard; cDNA; 1234 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #119.
PN US2003049749-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 4.1%; Score 35.4; DB 9; Length 1234;
RESULT 1327
ID ACF13680 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003064462-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 4.1%; Score 35.4; DB 9; Length 1234;
RESULT 1328
ID ACD41606 standard; cDNA; 1234 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #119.
PN US2003065159-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 4.1%; Score 35.4; DB 9; Length 1234;
RESULT 1329
ID ACF32019 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003064447-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 4.1%; Score 35.4; DB 9; Length 1234;
RESULT 1330
ID ACF23297 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003073184-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 4.1%; Score 35.4; DB 9; Length 1234;
RESULT 1331
ID ACF39987 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003064463-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 4.1%; Score 35.4; DB 9; Length 1234;
RESULT 1332
ID ACD45509 standard; cDNA; 1234 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #119.
PN US2003064451-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 4.1%; Score 35.4; DB 9; Length 1234;
RESULT 1333
ID ACF53166 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003068721-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 4.1%; Score 35.4; DB 9; Length 1234;
RESULT 1334
ID ACF27346 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003068699-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 4.1%; Score 35.4; DB 9; Length 1234;

Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1335
ID ACF45184 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003068707-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 4.1%; Score 35.4; DB 9; Length 1234;
RESULT 1336
ID ACF29802 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003073175-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 4.1%; Score 35.4; DB 9; Length 1234;
RESULT 1337
ID ACD89878 standard; cDNA; 1234 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #119.
PN US2003068695-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 4.1%; Score 35.4; DB 9; Length 1234;
RESULT 1338
ID ACD84659 standard; cDNA; 1234 BP.
DE Human PRO polynucleotide #119.
PN US2003068703-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 4.1%; Score 35.4; DB 9; Length 1234;
RESULT 1339
ID ACD98819 standard; cDNA; 1234 BP.
DE cDNA encoding human PRO polypeptide #119.
PN US2003068732-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 4.1%; Score 35.4; DB 9; Length 1234;
RESULT 1340
ID ACF77111 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003082717-A1.
PD 01-MAY-2003.
Query Match
Best Local Similarity 4.1%; Score 35.4; DB 9; Length 1234;
RESULT 1341
ID ACF76804 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003104548-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 4.1%; Score 35.4; DB 9; Length 1234;
RESULT 1342
ID ACF49789 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003104542-A1.
PD 05-JUN-2003.
Query Match
Best Local Similarity 4.1%; Score 35.4; DB 9; Length 1234;
RESULT 1343
ID ACF50096 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003104543-A1.
PD 05-JUN-2003.
Query Match
Best Local Similarity 4.1%; Score 35.4; DB 9; Length 1234;
RESULT 1344
ID ACD09495 standard; cDNA; 1234 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #119.

PN US2003036127-A1.
PD 20-FEB-2003.
Query Match 4.1%; Score 35.4; DB 9; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1345
ID ACD08574 standard; cDNA; 1234 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #119.
PN US2003040061-A1.
PD 27-FEB-2003.
Query Match 4.1%; Score 35.4; DB 9; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1346
ID ACH03607 standard; cDNA; 1234 BP.
DE Human secreted/transmembrane polypeptide PRO 3566 cDNA.
PN US2003018172-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 4.1%; Score 35.4; DB 9; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1347
ID ACF12288 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003036130-A1.
PD 20-FEB-2003.
Query Match 4.1%; Score 35.4; DB 9; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1348
ID ACC94796 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003054468-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.1%; Score 35.4; DB 9; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1349
ID ACD22515 standard; cDNA; 1234 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #119.
PN US2003054470-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.1%; Score 35.4; DB 9; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1350
ID ACF15215 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003044917-A1.
PD 06-MAR-2003.
Query Match 4.1%; Score 35.4; DB 9; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1351
ID ACC97310 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003044929-A1.
PD 06-MAR-2003.
Query Match 4.1%; Score 35.4; DB 9; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1352
ID ACC92340 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003059880-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.1%; Score 35.4; DB 9; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1353
ID ACF13987 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003064465-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.1%; Score 35.4; DB 9; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1354

ID ACF14294 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003054478-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.1%; Score 35.4; DB 9; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1355
ID ACF09525 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003068718-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.1%; Score 35.4; DB 9; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1356
ID ACD45816 standard; cDNA; 1234 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #119.
PN US2003064454-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.1%; Score 35.4; DB 9; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1357
ID ACD47965 standard; cDNA; 1234 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #119.
PN US2003064461-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.1%; Score 35.4; DB 9; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1358
ID ACD67696 standard; cDNA; 1234 BP.
DE cDNA encoding human PRO polypeptide #119.
PN US2003068724-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.1%; Score 35.4; DB 9; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1359
ID ACF25504 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003068727-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.1%; Score 35.4; DB 9; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1360
ID ACF29188 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003068772-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.1%; Score 35.4; DB 9; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1361
ID ACD84966 standard; cDNA; 1234 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #119.
PN US2003068714-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.1%; Score 35.4; DB 9; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1362
ID ACD84045 standard; cDNA; 1234 BP.
DE Human PRO polynucleotide #119.
PN US2003068758-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.1%; Score 35.4; DB 9; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1363
ID ACD88036 standard; cDNA; 1234 BP.

DE Human secreted/transmembrane protein (PRO) cDNA #119.
PN US2003068776-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC. 4.1%; Score 35.4; DB 9; Length 1234;
Query Match Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1364
ID ACF30723 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003069407-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC. 4.1%; Score 35.4; DB 9; Length 1234;
Query Match Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1365
ID ACF32326 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003104555-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC. 4.1%; Score 35.4; DB 9; Length 1234;
Query Match Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1366
ID ACH11986 standard; cDNA; 1234 BP.
DE cDNA encoding human PRO polypeptide #119.
PN US2003049768-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC. 4.1%; Score 35.4; DB 9; Length 1234;
Query Match Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1367
ID ACH12293 standard; cDNA; 1234 BP.
DE cDNA encoding human PRO polypeptide #119.
PN US2003049771-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC. 4.1%; Score 35.4; DB 9; Length 1234;
Query Match Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1368
ID ADA19925 standard; cDNA; 1234 BP.
DE Novel human secreted and transmembrane protein PRO3566 cDNA.
PN US2003069394-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC. 4.1%; Score 35.4; DB 9; Length 1234;
Query Match Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1369
ID ACD40685 standard; cDNA; 1234 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #119.
PN US2003032134-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC. 4.1%; Score 35.4; DB 9; Length 1234;
Query Match Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1370
ID ADB17308 standard; cDNA; 1234 BP.
DE Human cDNA clone (seqID 63) encoding the transmembrane PRO protein.
PN US2003050465-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC. 4.1%; Score 35.4; DB 9; Length 1234;
Query Match Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1371
ID ACF18157 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003054481-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC. 4.1%; Score 35.4; DB 9; Length 1234;
Query Match Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1372
ID ACF08604 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003049778-A1.

PD 13-MAR-2003.
PA (GETH) GENENTECH INC. 4.1%; Score 35.4; DB 9; Length 1234;
Query Match Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1373
ID ACF31405 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003049782-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC. 4.1%; Score 35.4; DB 9; Length 1234;
Query Match Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1374
ID ACF52245 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003054476-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC. 4.1%; Score 35.4; DB 9; Length 1234;
Query Match Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1375
ID ACD50114 standard; cDNA; 1234 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #119.
PN US2003068733-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC. 4.1%; Score 35.4; DB 9; Length 1234;
Query Match Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1376
ID ACF38817 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003068692-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC. 4.1%; Score 35.4; DB 9; Length 1234;
Query Match Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1377
ID ACF26732 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003068709-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC. 4.1%; Score 35.4; DB 9; Length 1234;
Query Match Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1378
ID ACF24832 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003068716-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC. 4.1%; Score 35.4; DB 9; Length 1234;
Query Match Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1379
ID ACF46412 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003068740-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC. 4.1%; Score 35.4; DB 9; Length 1234;
Query Match Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1380
ID ACF27960 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003068751-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC. 4.1%; Score 35.4; DB 9; Length 1234;
Query Match Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1381
ID ACD89264 standard; cDNA; 1234 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #119.
PN US2003068684-A1.
PD 10-APR-2003.

PA (GETH) GENENTECH INC.
Query Match 4.1%; Score 35.4; DB 9; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1382
ID ACF63836 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003073179-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.1%; Score 35.4; DB 9; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1383
ID ACF60476 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003087374-A1.
PD 08-MAY-2003.
Query Match 4.1%; Score 35.4; DB 9; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1384
ID ACH12600 standard; cDNA; 1234 BP.
DE cDNA encoding human PRO polypeptide #119.
PN US2003049773-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.1%; Score 35.4; DB 9; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1385
ID ACH10023 standard; cDNA; 1234 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #119.
PN US2003049777-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.1%; Score 35.4; DB 9; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1386
ID ACD03878 standard; cDNA; 1234 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #119.
PN US2003040055-A1.
PD 27-FEB-2003.
Query Match 4.1%; Score 35.4; DB 9; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1387
ID ACD10416 standard; cDNA; 1234 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #119.
PN US2003036164-A1.
PD 20-FEB-2003.
Query Match 4.1%; Score 35.4; DB 9; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1388
ID ACD12058 standard; cDNA; 1234 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #119.
PN US2003040074-A1.
PD 27-FEB-2003.
Query Match 4.1%; Score 35.4; DB 9; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1389
ID ACF42443 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003054480-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.1%; Score 35.4; DB 9; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1390
ID ACF18464 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003059885-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.1%; Score 35.4; DB 9; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1391
ID ACF02254 standard; cDNA; 1234 BP.

DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003049740-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.1%; Score 35.4; DB 9; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1392
ID ACF21762 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003049770-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.1%; Score 35.4; DB 9; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1393
ID ACF10446 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003073169-A1.
PD 17-APR-2003.
Query Match 4.1%; Score 35.4; DB 9; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1394
ID ACF33898 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003064457-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.1%; Score 35.4; DB 9; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1395
ID ACF44860 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003068711-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.1%; Score 35.4; DB 9; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1396
ID ACD90492 standard; cDNA; 1234 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #119.
PN US2003049745-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.1%; Score 35.4; DB 9; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1397
ID ACD91105 standard; cDNA; 1234 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #119.
PN US2003049751-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.1%; Score 35.4; DB 9; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1398
ID ACD12058 standard; cDNA; 1234 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #119.
PN US2003040074-A1.
PD 27-FEB-2003.
Query Match 4.1%; Score 35.4; DB 9; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1399
ID ACD87115 standard; cDNA; 1234 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #119.
PN US2003068773-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.1%; Score 35.4; DB 9; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1400
ID ACF60169 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003073185-A1.

PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 4.1%; Score 35.4; DB 9; Length 1234;
PD 10-APR-2003.
ID ACF46719 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003087373-A1.
PD 08-MAY-2003.
Query Match
Best Local Similarity 4.1%; Score 35.4; DB 9; Length 1234;
PD 22-MAY-2003.
ID ACF75576 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003096353-A1.
PD 22-MAY-2003.
Query Match
Best Local Similarity 4.1%; Score 35.4; DB 9; Length 1234;
PD 17-APR-2003.
ID ADA79781 standard; cDNA; 1234 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #119.
PN US2003073173-A1.
PD 17-APR-2003.
Query Match
Best Local Similarity 4.1%; Score 35.4; DB 9; Length 1234;
PD 20-MAR-2003.
ID ACF17236 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003054458-A1.
PD 20-MAR-2003.
Query Match
Best Local Similarity 4.1%; Score 35.4; DB 9; Length 1234;
PD 27-MAR-2003.
ID ACF22990 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003059886-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 4.1%; Score 35.4; DB 9; Length 1234;
PD 13-MAR-2003.
ID ACF07990 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003049758-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 4.1%; Score 35.4; DB 9; Length 1234;
PD 13-MAR-2003.
ID ACF08297 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003049772-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 4.1%; Score 35.4; DB 9; Length 1234;
PD 03-APR-2003.
ID ACF40601 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003064448-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 4.1%; Score 35.4; DB 9; Length 1234;
PD 03-APR-2003.
ID ACF53780 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003064456-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 4.1%; Score 35.4; DB 9; Length 1234;
PD 03-APR-2003.
ID ACF61397 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003096359-A1.

ID ACD47044 standard; cDNA; 1234 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #119.
PN US2003068693-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 4.1%; Score 35.4; DB 9; Length 1234;
PD 10-APR-2003.
ID ACF47947 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003068735-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 4.1%; Score 35.4; DB 9; Length 1234;
PD 10-APR-2003.
ID ACF47333 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003068753-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 4.1%; Score 35.4; DB 9; Length 1234;
PD 10-APR-2003.
ID ACF46105 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003068742-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 4.1%; Score 35.4; DB 9; Length 1234;
PD 10-APR-2003.
ID ACD86194 standard; cDNA; 1234 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #119.
PN US2003068756-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 4.1%; Score 35.4; DB 9; Length 1234;
PD 01-MAY-2003.
ID ACF52552 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003082715-A1.
PD 01-MAY-2003.
Query Match
Best Local Similarity 4.1%; Score 35.4; DB 9; Length 1234;
PD 01-MAY-2003.
ID ACF52859 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003082716-A1.
PD 01-MAY-2003.
Query Match
Best Local Similarity 4.1%; Score 35.4; DB 9; Length 1234;
PD 01-MAY-2003.
ID ACF64852 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003068737-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 4.1%; Score 35.4; DB 9; Length 1234;
PD 05-JUN-2003.
ID ACF76497 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003104547-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 4.1%; Score 35.4; DB 9; Length 1234;
PD 05-JUN-2003.
ID ACF61397 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003096359-A1.

PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 4.1%; Score 35.4; DB 9; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1420
ID ACF61704 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003100061-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 4.1%; Score 35.4; DB 9; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1421
ID ACD30735 standard; cDNA; 1234 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #119.
PN US2003032125-A1.
PD 13-FEB-2003.
Query Match 4.1%; Score 35.4; DB 9; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1422
ID ACD31656 standard; cDNA; 1234 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #119.
PN US2003054454-A1.
PD 20-MAR-2003.
Query Match 4.1%; Score 35.4; DB 9; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1423
ID ACD32577 standard; cDNA; 1234 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #119.
PN US2003054477-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.1%; Score 35.4; DB 9; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1424
ID ADA20097 standard; cDNA; 1234 BP.
DE Novel human secreted and transmembrane protein PRO3566 cDNA.
PN US2003055222-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.1%; Score 35.4; DB 9; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1425
ID ACD82121 standard; cDNA; 1234 BP.
DE Human secreted/transmembrane polypeptide PRO 3566 cDNA.
PN US2003060601-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.1%; Score 35.4; DB 9; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1426
ID ACF17543 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003054460-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.1%; Score 35.4; DB 9; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1427
ID ACF07376 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003049753-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.1%; Score 35.4; DB 9; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1428
ID ACF20534 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003049763-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.1%; Score 35.4; DB 9; Length 1234;

Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1429
ID ACF20841 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003073172-A1.
PD 17-APR-2003.
Query Match 4.1%; Score 35.4; DB 9; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1430
ID ACF21148 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003073172-A1.
PD 17-APR-2003.
Query Match 4.1%; Score 35.4; DB 9; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1431
ID ACD47658 standard; cDNA; 1234 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #119.
PN US2003068700-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.1%; Score 35.4; DB 9; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1432
ID ACF47640 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003068736-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.1%; Score 35.4; DB 9; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1433
ID ACF53473 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003068679-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.1%; Score 35.4; DB 9; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1434
ID ACD86808 standard; cDNA; 1234 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #119.
PN US2003068767-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.1%; Score 35.4; DB 9; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1435
ID ACH05056 standard; cDNA; 1234 BP.
DE cDNA encoding human PRO polypeptide #119.
PN US2003073182-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.1%; Score 35.4; DB 9; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1436
ID ACF44553 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003104557-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 4.1%; Score 35.4; DB 9; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1437
ID ADA81508 standard; cDNA; 1234 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #119.
PN US2003092121-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 4.1%; Score 35.4; DB 9; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1438
ID ACD22208 standard; cDNA; 1234 BP.


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DE Human secreted/transmembrane protein (PRO) cDNA #119.
PN US2003027276-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 4.1%; Score 35.4; DB 9; Length 1234;
PA (GETH ) GENENTECH INC.
RESULT 1439
ID ACD24555 standard; cDNA; 1234 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #119.
PN US2003044920-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 4.1%; Score 35.4; DB 9; Length 1234;
PA (GETH ) GENENTECH INC.
RESULT 1440
ID ACD39758 standard; cDNA; 1234 BP.
DE cDNA encoding human PRO polypeptide #119.
PN US2003027265-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 4.1%; Score 35.4; DB 9; Length 1234;
PA (GETH ) GENENTECH INC.
RESULT 1441
ID ACD40065 standard; cDNA; 1234 BP.
DE cDNA encoding human PRO polypeptide #119.
PN US2003054461-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 4.1%; Score 35.4; DB 9; Length 1234;
RESULT 1442
ID ACF13373 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003064446-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 4.1%; Score 35.4; DB 9; Length 1234;
RESULT 1443
ID ACF03175 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003049744-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 4.1%; Score 35.4; DB 9; Length 1234;
RESULT 1444
ID ACF78646 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003049783-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 4.1%; Score 35.4; DB 9; Length 1234;
RESULT 1445
ID ACF11367 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003073171-A1.
PD 17-APR-2003.
Query Match
Best Local Similarity 4.1%; Score 35.4; DB 9; Length 1234;
RESULT 1446
ID ACF50710 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003032121-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 4.1%; Score 35.4; DB 9; Length 1234;
RESULT 1447
ID ACF34205 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003064458-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 4.1%; Score 35.4; DB 9; Length 1234;
RESULT 1448
ID ACD46430 standard; cDNA; 1234 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #119.
PN US2003064460-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 4.1%; Score 35.4; DB 9; Length 1234;
RESULT 1449
ID ACD48272 standard; cDNA; 1234 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #119.
PN US2003064464-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 4.1%; Score 35.4; DB 9; Length 1234;
RESULT 1450
ID ACF27653 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003068702-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 4.1%; Score 35.4; DB 9; Length 1234;
RESULT 1451
ID ACF24525 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003068734-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 4.1%; Score 35.4; DB 9; Length 1234;
RESULT 1452
ID ACD85580 standard; cDNA; 1234 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #119.
PN US2003068719-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 4.1%; Score 35.4; DB 9; Length 1234;
RESULT 1453
ID ACD90185 standard; cDNA; 1234 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #119.
PN US2003068729-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 4.1%; Score 35.4; DB 9; Length 1234;
RESULT 1454
ID ACD83738 standard; cDNA; 1234 BP.
DE Human PRO polynucleotide #119.
PN US2003068738-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 4.1%; Score 35.4; DB 9; Length 1234;
RESULT 1455
ID ACF49175 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003104540-A1.
PD 05-JUN-2003.
Query Match
Best Local Similarity 4.1%; Score 35.4; DB 9; Length 1234;
RESULT 1456
ID ACH07260 standard; cDNA; 1234 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #119.
PN US2003049742-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 4.1%; Score 35.4; DB 9; Length 1234;
RESULT 1457
ID ACH07567 standard; cDNA; 1234 BP.
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DE Human secreted/transmembrane protein (PRO) cdna #119.
PN US2003049747-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.1%; Score 35.4; DB 9; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1458
ID ACH08181 standard; cdna; 1234 BP.
DE Human secreted/transmembrane protein (PRO) cdna #119.
PN US2003049750-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.1%; Score 35.4; DB 9; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1459
ID ACH11372 standard; cdna; 1234 BP.
DE cDNA encoding human PRO polypeptide #119.
PN US2003049766-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.1%; Score 35.4; DB 9; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1460
ID ACH11679 standard; cdna; 1234 BP.
DE cDNA encoding human PRO polypeptide #119.
PN US2003049767-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.1%; Score 35.4; DB 9; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1461
ID ACH10330 standard; cdna; 1234 BP.
DE Human secreted/transmembrane protein (PRO) cdna #119.
PN US2003049779-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.1%; Score 35.4; DB 9; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1462
ID ACF01333 standard; cdna; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cdna, SEQ ID NO:237.
PN US2003040059-A1.
PD 27-FEB-2003.
Query Match 4.1%; Score 35.4; DB 9; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1463
ID ACF40908 standard; cdna; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cdna, SEQ ID NO:237.
PN US2003040078-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 4.1%; Score 35.4; DB 9; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1464
ID ACD24248 standard; cdna; 1234 BP.
DE Human secreted/transmembrane protein (PRO) cdna #119.
PN US2003044918-A1.
PD 06-MAR-2003.
Query Match 4.1%; Score 35.4; DB 9; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1465
ID ACD31349 standard; cdna; 1234 BP.
DE Human secreted/transmembrane protein (PRO) cdna #119.
PN US2003032132-A1.
PD 13-FEB-2003.
Query Match 4.1%; Score 35.4; DB 9; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1466
ID ACF17850 standard; cdna; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cdna, SEQ ID NO:237.
PN US2003054462-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.

Query Match 4.1%; Score 35.4; DB 9; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1467
ID ACF12633 standard; cdna; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cdna, SEQ ID NO:237.
PN US2003064445-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.1%; Score 35.4; DB 9; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1468
ID ACF40294 standard; cdna; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cdna, SEQ ID NO:237.
PN US2003064449-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.1%; Score 35.4; DB 9; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1469
ID ACF48254 standard; cdna; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cdna, SEQ ID NO:237.
PN US2003064441-A1.
PD 03-APR-2003.
Query Match 4.1%; Score 35.4; DB 9; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1470
ID ACF38203 standard; cdna; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cdna, SEQ ID NO:237.
PN US2003068696-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.1%; Score 35.4; DB 9; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1471
ID ACF25139 standard; cdna; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cdna, SEQ ID NO:237.
PN US2003068712-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.1%; Score 35.4; DB 9; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1472
ID ACF27039 standard; cdna; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cdna, SEQ ID NO:237.
PN US2003068730-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.1%; Score 35.4; DB 9; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1473
ID ACF29495 standard; cdna; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cdna, SEQ ID NO:237.
PN US2003073174-A1.
PD 17-APR-2003.
Query Match 4.1%; Score 35.4; DB 9; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1474
ID ACD87729 standard; cdna; 1234 BP.
DE Human secreted/transmembrane protein (PRO) cdna #119.
PN US2003068775-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.1%; Score 35.4; DB 9; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1475
ID ACF76190 standard; cdna; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cdna, SEQ ID NO:237.
PN US2003104545-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 4.1%; Score 35.4; DB 9; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1476

RESULT 1486
ID ACC94489 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003054467-A1.
PD 05-JUN-2003.
Query Match 4.1%; Score 35.4; DB 9; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1477
ID ACF43939 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003104554-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 4.1%; Score 35.4; DB 9; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1478
ID ACH06284 standard; cDNA; 1234 BP.
DE cDNA encoding human PRO polypeptide #119.
PN US2003049762-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.1%; Score 35.4; DB 9; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1479
ID ACH06591 standard; cDNA; 1234 BP.
DE cDNA encoding human PRO polypeptide #119.
PN US2003049765-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.1%; Score 35.4; DB 9; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1480
ID ADA93306 standard; cDNA; 1234 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #119.
PN US2003049752-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.1%; Score 35.4; DB 9; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1481
ID ACC92647 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003032133-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 4.1%; Score 35.4; DB 9; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1482
ID ACC93261 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003032136-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 4.1%; Score 35.4; DB 9; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1483
ID ACF19306 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003036129-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 4.1%; Score 35.4; DB 9; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1484
ID ACD12997 standard; cDNA; 1234 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #119.
PN US2003040053-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 4.1%; Score 35.4; DB 9; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1485
ID ACF06455 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003040057-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 4.1%; Score 35.4; DB 9; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;

RESULT 1486
ID ACC94489 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003054467-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.1%; Score 35.4; DB 9; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1487
ID ACC97917 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003044932-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.1%; Score 35.4; DB 9; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1488
ID ACC94182 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003027270-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 4.1%; Score 35.4; DB 9; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1489
ID ACF42136 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003054469-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.1%; Score 35.4; DB 9; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1490
ID ACB31042 standard; cDNA; 1234 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #119.
PN US2003032126-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 4.1%; Score 35.4; DB 9; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1491
ID ACD43071 standard; cDNA; 1234 BP.
DE cDNA encoding human PRO polypeptide #119.
PN US2003054463-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.1%; Score 35.4; DB 9; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1492
ID ACD43378 standard; cDNA; 1234 BP.
DE cDNA encoding human PRO polypeptide #119.
PN US2003054466-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.1%; Score 35.4; DB 9; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1493
ID ACF14908 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003059879-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.1%; Score 35.4; DB 9; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1494
ID ACF01640 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003049738-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.1%; Score 35.4; DB 9; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1495
ID ACF31712 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003064469-A1.
PD 03-APR-2003.

PA (GETH) GENENTECH INC.
Query Match 4.1%; Score 35.4; DB 9; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1496
ID ACD67389 standard; cDNA; 1234 BP.
DE cDNA encoding human PRO polypeptide #119.
PN US2003064453-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.1%; Score 35.4; DB 9; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1497
ID ACD48579 standard; cDNA; 1234 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #119.
PN US2003064456-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.1%; Score 35.4; DB 9; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1498
ID ACD48886 standard; cDNA; 1234 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #119.
PN US2003064468-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.1%; Score 35.4; DB 9; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1499
ID ACF51324 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003068760-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.1%; Score 35.4; DB 9; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1500
ID AEF74278 standard; cDNA; 1234 BP.
DE Human PRO3566 encoding cDNA SEQ ID NO:63.
PN US2005260647-A1.
PD 24-NOV-2005.
PA (EATO/) EATON D L.
PA (FILV/) FILVAROFF E.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GRIM/) GRIMALDI J C.
PA (GURN/) GURNEY A L.
PA (WATA/) WATANABE C K.
PA (WOOD/) WOOD W L.
Query Match 4.1%; Score 35.4; DB 15; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;

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GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: August 3, 2006, 09:03:50 ; Search time 5165 Seconds
(without alignments)

Title: US-10-015-967-1
 Perfect score: 870
 Sequence: 1 ctgcgctccaatcggaacg.....tcaaaaaaaaaaaaaaaaaa 870

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 96473596

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Minimum DB seq length: 0
Maximum DB seq length: 20000000000
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries

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1: gb_est1.*
2: gb_est3.*
3: gb_est4.*
4: gb_est5.*
5: gb_est6.*
6: gb_hic.*
7: gb_est2.*
8: gb_est7.*
9: gb_est8.*
10: gb_est9.*
11: gb_gss1.*
12: gb_gss2.*
13: gb_gss3.*
14: gb_gss4.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query			DB	ID	Description
		Match	Length	†			
C	1	725	83.3	748	4	CB242167	UI-CF-FNO1
	2	685.8	78.8	715	3	BM982101	UI-CF-EN1
	3	682.8	78.5	753	3	BM978124	UI-CF-EC1
C	4	679.4	78.1	693	10	DR422006	navo06910
	5	677	77.8	677	3	BM769732	K-EST0053
	6	675.6	77.7	820	2	BI770944	603059769
C	7	671	77.1	671	4	BX102380	BX102380
	8	666	76.6	666	3	BM831028	K-EST0104
	9	664	76.3	664	3	BM854000	K-EST0136
C	10	622	71.5	628	9	DN998063	TC105256
	11	621.4	71.4	628	9	DN998245	TC124609
	12	607.8	69.9	631	5	CD698783	EST5305_h
C	13	607.2	69.8	628	3	BM746867	K-EST0021
	14	590.4	67.9	592	3	BU682452	UI-CF-EC1
	15	589	67.7	589	9	DB236758	DB236758
C	16	582.6	67.0	613	2	BG536626	602586231
	17	579	66.6	613	3	BM766904	K-EST0048
	18	575.6	66.2	594	3	BM743525	K-EST0016
C	19	573.8	66.0	578	3	BM979898	UI-CF-EN1

93	266.8	30.7	270	3	BM855784	BM855784	K-EST0139
94	264.4	30.4	421	4	CB434699	CB434699	G11358 MA
95	263	30.2	263	7	BF055365	BF055365	7J78F09 X
96	263	30.2	263	4	BE645174	BE645174	7E64A07 X
97	262.2	30.1	643	4	BY731153	BY731153	BY731153
98	262.2	30.1	669	6	AK143005	AK143005	Mus muscu
99	259.4	29.8	479	7	BE624584	BE624584	uu23h11.Y
100	258.6	29.7	605	1	AA537274	AA537274	vk46B02 .Y
101	258.4	29.7	575	4	CB450481	CB450481	705144 MA
102	258.2	29.7	541	4	BX520414	BX520414	BX520414
103	257.8	29.6	466	1	AA881369	AA881369	vx31g04. r
104	257.8	29.6	484	1	AA7899593	AA7899593	vw61E07. r
105	255	29.3	255	1	AI2107071	AI2107071	qf80E02. X
106	253.4	29.1	433	7	BE197231	BE197231	ug73b06. Y
107	252.8	29.1	913	10	DM047460	DM047460	DAY20. 17
108	247.4	28.4	834	4	CB952075	CB952075	AGENCOURT
109	245.8	28.3	298	5	CD707468	CD707468	EST23995
110	241.2	27.7	271	7	BE181362	BE181362	CM0-HT063
111	240.4	27.6	829	2	BF1078998	BF1078998	602873258
112	240.4	27.6	1279	2	BG535485	BG535485	602563170
113	239.2	27.5	556	8	CK980826	CK980826	4112905 B
114	238	27.4	242	1	AA477092	AA477092	zu35g03. r
115	234	26.9	251	2	BF743524	BF743524	QVO-BT084
116	224.4	25.8	390	10	DM092442	DM092442	000731B1TN
117	220	25.3	533	4	CB420505	CB420505	593464 MA
118	219	25.2	254	7	BF789442	BF789442	110-ST016
119	218.2	25.1	267	2	AP743520	AP743520	QVO-BT084
120	218	25.1	232	1	AI474243	AI474243	tg84c11. x
121	213.8	24.6	227	1	AI680037	AI680037	tu24C01. x
122	210.6	24.2	373	10	DM071286	DM071286	000731B1TN
123	209.6	24.1	472	4	BF089449	BF089449	PM3-HT093
124	203	23.3	242	4	CB435186	CB435186	615242 MA
125	201.2	23.1	579	12	CG691642	CG691642	FHCRC-GT-
126	195	22.4	253	7	BF088641	BF088641	RC0-HT088
127	193.2	22.2	279	1	AI758852	AI758852	ty16C01. x
128	190.4	21.9	241	7	BF089451	BF089451	PM3-HT093
129	189	21.7	191	4	CO0521	CO0521	HUMGS000804
130	185.4	21.3	422	7	BF652670	BF652670	QV1-UM003
131	176.2	20.3	223	7	AW797203	AW797203	QV1-UM003
132	175.6	20.2	311	4	CB869626	CB869626	AMGNNUC.T
133	139.8	16.1	144	2	AA074399	AA074399	zmi6E08. s
134	136.4	15.7	424	1	BF845955	BF845955	QV1-EN005
135	136.2	15.7	213	2	BG338127	BG338127	IAbol1F12
136	133.6	15.4	415	3	BQ380575	BQ380575	QV1-UT009
137	126.6	14.6	401	1	AI276273	AI276273	g165G05. x
138	120.4	13.8	465	1	AI463349	AI463349	vw61E07. x
139	118	13.6	167	7	AW797186	AW797186	QV1-UM003
140	114	13.1	143	3	DA763751	DA763751	UI-CF-DU0
141	103.8	11.9	571	9	BU674375	BU674375	DA763751
142	100.4	11.5	631	12	CE3250770	CE3250770	tgcr-g98-
143	93.6	10.8	360	1	AI375133	AI375133	tc09G06. x
144	89.6	10.3	251	4	CB220287	CB220287	IAbol19G09
145	82.6	9.5	454	14	CR873527	CR873527	Sub scrof
146	78.4	9.0	398	12	CG491802	CG491802	OST293360
147	78	9.0	628	5	CD696654	CD696654	EST31377
148	69.8	8.0	610	14	CR833969	CR833969	GROAAA67D
149	69.2	8.0	596	2	BG381659	BG381659	UI-R-CT0-
150	69	7.9	485	14	DU513069	DU513069	109860983
151	66.6	7.7	710	11	AZ360058	AZ360058	2M0227E20
152	65.4	7.5	696	11	AZ804554	AZ804554	2M065806
153	65	7.5	364	3	BU677228	BU677228	UI-CF-DU1
154	58.2	6.7	1080	14	CNS00EPP	CNS00EPP	DN900142
155	55.8	6.4	1101	14	CNS00LT2	CNS00LT2	naq01d04.
156	54	6.2	478	8	CNT30376	CNT30376	DT785142
157	49.2	5.7	1272	9	DN810334	DN810334	124579094
158	49	5.6	329	1	AI810721	AI810721	HW_loin_3
159	48	5.5	869	9	BE964633	BE964633	CJ42368
160	47.8	5.5	563	9	DN900142	DN900142	CJ42368
161	47.8	5.5	836	10	DT785142	DT785142	DT785142
162	47.4	5.4	1300	10	DT792398	DT792398	HW_loin_3
163	46.4	5.3	835	5	CJ42368	CJ42368	HW_loin_3
164	46.2	5.3	371	3	BQ196067	BQ196067	CJ42368
165	46.2	5.3	959	14	CNS01407	CNS01407	DT785142

45.6	5.2	5.17	4	C90175	C90175 Dict
45.6	5.2	1101	14	CNS00LOO	AL068607 Drosophill
45.6	5.2	1101	14	CNS0106X	AL098595 Drosophill
45.2	5.2	509	9	DN254243	DN254243 Meso02318
45.2	5.2	912	9	DN2569400	DN2569400 938112657
45.2	5.2	957	10	DT8042463	DT8042463 127363864
45	5.2	971	9	DN561756	DN561756 88080644
44.6	5.1	389	1	A1301631	A1301631 qnl71h09.x
44.4	5.1	431	14	CNS0406O	AL293145 Tetraodon
44.4	5.1	993	2	BG6223358	BG6223358 602647045
44.2	5.1	386	8	CV999880	CV999880 1v53504.b
44.2	5.1	1316	7	CBX631051	BE965081 601658868
44	5.1	465	9	CR8031081	CX803105 JGI_CAAJ1
44	5.1	808	14	DN958240	DN958240 225373 To
44	5.1	837	8	CN169807	CN169807 AGENCOURT
44	5.1	989	11	A2536271	A2536271 ENTBZ25TR
44	5.1	1033	9	DN573003	DN573003 92937986
44	5.1	3431	6	AK155463	AK155463 Mus muscu
43.8	5.0	684	11	AQ894677	AQ894677 HS_3143_B
43.8	5.0	892	9	DN573579	DN573579 92269141
43.8	5.0	895	14	CNS0071A	AL066286 Drosophill
43.8	5.0	898	14	CNS00JQC	AL076805 Drosophill
43.8	5.0	923	3	BU588149	BU588149 AGENCOURT
43.8	5.0	939	14	CNS00CNG	AL059400 Drosophill
43.8	5.0	1101	14	CNS0181N	AL108773 Drosophill
43.6	5.0	302	10	DN7365008	DN7365008 ZO_Ee000
43.6	5.0	640	9	DN414095	DN414095 LiFB4215-0
43.4	5.0	258	11	AZ808132	AZ808132 2M0071H07
43.4	5.0	355	2	B1111761	B1111761 602897921
43.4	5.0	428	5	CJ310586	CJ310586 C3J10586
43.4	5.0	640	8	CX331766	CX331766 JGI_XZT17
43.4	5.0	652	9	DN837829	DN837829 nad29a12.
43.2	5.0	456	3	BQ197844	BQ197844 NXVL121.D
43.2	5.0	884	14	CNS006UO	AL065923 Drosophill
43	4.9	615	2	B1521894	B1521894 603081323
43	4.9	861	9	DN872401	DN872401 aden1907.
43	4.9	873	5	CD251221	CD251221 AGENCOURT
43	4.9	967	11	BH154293	BH154293 ENTQV43TF
42.8	4.9	412	9	DN903185	DN903185 nad44h08.
42.8	4.9	474	7	BE848199	BE848199 uw36d05.Y
42.8	4.9	485	14	DE136007	DE136007 Oryzias.Y
42.8	4.9	683	4	BY724873	BY724873 BY724873
42.8	4.9	761	14	CNS02MEY	AL204019 Tetraodon
42.8	4.9	802	5	CK128354	CK128354 AGENCOURT
42.8	4.9	802	5	CK128354	BE966081 601659991
42.8	4.9	1322	7	AA162707	AA162707 mna42c02.r
42.6	4.9	155	1	CA281558	CX428158 JGI_XZG18
42.6	4.9	354	9	CX428158	BE231815 136644.WA
42.6	4.9	379	7	CJ321815	CJ321550 C3J21550
42.6	4.9	410	5	CJ321550	CJ321550 C3J21550
42.6	4.9	413	5	CF047793	CF047793 CSECS068E
42.6	4.9	425	1	AT196113	AT196113 wh42807.X
42.6	4.9	535	10	DT396095	DT396095 JGI_CABH1
42.6	4.9	635	3	BU063136	BU063136 For_2.L12
42.6	4.9	727	4	CA164504	CA164504 SQTJFT205
42.6	4.9	826	8	CR433419	CR433419 CR433419
42.6	4.9	855	14	AG135519	AG135519 Pan trogl
42.4	4.9	280	8	CN211523	CN211523 rzhswabO
42.4	4.9	438	8	CO895118	CO895118 BowGen_23
42.4	4.9	601	4	BX550992	BX550992 BX550992
42.4	4.9	619	2	BT199499	BT199499 HL34802.E
42.4	4.9	626	9	DN866591	DN866591 naf37h04.
42.4	4.9	821	14	CNS015G1	AL105420 Drosophill
42.4	4.9	821	14	AL047047	AL047047 DKF2P586O
42.4	4.9	821	14	CNS015G1	AL105420 Drosophill
42.4	4.9	866	5	CK413099	CK413099 AUP_Ipg11
42.4	4.9	913	14	AG396212	AG396212 Mus muscu
42.4	4.9	926	2	B1524254	B1524254 603052055
42.4	4.9	952	2	BG555702	BG555702 dfc19g02.x
42.2	4.9	95	2	BG555702	BG555702 dfc19g02.x
42.2	4.9	379	4	C90082	C90082 C90082 Dict
42.2	4.9	423	4	CB280289	CB280289 ru43h09.Y
42.2	4.9	455	5	CJ263805	CJ263805 C3J263805
42.2	4.9	455	5	CJ263805	CJ263805 C3J263805
42.2	4.9	508	4	CA365670	CA365670 640857 NC
42.2	4.9	517	9	DN868818	DN868818 nac36d04.
42.2	4.9	534	3	BQ058821	BQ058821 il10d05.Y

239	42.2	4.9	536	9	CX733097	CX733097 oc39b09.y	312	4.7	353	5	CF382108	CF382108 lab96h07.
240	42.2	4.9	544	4	CB979855	CB979855 CAB70001_	313	4.7	412	5	CJ310210	CJ310210 CJ310210
C 241	42.2	4.9	694	10	DV624532	DV624532 94087.1 C	314	4.7	435	5	CJ305667	CJ305667 CJ305667
C 242	42.2	4.9	837	9	DN053786	DN053786 JGI CABAB	315	4.7	470	9	CX572103	CX572103 TTR000183
C 243	42.2	4.9	1000	12	CL111647	CL111647 TSB1-5539	316	4.7	502	10	DT928899	DT928899 BMSB11813
C 244	42	4.8	303	8	CO081908	CO081908 GR_Ra46E	317	4.7	544	5	CK789750	CK789750 AGENCOURT
245	42	4.8	342	9	CX368327	CX368327 LJB3731-0	318	4.7	548	4	CB723280	CB723280 UI-M-GKO-
246	42	4.8	419	3	BU551636	BU551636 mail18d05.	319	4.7	551	8	CO814978	CO814978 AGENCOURT
247	42	4.8	552	5	CK086699	CK086699 AmeF214 L	C 320	4.7	620	8	CR431617	CR431617 CR431617
248	42	4.8	859	14	CNS0004Y	AL055406 Drosophila	321	4.7	652	10	DT101207	DT101207 JGI ANNS
C 249	42	4.8	1101	14	CNS00KCF	AL077499 Drosophila	322	4.7	688	8	CV529650	CV529650 ALV_011B
C 250	42	4.8	1238	13	CL646737	CL646737 CH213-122	323	4.7	717	8	CN842704	CN842704 AGENCOURT
251	41.8	4.8	176	5	CK376859	CK376859 lan68h02.	324	4.7	744	5	CK797902	CK797902 AGENCOURT
C 252	41.8	4.8	279	10	BR430456	BR430456 max30g06.	325	4.7	786	8	CX134193	CX134193 AGENCOURT
C 253	41.8	4.8	317	4	DX481768	DX481768 DKFZP6861	326	4.7	810	3	BU944974	BU944974 AGENCOURT
C 254	41.8	4.8	423	9	BF724797	BF724797 bx08g10.x	327	4.7	849	2	BG110577	BG110577 602281019
C 255	41.8	4.8	448	9	DN866491	DN866491 nsc22b04.	C 328	4.7	859	14	CNS00KLL	AL077728 Drosophila
256	41.8	4.8	615	10	DT841689	DT841689 LB00460.C	C 329	4.7	893	8	CR564211	CR564211 CR564211
C 257	41.8	4.8	678	14	CR003486	CR003486 Forward s	330	4.7	928	5	CK022959	CK022959 AGENCOURT
C 258	41.8	4.8	719	11	B21675	B21675 F17P15-Sp6	331	4.7	937	14	AG466365	AG466365 Mus muscu
C 259	41.8	4.8	913	5	CK416843	CK416843 AUF IPint	C 332	4.7	938	10	DM637916	DM637916 CLJ368-C2
C 260	41.8	4.8	935	13	CZ519146	CZ519146 GNM2-8211	C 333	4.7	951	10	DT799609	DT799609 126446838
261	41.8	4.8	1030	13	CL492173	CL492173 SAIL_564	C 334	4.7	104	2	BJ366707	BJ366707 BJ366707
262	41.8	4.8	1041	10	DT798111	DT798111 126435162	335	4.7	195	5	CF546382	CF546382 labg72803.
C 263	41.8	4.8	1101	14	CNS000D1	AL065414 Drosophila	C 336	4.7	315	5	CF318708	CF318708 HD--08-P0
C 264	41.8	4.8	1101	14	CNS0167Y	AL106840 Drosophila	337	4.7	362	10	DV079721	DV079721 B15SFWldg
C 265	41.8	4.8	1766	7	BF683714	BF683714 602139978	338	4.7	384	8	CX311212	CX311212 JGI X2T11
C 266	41.6	4.8	158	5	CF383869	CF383869 lac11c07.	C 339	4.7	386	8	CX125202	CX125202 1325194 N
C 267	41.6	4.8	316	10	DR446496	DR446496 AR1032E06	340	4.7	421	8	CX026756	CX026756 1338219 N
268	41.6	4.8	377	12	CE245314	CE245314 tigr-g88-	341	4.7	447	4	BY465334	BY465334 BY465334
269	41.6	4.8	381	5	CK381710	CK381710 lag990g09.	C 342	4.7	475	4	BX566461	BX566461 BX566461
270	41.6	4.8	385	5	CK381768	CK381768 lag28a04.	C 343	4.7	483	14	CR368821	CR368821 GR0A4617A
C 271	41.6	4.8	405	5	CF354661	CF354661 lac16b05.	C 344	4.7	507	4	CA344051	CA344051 674365 NC
C 272	41.6	4.8	489	1	AL664772	AL664772 AL664772	345	4.7	510	4	CA344051	CA344051 674365 NC
273	41.6	4.8	572	1	AL727326	AL727326 AL727326	346	4.7	547	8	CN728405	CN728405 13JKNW2
274	41.6	4.8	591	9	DN975655	DN975655 CT07_85 T	347	4.7	563	9	DN895807	DN895807 nap01C03-
C 275	41.6	4.8	596	9	DN870799	DN870799 nad09b10.	C 348	4.7	592	3	BM671350	BM671350 UI-E-CKI-
C 276	41.6	4.8	737	12	CF910523	CF910523 t061n19ba	C 349	4.7	617	4	BF560294	BF560294 BX560294
C 277	41.6	4.8	921	5	CF595473	CF595473 AGENCOURT	C 350	4.7	752	5	CF519392	CF519392 AGENCOURT
C 278	41.4	4.8	252	8	CX068628	CX068628 1320073 N	C 351	4.7	756	4	CB243933	CB243933 UI-CF-FN0
279	41.4	4.8	256	2	BJ680202	BJ680202 BJ680202	C 352	4.7	790	10	DT254385	DT254385 JGI CANU6
C 280	41.4	4.8	434	3	BU958142	BU958142 AGENCOURT	C 353	4.7	843	4	BX710027	BX710027 BX710027
C 281	41.4	4.8	462	1	AI125744	AI125744 q991b02.x	C 354	4.7	876	10	DR549024	DR549024 WS03214.C
C 282	41.4	4.8	496	10	DT424714	DT424714 JGI CABY5	C 355	4.7	921	10	DT068969	DT068969 AGENCOURT
C 283	41.4	4.8	595	1	AM035555	AM035555 AM035555	C 356	4.7	964	10	DT776388	DT776388 125250650
C 284	41.4	4.8	690	8	CV666124	CV666124 LCPB04EX0	C 357	4.7	1083	7	BE965014	BE965014 601658792
C 285	41.4	4.8	951	14	CNS0157Z	AL105905 Drosophila	C 358	4.7	1117	2	BG766575	BG766575 602733344
286	41.4	4.8	1056	12	CC306139	CC306139 CH261-129	C 359	4.7	1438	2	BF781133	BF781133 602106779
C 287	41.4	4.8	1101	14	CNS0039E	AL063919 Drosophila	C 360	4.7	1645	7	BE962684	BE962684 601656058
C 288	41.4	4.8	1101	14	CNS0180X	AL108747 Drosophila	C 361	4.7	4022	6	BC029662	BC029662 Homo sapi
C 289	41.2	4.7	234	5	CF511149	CF511149 Cabud0002	362	4.7	153	5	CK374496	CK374496 lai78c08.
290	41.2	4.7	289	2	EG018795	EG018795 dsa56e11.	C 363	4.7	225	1	AA724507	AA724507 a104g08.8
291	41.2	4.7	405	5	CF639220	CF639220 D12.G10 F	364	4.7	235	3	BQ610416	BQ610416 sap41804.
292	41.2	4.7	430	8	CN831162	CN831162 EL845 Bra	C 365	4.7	245	2	BI291129	BI291129 UI-R-DK0-
C 293	41.2	4.7	544	8	CO881720	CO881720 BovGen.10	366	4.7	271	2	CG146874	CG146874 mab96f09.
C 294	41.2	4.7	566	7	BF410536	BF410536 UI-R-CAO-	367	4.7	314	5	CF754869	CF754869 lae07d02.
C 295	41.2	4.7	594	5	CK935674	CK935674 CGF100455	368	4.7	327	8	CO182751	CO182751 EC23873.5
296	41.2	4.7	599	3	BQ746546	BQ746546 UI-M-PAO-	369	4.7	332	5	CK384472	CK384472 lah25d06.
C 297	41.2	4.7	625	14	CNS036A2	AL229763 Tetraodon	370	4.7	338	8	CO192780	CO192780 EC34473.5
298	41.2	4.7	706	10	DY360654	DY360654 ZO_Ed000	371	4.7	346	5	CF382593	CF382593 lac88g07.
299	41.2	4.7	716	13	CL514121	CL514121 SAIL_883	372	4.7	383	5	CF382551	CF382551 lac88a12.
C 300	41.2	4.7	792	10	DT773642	DT773642 125583905	373	4.7	385	5	CF356034	CF356034 lab77b02.
C 301	41.2	4.7	844	5	CF883043	CF883043 ttrc032x3	374	4.7	395	8	CR544106	CR544106 DKFZP470M
302	41.2	4.7	928	13	CZ510468	CZ510468 GNM2-5812	375	4.7	410	3	BM567429	BM567429 k15a09.y
C 303	41.2	4.7	960	4	BX375427	BX375427 BX375427	C 376	4.7	417	2	BI293909	BI293909 UI-R-DK0-
304	41.2	4.7	987	14	CNS000418	AL066537 Drosophila	C 377	4.7	439	7	AW632847	AW632847 b101a07.x
305	41.2	4.7	1004	10	DV072413	DV072413 VP01_12 O	378	4.7	448	5	CF621874	CF621874 lae68d10.
C 306	41.2	4.7	1334	10	DV786702	DV786702 Hw_liver_	379	4.7	448	5	CF803224	CF803224 r395g04.y
C 307	41.2	4.7	3347	6	AK139104	AK139104 Mus_muscu	380	4.7	449	3	BP483514	BP483514 BP483514
308	41	4.7	158	5	CF353009	CF353009 lab60e05.	C 381	4.7	471	1	AI890026	AI890026 wmg0g06.x
309	41	4.7	273	7	AW164794	AW164794 se77h06.y	C 382	4.7	493	5	CF546442	CF546442 lae73f11.
310	41	4.7	277	1	AU261831	AU261831 AU261831	C 383	4.7	505	7	AW632884	AW632884 b101d08.x
311	41	4.7	300	4	BX476421	BX476421 DKFZP686A	384	4.7	509	8	CO883450	CO883450 BovGen_11

385	40.6	4.7	533	11	AZ052908	RPCI-23-4	458	40	4.6	394	5	CF383901	CF383901 lac11903.
386	40.6	4.7	568	5	CF554171	AGENCOURT	459	40	4.6	414	5	CJ322462	CJ322462 CJ322462
387	40.6	4.7	596	3	BM936065	UI-N-B21-	C 460	40	4.6	416	9	DN872226	DN872226 nad18f09.
388	40.6	4.7	636	12	CC563671	CH240 475	461	40	4.6	421	3	BU774346	BU774346 SJEGKA06
389	40.6	4.7	652	2	BI274223	UI-R-CW0-	462	40	4.6	456	4	CA451405	CA451405 UI-M-FV0-
390	40.6	4.7	662	1	AL889632	AL889632	C 463	40	4.6	456	4	CB461292	CB461292 721246 MA
391	40.6	4.7	776	14	AG607515	Mus muscu	464	40	4.6	472	2	BJ338254	BJ338254 BJ338254
392	40.6	4.7	781	14	CNS009DO	AL053444 Drosophil	C 465	40	4.6	480	1	AA956345	AA956345 UI-R-E1-f
393	40.6	4.7	792	8	CV470318	CV470318 43157.1 C	466	40	4.6	485	1	AU051956	AU051956 AU051956
394	40.6	4.7	851	3	BU954498	AGENCOURT	467	40	4.6	495	1	AM031205	AM031205 AM031205
395	40.6	4.7	869	14	DX075355	KB-B086E2	468	40	4.6	508	8	CN986100	CN986100 61682 125
396	40.6	4.7	872	4	EX752799	EX752799	C 469	40	4.6	512	14	CR801511	CR801511 GROAA20C
397	40.6	4.7	904	10	DT770997	DT770997 125680637	C 470	40	4.6	512	14	CR801511	CR801511 CT12 22 T
398	40.6	4.7	929	4	EX760619	EX760619	C 471	40	4.6	547	9	DN975983	DN975983 CT12 22 T
399	40.6	4.7	954	10	DT804783	DT804783 127377390	472	40	4.6	550	2	BI293646	BI293646 UI-R-DK0-
400	40.6	4.7	1101	14	CNS00HTH	AL074023 Drosophil	473	40	4.6	558	1	AJ931852	AJ931852 AJ931852
401	40.6	4.7	1101	14	CNS01720	AL107514 Drosophil	474	40	4.6	563	8	CX328448	CX328448 JGI XZT67
402	40.6	4.7	1149	10	DV623046	DV623046 92457.1 C	C 475	40	4.6	573	4	CB615111	CB615111 AMGNNUC-U
403	40.6	4.7	1204	14	AG332691	AG332691 Mus muscu	476	40	4.6	591	10	DT835946	DT835946 LB00432.C
404	40.4	4.6	174	5	CF606084	RADIC01_0	477	40	4.6	605	4	CB588300	CB588300 AGENCOURT
405	40.4	4.6	249	9	CF799674	CF799674 JGI CAATJ_1	478	40	4.6	614	5	CK793633	CK793633 AGENCOURT
406	40.4	4.6	372	5	CF583967	CF583967 AGENCOURT	C 479	40	4.6	622	1	AI587114	AI587114 trs3d05.x
407	40.4	4.6	389	2	BG237082	BG237082 saa97a09.	C 480	40	4.6	637	10	DM260609	DM260609 UI-S-GG1-
408	40.4	4.6	415	5	CJ304128	CJ304128	C 481	40	4.6	645	11	AZ421486	AZ421486 IM0199G17
409	40.4	4.6	482	4	EX549422	EX549422 BX549422	C 482	40	4.6	669	9	DN815169	DN815169 ACAC-aac2
410	40.4	4.6	500	5	CK379767	CK379767 lai58c03.	C 483	40	4.6	669	10	DM235562	DM235562 UI-S-GB1-
411	40.4	4.6	578	10	DR404052	DR404052 CSAG-PNP1	484	40	4.6	697	1	AM066156	AM066156 AM066156
412	40.4	4.6	590	9	CX573023	CX573023 TTE000164	485	40	4.6	768	5	CJ439911	CJ439911 CJ439911
413	40.4	4.6	625	11	B29043	B29043 T24J14TF TA	486	40	4.6	802	3	BU556118	BU556118 AGENCOURT
414	40.4	4.6	625	14	CNS036A2	AL229763 Tetraodon	C 487	40	4.6	819	14	AG469163	AG469163 Mus muscu
415	40.4	4.6	753	9	DN838005	DN838005 Smoc-1_02	C 488	40	4.6	879	14	CNS00BVO	AL058074 Drosophil
416	40.4	4.6	838	3	BU587874	BU587874 AGENCOURT	C 489	40	4.6	897	10	DT772513	DT772513 125665216
417	40.4	4.6	851	9	DN582583	DN582583 94374127	490	40	4.6	930	10	DV075519	DV075519 WT1291190
418	40.4	4.6	931	5	CK413737	CK413737 AUF IPG11	C 491	40	4.6	935	10	DV055423	DV055423 DL001_14
419	40.4	4.6	997	9	DN571222	DN571222 901F5088	C 492	40	4.6	951	10	DT782856	DT782856 125636838
420	40.4	4.6	1037	10	DV075133	DV075133 WT1291190	493	40	4.6	958	10	DV069817	DV069817 VP01_02 L
421	40.4	4.6	1152	2	BG309087	BG309087 HVSMEC000	494	40	4.6	959	10	DV069681	DV069681 VP01_02 C
422	40.4	4.6	1184	2	DT088615	DT088615 602853168	495	40	4.6	968	10	DV071065	DV071065 VP01_08 I
423	40.4	4.6	1221	14	CNS0169U	AL106476 Drosophil	496	40	4.6	993	10	DV053532	DV053532 DL001_07
424	40.4	4.6	1615	6	AK043740	AK043740 Mus muscu	497	40	4.6	994	10	DV073491	DV073491 VP01_16 L
425	40.2	4.6	155	5	CF3331482	CF3331482 NACL-07-	498	40	4.6	995	10	DV071636	DV071636 VP01_10 C
426	40.2	4.6	180	5	CK377194	CK377194 lah99e05.	499	40	4.6	1004	10	DV047751	DV047751 DAX20 18
427	40.2	4.6	242	2	BM43460	BM43460 rr38g10.y	500	40	4.6	1022	10	DV051526	DV051526 DAX35-03
428	40.2	4.6	249	4	CB964409	CB964409 Ac2282 Ra	501	40	4.6	1042	10	DV074506	DV074506 VP01_19 J
429	40.2	4.6	275	10	DV769182	DV769182 ILLUMIGEN	502	40	4.6	1042	10	DV074507	DV074507 VP01_19 J
430	40.2	4.6	291	3	BQ785586	BQ785586 saq80c10.	503	40	4.6	1069	10	DV073397	DV073397 VP01_16 G
431	40.2	4.6	340	5	CF529645	CF529645 UI-1-BC1p	C 504	40	4.6	1101	14	CNS0006J	AL062049 Drosophil
432	40.2	4.6	387	1	AI139546	AI139546 MA003804.	505	40	4.6	1101	14	CNS01844	AL108862 Drosophil
433	40.2	4.6	418	1	AI395043	AI395043 MA02273.	506	40	4.6	1102	10	DV074951	DV074951 VP01_20 K
434	40.2	4.6	447	4	CA945634	CA945634 UI-M-FD0-	C 507	40	4.6	1147	9	DR124836	DR124836 49114046-
435	40.2	4.6	488	10	DV865683	DV865683 CRP5415 C	508	40	4.6	1167	10	DV047372	DV047372 DAX20 17
436	40.2	4.6	494	3	BQ521094	BQ521094 NISC n109	C 509	40	4.6	1495	7	BF541123	BF541123 602068734
437	40.2	4.6	569	8	CO100558	CO100558 Rag_Ea25P	510	40	4.6	3138	6	HSM807377	AA162226 mm44g01.r
438	40.2	4.6	589	9	DN877170	DN877170 nae11g06.	511	39.8	4.6	172	1	AA162226	AA162226 mm44g01.r
439	40.2	4.6	615	4	CB194319	CB194319 AGENCOURT	512	39.8	4.6	206	10	DV862573	DV862573 CRP2305 C
440	40.2	4.6	646	10	DT110892	DT110892 JGI ANNO1	513	39.8	4.6	280	8	CN472566	CN472566 USDA-FP 1
441	40.2	4.6	713	1	AJ815888	AJ815888 AJ815888	514	39.8	4.6	305	9	DN798248	DN798248 USDA-FP7A
442	40.2	4.6	849	10	DT771619	DT771619 125662369	515	39.8	4.6	356	5	CK936931	CK936931 CGF100451
443	40.2	4.6	884	10	DT771925	DT771925 1256644003	516	39.8	4.6	396	2	BI941650	BI941650 sc82c02.y
444	40.2	4.6	943	4	CB202689	CB202689 AGENCOURT	517	39.8	4.6	396	3	BM999663	BM999663 UI-H-DIO-
445	40.2	4.6	1024	9	DN575349	DN575349 90166492	C 518	39.8	4.6	399	7	AW015241	AW015241 UI-H-BIOp
446	40.2	4.6	1173	2	BG290683	BG290683 602388977	519	39.8	4.6	407	7	BE787416	BE787416 601479554
447	40.2	4.6	1203	2	BM466037	BM466037 AGENCOURT	C 520	39.8	4.6	487	4	BX555510	BX555510 BX555510
448	40.2	4.6	2362	6	CR859135	CR859135 Pongso PV9	521	39.8	4.6	514	9	CX368966	CX368966 JGI XZT54
449	40.2	4.6	130	1	AU037910	AU037910	522	39.8	4.6	546	9	CK740718	CK740718 JGI XZT54
450	40.2	4.6	152	5	CK428770	CK428770 lai16c03.	523	39.8	4.6	553	3	BM860273	BM860273 fy36c02.y
451	40.2	4.6	162	8	CN796620	CN796620 DK801055	524	39.8	4.6	580	4	CA337315	CA337315 NISC lv11
452	40.2	4.6	169	8	CN797086	CN797086 DK800781	525	39.8	4.6	580	8	CO804381	CO804381 AGENCOURT
453	40.2	4.6	245	9	DN237176	DN237176 EST00301	526	39.8	4.6	620	8	CV920665	CV920665 PH048A C
454	40.2	4.6	251	2	BJ702291	BJ702291	C 527	39.8	4.6	733	4	CB510691	CB510691 sbalrnh50
455	40.2	4.6	298	3	BU587978	BU587978 AGENCOURT	528	39.8	4.6	753	4	CBS599054	CBS599054 AGENCOURT
456	40.2	4.6	375	5	CF425838	CF425838 lad45a03.	529	39.8	4.6	845	5	CK397453	CK397453 AGENCOURT
457	40.2	4.6	377	5	CF804787	CF804787 lad79h06.	530	39.8	4.6	857	8	CN384732	CN384732 LE2TR01L1

C 531	39.8	4.6	954	10	DT802126	DT802126 126488246	C 604	39.6	4.6	1193	2	BG428284	BG428284 602498959
C 532	39.8	4.6	996	10	DT784459	DT784459 127494684	C 605	39.6	4.6	1207	9	DR149283	DR149283 49350707
C 533	39.8	4.6	997	14	CNS005TE	AL060767 Drosophila	C 606	39.6	4.6	2769	6	CR858102	Pongo pyg
C 534	39.8	4.6	1025	10	DT780188	DT780188 125260844	C 607	39.4	4.5	166	2	BI703589	rs73c03.y
C 535	39.6	4.6	185	2	BI943092	BI943092 828912.y	C 608	39.4	4.5	186	9	DN872128	nad18a08.
C 536	39.6	4.6	200	1	AU038268	AU038268 AU038268	C 609	39.4	4.5	209	3	BUS530885	BUS530885 AGENCOURT
C 537	39.6	4.6	210	5	CF123088	CF123088 UT-HF-CHO	C 610	39.4	4.5	212	5	CF613319	CF613319 1a127H09.
C 538	39.6	4.6	220	10	DM445757	DM445757 HHAGE0434	C 611	39.4	4.5	231	7	AW235745	xm45c08.x
C 539	39.6	4.6	241	10	DN076574	DN076574 F21SFmldg	C 612	39.4	4.5	236	8	CV953285	Pvtpvb 98
C 540	39.6	4.6	245	9	DN237176	DN237176 EST00301	C 613	39.4	4.5	296	8	CV953285	Pvtpvb 98
C 541	39.6	4.6	258	7	AW598484	AW598484 E344D05.y	C 614	39.4	4.5	306	2	BI945447	eb86912.y
C 542	39.6	4.6	289	10	DM866666	DM866666 CRP6398	C 615	39.4	4.5	306	2	BUS42579	AGENCOURT
C 543	39.6	4.6	301	3	BM880539	BM880539 r23802.y	C 616	39.4	4.5	308	3	BUS30904	AGENCOURT
C 544	39.6	4.6	302	3	BO453074	BO453074 s095e07.	C 617	39.4	4.5	316	2	BM286318	BM286318 526323 MA
C 545	39.6	4.6	311	1	AI965701	AI965701 sc77c09.y	C 618	39.4	4.5	321	5	CF330989	NACL--06-
C 546	39.6	4.6	313	3	BQ012596	BQ012596 UI-1-BC1p	C 619	39.4	4.5	325	5	CK151023	CsmgEST02
C 547	39.6	4.6	313	4	CA444611	CA444611 UI-H-DTL	C 620	39.4	4.5	390	1	AL120526	DKF2p7610
C 548	39.6	4.6	319	8	CO774070	CO774070 ILLUMIGEN	C 621	39.4	4.5	392	7	AW569872	8182f06.y
C 549	39.6	4.6	324	8	CN478726	CN478726 UT-CF-FNO	C 622	39.4	4.5	416	8	AX190001	70-E01341
C 550	39.6	4.6	332	5	CF314491	CF314491 HD--03-A1	C 623	39.4	4.5	423	2	BJ366859	BJ366859
C 551	39.6	4.6	350	1	AM004320	AM004320 AM004320	C 624	39.4	4.5	446	1	AI253147	q38b08.x
C 552	39.6	4.6	382	5	CK381708	CK381708 lsg9907.	C 625	39.4	4.5	463	8	CK327218	JGI_XZT15
C 553	39.6	4.6	384	5	CK379579	CK379579 lal13e03.	C 626	39.4	4.5	470	7	BF117517	uz38a05.y
C 554	39.6	4.6	389	3	BM731463	BM731463 sal180c07.	C 627	39.4	4.5	481	12	CC766090	CH240_131
C 555	39.6	4.6	392	5	CF331891	CF331891 NACL--08-	C 628	39.4	4.5	482	9	CK367911	UI-M-HK0-
C 556	39.6	4.6	403	9	DN882833	DN882833 rsf10d09.	C 629	39.4	4.5	486	9	CK393284	JGI_XZT40
C 557	39.6	4.6	405	5	CF927527	CF927527 lsf54c10.	C 630	39.4	4.5	487	10	DR391327	USDA-PP_1
C 558	39.6	4.6	435	3	BQ526909	BQ526909 NISC.ro19	C 631	39.4	4.5	488	3	BP381442	BP381442
C 559	39.6	4.6	444	4	CA803547	CA803547 ESG01lc.E	C 632	39.4	4.5	489	7	AM642784	cm22e06.w
C 560	39.6	4.6	459	3	BQ476192	BQ476192 curculio1	C 633	39.4	4.5	491	8	CK041175	1354595.N
C 561	39.6	4.6	462	7	BF398814	BF398814 UI-R-CAL-	C 634	39.4	4.5	495	11	AQ986347	RPCI-23-3
C 562	39.6	4.6	484	7	BX513394	BX513394 BX513394	C 635	39.4	4.5	514	5	CF328406	NACL--03-
C 563	39.6	4.6	484	7	AW558854	AW558854 LQ30H05-	C 636	39.4	4.5	522	9	CK572465	TTE000363
C 564	39.6	4.6	496	8	CO776081	CO776081 JH02005D0	C 637	39.4	4.5	524	5	CF316197	HD--05-G0
C 565	39.6	4.6	499	5	CF529813	CF529813 UI-1-BC1p	C 638	39.4	4.5	527	2	BI082991	602874496
C 566	39.6	4.6	500	9	DN348514	DN348514 LTB3578-0	C 639	39.4	4.5	530	9	DN873278	nad25e07.
C 567	39.6	4.6	532	4	CB619869	CB619869 OSIIIEa04L	C 640	39.4	4.5	555	10	DT458643	GH_ONJ36H1
C 568	39.6	4.6	545	3	BM734127	BM734127 k111804.y	C 641	39.4	4.5	698	4	BT703217	BT703217
C 569	39.6	4.6	568	4	CA416240	CA416240 UI-H-PEO-	C 642	39.4	4.5	726	8	CR421659	CR421659
C 570	39.6	4.6	575	3	BQ775524	BQ775524 UI-H-FHO-	C 643	39.4	4.5	758	8	CR421659	CR421659
C 571	39.6	4.6	589	3	BQ013151	BQ013151 UI-1-BC1p	C 644	39.4	4.5	762	4	BT700523	BT700523
C 572	39.6	4.6	591	4	CA421998	CA421998 UI-H-FGO-	C 645	39.4	4.5	785	14	AG511813	Mus muscu
C 573	39.6	4.6	606	9	CX442823	CX442823 JGI_XZG84	C 646	39.4	4.5	796	14	AG542918	Mus muscu
C 574	39.6	4.6	611	10	DL171893	DL171893 ZM_BFB017	C 647	39.4	4.5	796	14	AG542918	Mus muscu
C 575	39.6	4.6	653	5	CK541111	CK541111 rswh00.00	C 648	39.4	4.5	808	12	CG499135	CG499135
C 576	39.6	4.6	665	4	CB290025	CB290025 UI-M-F10-	C 649	39.4	4.5	819	4	BT710613	BT710613
C 577	39.6	4.6	671	3	BU676109	BU676109 UI-CF-DUI-	C 650	39.4	4.5	833	2	BF791937	BF791937
C 578	39.6	4.6	683	4	CA505570	CA505570 UI-R-FS1-	C 651	39.4	4.5	857	1	AG923328	AG923328
C 579	39.6	4.6	685	3	BM683048	BM683048 UI-E-E01-	C 652	39.4	4.5	862	14	AG463906	AG463906
C 580	39.6	4.6	685	3	BQ683109	BQ683109 UI-CF-EN1	C 653	39.4	4.5	873	14	DU860232	DU860232
C 581	39.6	4.6	686	3	BQ045403	BQ045403 UI-CF-EN1	C 654	39.4	4.5	889	4	BT700931	BT700931
C 582	39.6	4.6	686	3	BQ575797	BQ575797 UI-H-EZ1-	C 655	39.4	4.5	922	14	AG864076	AG864076
C 583	39.6	4.6	708	3	BQ678435	BQ678435 UI-CF-ECO	C 656	39.4	4.5	927	9	DN571108	DN571108
C 584	39.6	4.6	713	8	CO894039	CO894039 BovGen.22	C 657	39.4	4.5	928	10	DT782859	DT782859
C 585	39.6	4.6	720	4	CA418566	CA418566 UI-H-EZ1-	C 658	39.4	4.5	936	10	DV069480	DV069480
C 586	39.6	4.6	720	4	CB305432	CB305432 UI-CF-EN1	C 659	39.4	4.5	951	10	DV041273	DV041273
C 587	39.6	4.6	721	3	BU681018	BU681018 UI-CF-EC1	C 660	39.4	4.5	961	7	BE890494	BE890494
C 588	39.6	4.6	732	4	CA944758	CA944758 UI-CF-FNO	C 661	39.4	4.5	1011	14	CNS005L1	CNS005L1
C 589	39.6	4.6	754	1	AJ410647	AJ410647 AJ410647	C 662	39.4	4.5	1034	14	CNS01611	CNS01611
C 590	39.6	4.6	762	9	DL128525	DL128525 49025125	C 663	39.4	4.5	1035	14	CNS002D5	CNS002D5
C 591	39.6	4.6	768	4	CA417824	CA417824 UI-H-PEO-	C 664	39.4	4.5	1049	2	BG393206	BG393206
C 592	39.6	4.6	789	9	DL125270	DL125270 49113031	C 665	39.4	4.5	1100	14	CNS00G3S	CNS00G3S
C 593	39.6	4.6	790	9	DL126699	DL126699 49306621	C 666	39.2	4.5	1101	14	CNS00FXE	CNS00FXE
C 594	39.6	4.6	886	4	BX748883	BX748883 brain.EST	C 667	39.2	4.5	215	8	CK058264	CK058264
C 595	39.6	4.6	888	8	CO763934	CO763934 StrPN691.	C 668	39.2	4.5	216	7	BF613033	BF613033
C 596	39.6	4.6	898	5	CD305481	CD305481 StrPN691.	C 669	39.2	4.5	222	2	BG945637	BG945637
C 597	39.6	4.6	905	14	AG396436	AG396436 Mus muscu	C 670	39.2	4.5	233	2	BI843156	BI843156
C 598	39.6	4.6	928	10	DT785774	DT785774 126368860	C 671	39.2	4.5	241	1	AI340570	AI340570
C 599	39.6	4.6	959	10	DV050388	DV050388 DAY35S.09	C 672	39.2	4.5	242	1	AL036146	AL036146
C 600	39.6	4.6	962	10	DT793540	DT793540 126552469	C 673	39.2	4.5	256	1	AI570164	AI570164
C 601	39.6	4.6	969	4	CA971584	CA971584 AGENCOURT	C 674	39.2	4.5	258	7	AW268744	AW268744
C 602	39.6	4.6	1073	3	BQ930284	BQ930284 AGENCOURT	C 675	39.2	4.5	266	9	DN274839	DN274839
C 603	39.6	4.6	1156	13	CL640910	CL640910 CH213-131	C 676	39.2	4.5	308	1	AL037521	AL037521

C 604	39.6	4.6	1193	2	BG428284	BG428284 602498959
C 605	39.6	4.6	1207	9	DR149283	DR149283 49350707
C 606	39.6	4.6	2769	6	CR858102	Pongo pyg
C 607	39.4	4.5	166	2	BI703589	rs73c03.y
C 608	39.4	4.5	186	9	DN872128	nad18a08.
C 609	39.4	4.5	209	3	BUS530885	BUS530885 AGENCOURT
C 610	39.4	4.5	212	5	CF613319	CF613319 1a127H09.
C 611	39.4	4.5	231	7	AW235745	xm45c08.x
C 612	39.4	4.5	236	8	CV953285	Pvtpvb 98
C 613	39.4	4.5	296	8	CV953285	Pvtpvb 98
C 614	39.4	4.5	306	2	BI945447	eb86912.y
C 615	39.4	4.5	306	2	BUS42579	AGENCOURT
C 616	39.4	4.5	308	3	BUS30904	AGENCOURT
C 617	39.4	4.5	316	2	BM286318	BM286318 526323 MA
C 618	39.4	4.5	321	5	CF330989	NACL--06-
C 619	39.4	4.5	325	5	CK151023	CsmgEST02
C 620	39.4	4.5	390	1	AL120526	DKF2p7610
C 621	39.4	4.5	392	7	AW569872	8182f06.y
C 622	39.4	4.5	416	8	AX190001	70-E01341
C 623	39.4	4.5	423	2	BJ366859	BJ366859
C 624	39.4	4.5	446	1	AI253147	q38b08.x
C 625	39.4	4.5	463	8	CK327218	JGI_XZT15
C 626	39.4	4.5	470	7	BF117517	uz38a05.y
C 627	39.4	4.5	481	12	CC766090	CH240_131
C 628	39.4	4.5	482	9	CK367911	UI-M-HK0-
C 629	39.4	4.5	486	9	CK393284	JGI_XZT40
C 630	39.4	4.5	487	10	DR391327	USDA-PP_1
C 631	39.4	4.5	488	3	BP381442	BP381442
C 632	39.4	4.5	489	7	AM642784	cm22e06.w
C 633	39.4	4.5	491	8	CK041175	1354595.N
C						

C 677	39.2	4.5	311	4	CB264177	750	39	4.5	340	5	CF621600	CF621600 lae62b07.
C 678	39.2	4.5	341	2	BG290300	C 751	39	4.5	371	7	AW189482	AW189482 xl07c04.x
C 679	39.2	4.5	348	9	DN896823	C 752	39	4.5	372	7	BE097001	UI-R-B50-
C 680	39.2	4.5	375	5	CF803697	C 753	39	4.5	377	5	CF326815	NACL-01-
C 681	39.2	4.5	378	2	BW319775	C 754	39	4.5	398	1	AA999157	UI-R-C0-h
C 682	39.2	4.5	398	1	AJ499453	C 755	39	4.5	411	9	DN885393	naf29c12.
C 683	39.2	4.5	416	9	CV600093	C 756	39	4.5	428	5	CF545395	lae78g01.
C 684	39.2	4.5	419	4	CB345973	C 757	39	4.5	445	7	BE105623	UI-R-BX0-
C 685	39.2	4.5	442	7	AM597567	C 758	39	4.5	453	1	AI096778	qb56e07.x
C 686	39.2	4.5	443	5	KA18085	C 759	39	4.5	457	7	AW529488	UI-R-BT1-
C 687	39.2	4.5	453	8	CK062681	C 760	39	4.5	474	8	AX294096	C05011A09
C 688	39.2	4.5	455	12	BI359777	C 761	39	4.5	489	1	AL892912	BI523035 603175533
C 689	39.2	4.5	462	2	CF190319	C 762	39	4.5	498	2	AL892912	AL892912
C 690	39.2	4.5	496	3	BQ770924	C 763	39	4.5	499	4	EX779765	EX779765
C 691	39.2	4.5	518	1	AM016574	C 764	39	4.5	503	5	CK377125	BE111550
C 692	39.2	4.5	532	10	DF833093	C 765	39	4.5	511	7	BE111550	UI-R-BJ1-
C 693	39.2	4.5	533	8	CF321773	C 766	39	4.5	512	9	DN366000	DN366000
C 694	39.2	4.5	539	5	CF308013	C 767	39	4.5	514	3	BQ389814	NISC mq09
C 695	39.2	4.5	544	3	BQ398892	C 768	39	4.5	530	9	CF370039	CF370039 JGI_XZT55
C 696	39.2	4.5	545	8	CO753692	C 769	39	4.5	536	5	CK815132	RA89gc614
C 697	39.2	4.5	548	4	CB964126	C 770	39	4.5	539	4	CA318931	UI-M-FV0-
C 698	39.2	4.5	549	7	BE648293	C 771	39	4.5	548	9	DN366887	DN366887
C 699	39.2	4.5	549	8	CN727743	C 772	39	4.5	557	9	DN365974	LI83629-0
C 700	39.2	4.5	565	2	BJ929052	C 773	39	4.5	571	7	BE105735	UI-R-B01-
C 701	39.2	4.5	568	10	DF833077	C 774	39	4.5	576	9	CF375149	JGI_XZT58
C 702	39.2	4.5	586	10	DF651269	C 775	39	4.5	579	12	CC961073	CC961073
C 703	39.2	4.5	592	10	DS539846	C 776	39	4.5	596	10	DR976032	SKin-13-H
C 704	39.2	4.5	592	10	DM287773	C 777	39	4.5	647	7	BF399390	UI-R-CAI-
C 705	39.2	4.5	594	4	CB288148	C 778	39	4.5	649	1	AL881138	AL881138
C 706	39.2	4.5	603	3	BUI39582	C 779	39	4.5	659	8	CO117171	GR_Eb019
C 707	39.2	4.5	627	10	DF833785	C 780	39	4.5	677	4	EX726217	EX726217
C 708	39.2	4.5	650	14	CR836996	C 781	39	4.5	684	11	BZ061492	BZ061492
C 709	39.2	4.5	659	8	CV905600	C 782	39	4.5	687	8	CO042482	UI-M-FC0-
C 710	39.2	4.5	679	1	DR039981	C 783	39	4.5	692	2	BI289100	UI-R-DK0-
C 711	39.2	4.5	680	9	AL884087	C 784	39	4.5	699	4	EX750709	EX750709
C 712	39.2	4.5	680	3	BW724975	C 785	39	4.5	716	1	AV702427	AV702427
C 713	39.2	4.5	685	13	CF633535	C 786	39	4.5	737	14	AG242050	Mus muscu
C 714	39.2	4.5	688	4	CA419138	C 787	39	4.5	739	10	DR476428	DR476428
C 715	39.2	4.5	688	10	DR712787	C 788	39	4.5	749	8	CV469923	42688-1 C
C 716	39.2	4.5	707	8	CV472320	C 789	39	4.5	749	9	CV454181	JGI_XZG55
C 717	39.2	4.5	720	10	DR821106	C 790	39	4.5	772	14	CNS02HPA	Al197911 Tetradon
C 718	39.2	4.5	755	8	DR797445	C 791	39	4.5	797	3	BQ145169	AL145169 NF011B05G
C 719	39.2	4.5	776	3	BW743213	C 792	39	4.5	798	13	DU100472	JBNy021M1
C 720	39.2	4.5	780	7	AV733831	C 793	39	4.5	804	8	CO875720	BovGen.04
C 721	39.2	4.5	805	14	CNS009F8	C 794	39	4.5	813	3	BQ145175	NF011B0GG
C 722	39.2	4.5	816	3	BQ781132	C 795	39	4.5	852	11	BZ0766	BZ0766
C 723	39.2	4.5	880	5	CK156543	C 796	39	4.5	878	10	DT783805	DT783805
C 724	39.2	4.5	894	12	CG766346	C 797	39	4.5	885	10	DT783988	DT783988
C 725	39.2	4.5	921	10	DT068969	C 798	39	4.5	888	4	EX776606	EX776606
C 726	39.2	4.5	924	11	BH155735	C 799	39	4.5	890	4	EX752792	EX752792
C 727	39.2	4.5	953	9	DN573040	C 800	39	4.5	899	8	CR440269	CR440269
C 728	39.2	4.5	957	9	DN562197	C 801	39	4.5	899	10	DT801057	DT801057
C 729	39.2	4.5	972	2	BM464785	C 802	39	4.5	902	9	DN576815	DN576815
C 730	39.2	4.5	994	9	DN565593	C 803	39	4.5	904	12	CL059947	CL059947
C 731	39.2	4.5	1101	14	CNS0039G	C 804	39	4.5	936	10	DT779129	DT779129
C 732	39.2	4.5	1173	6	AF119859	C 805	39	4.5	938	9	DN575944	DN575944
C 733	39.2	4.5	1173	6	AF119859	C 806	39	4.5	948	9	DN574906	DN574906
C 734	39.2	4.5	127	6	CR861248	C 807	39	4.5	948	10	DV049457	DV049457
C 735	39.2	4.5	137	10	DN523132	C 808	39	4.5	959	10	DT773220	DT773220
C 736	39.2	4.5	151	9	DN154017	C 809	39	4.5	966	10	DV074671	DV074671
C 737	39.2	4.5	164	1	AT810589	C 810	39	4.5	978	10	DV054796	DV054796
C 738	39.2	4.5	170	5	CK617891	C 811	39	4.5	984	9	DN566597	DN566597
C 739	39.2	4.5	234	1	AJ766788	C 812	39	4.5	997	10	DV074672	DV074672
C 740	39.2	4.5	242	2	BI502406	C 813	39	4.5	1001	10	DV055332	DV055332
C 741	39.2	4.5	257	7	AW656503	C 814	39	4.5	1011	10	DN047455	DN047455
C 742	39.2	4.5	283	10	CR389239	C 815	39	4.5	1085	14	CNS0124K	AL101102 Drosophi1
C 743	39.2	4.5	298	5	CK395426	C 816	39	4.5	1094	10	DV054798	DV054798
C 744	39.2	4.5	312	1	AA909381	C 817	39	4.5	1101	14	CNS00781	AL067048 Drosophi1
C 745	39.2	4.5	314	2	BI846999	C 818	39	4.5	1275	14	AG333055	AG333055
C 746	39.2	4.5	319	10	DR558190	C 819	39	4.5	1275	14	AG333055	Mus muscu
C 747	39.2	4.5	321	5	CF228076	C 820	39	4.5	1275	14	AG333055	CR858060
C 748	39.2	4.5	324	5	CF423986	C 821	39	4.5	1275	14	AG333055	CR858060
C 749	39.2	4.5	329	5	CK404969	C 822	39	4.5	1275	14	AG333055	CR858060
C 750	39.2	4.5	329	5	CK404969	C 823	39	4.5	1275	14	AG333055	CR858060
C 751	39.2	4.5	329	5	CK404969	C 824	39	4.5	1275	14	AG333055	CR858060
C 752	39.2	4.5	329	5	CK404969	C 825	39	4.5	1275	14	AG333055	CR858060
C 753	39.2	4.5	329	5	CK404969	C 826	39	4.5	1275	14	AG333055	CR858060
C 754	39.2	4.5	329	5	CK404969	C 827	39	4.5	1275	14	AG333055	CR858060
C 755	39.2	4.5	329	5	CK404969	C 828	39	4.5	1275	14	AG333055	CR858060
C 756	39.2	4.5	329	5	CK404969	C 829	39	4.5	1275	14	AG333055	CR858060
C 757	39.2	4.5	329	5	CK404969	C 830	39	4.5	1275	14	AG333055	CR858060
C 758	39.2	4.5	329	5	CK404969	C 831	39	4.5	1275	14	AG333055	CR858060
C 759	39.2	4.5	329	5	CK404969	C 832	39	4.5	1275	14	AG333055	CR858060
C 760	39.2	4.5	329	5	CK404969	C 833	39	4.5	1275	14	AG333055	CR858060
C 761	39.2	4.5	329	5	CK404969	C 834	39	4.5	1275	14	AG333055	CR858060
C 762	39.2	4.5	329	5	CK404969	C 835	39	4.5	1275	14	AG333055	CR858060
C 763	39.2	4.5	329	5	CK404969	C 836	39	4.5	1275	14	AG333055	CR858060
C 764	39.2	4.5	329	5	CK404969	C 837	39	4.5	1275	14	AG333055	CR858060
C 765	39.2	4.5	329	5	CK404969	C 838	39	4.5	1275	14	AG333055	CR858060
C 766	39.2	4.5	329	5	CK404969	C 839	39	4.5	1275	14	AG333055	CR858060
C 767	39.2	4.5	329	5	CK404969	C 840	39	4.5	1275	14	AG333055	CR858060
C 768	39.2	4.5	329	5	CK404969	C 841	39	4.5	1275	14	AG333055	CR858060
C 769	39.2	4.5	329	5	CK404969	C 842	39	4.5	1275	14	AG333055	CR858060
C 770	39.2	4.5	329	5	CK404969	C 843	39	4.5	1275	14	AG333055	CR858060
C 771	39.2	4.5	329	5	CK404969	C 844	39	4.5	1275	14	AG333055	CR858060
C 772	39.2	4.5	329	5	CK404969	C 845	39	4.5	1275	14	AG333055	CR858060
C 773	39.2	4.5	329	5	CK404969	C 846	39	4.5	1275	14	AG333055	CR858060
C 774	39.2	4.5	329	5	CK404969	C 847	39	4.5	1275	14	AG333055	CR858060
C 775	39.2	4.5	329	5	CK404969	C 848	39	4.5	1275	14	AG333055	CR858060
C 776	39.2	4.5	329	5	CK404969	C 849	39	4.5	1275	14	AG333055	CR858060
C 777	39.2	4.5	329	5	CK404969	C 850	39	4.5	1275	14	AG333055	CR858060
C 778	39.2	4.5	329	5	CK404969	C 851	39	4.5	1275	14	AG333055	CR858060
C 779	39.2	4.5	329	5	CK404969	C 852	39	4.5				

823	38.8	4.5	293	2	BI502720	BI502720 BB170002A	C 896	38.6	4.4	477	3	BP120207	BP120207 BP120207
824	38.8	4.5	328	5	CD512549	CD512549 AGENCOURT	C 897	38.6	4.4	501	9	CX437427	CX437427 JGI XZGS59
C 825	38.8	4.5	348	12	CE477600	CE477600 tigr-gss-	C 898	38.6	4.4	507	7	AW135217	AW135217 UI-H-B11-
C 826	38.8	4.5	373	1	AI253178	AI253178 q238h10.x	C 899	38.6	4.4	507	9	CX338017	CX338017 JGI XZT59
C 827	38.8	4.5	377	1	AJ846519	AJ846519 AJ846519	C 900	38.6	4.4	510	9	CX805458	CX805458 JGI_CNAJ1
C 828	38.8	4.5	400	5	CJ127494	CJ127494 CJ127494	C 901	38.6	4.4	519	14	DR064043	DR064043 Oryzias1
C 829	38.8	4.5	413	8	CX330080	CX330080 JGI_XZT68	C 902	38.6	4.4	530	5	CK034703	CK034703 3585Sraic
C 830	38.8	4.5	432	4	CB559646	CB559646 AGENCOURT	C 903	38.6	4.4	543	5	CK414853	CK414853 AUP_Ippit
C 831	38.8	4.5	434	4	CB793407	CB793407 AGNUNC1U	C 904	38.6	4.4	561	8	KN051395	KN051395 v8_P2_f13
C 832	38.8	4.5	451	5	CK454293	CK454293 911581 WA	C 905	38.6	4.4	581	3	BP375614	BP375614 BP375614
C 833	38.8	4.5	453	4	CB046243	CB046243 NISC_gf03	C 906	38.6	4.4	585	3	BQ393240	BQ393240 NISC_rg02
C 834	38.8	4.5	516	2	BI183348	BI183348 UNL-P-FN-	C 907	38.6	4.4	601	3	BQ396673	BQ396673 NISC_rg22
C 835	38.8	4.5	521	4	CB257020	CB257020 51-B01084	C 908	38.6	4.4	606	4	CA325540	CA325540 UI-M-P20-
836	38.8	4.5	524	3	BU056256	BU056256 UI-M-P20-	C 909	38.6	4.4	620	7	BE965577	BE965577 601659613
837	38.8	4.5	531	7	AW632760	AW632760 92879 MAR	C 910	38.6	4.4	628	4	BE731709	BE731709 BX731709
838	38.8	4.5	542	5	CK429916	CK429916 OJ42912.y	C 911	38.6	4.4	629	9	CX872782	CX872782 HSC4_73
839	38.8	4.5	558	8	CV659314	CV659314 tak3905.	C 912	38.6	4.4	647	2	BI382924	BI382924 BFLG3_001
840	38.8	4.5	559	3	BU171114	BU171114 AGENCOURT	C 913	38.6	4.4	663	3	BQ523745	BQ523745 NISC_n123
841	38.8	4.5	594	5	CK935661	CK935661 CGF100455	C 914	38.6	4.4	676	11	AZ642505	AZ642505 IM0505L05
C 842	38.8	4.5	595	4	CAB04091	CAB04091 EGG0112a.	C 915	38.6	4.4	681	10	DM254197	DM254197 UI-S-GB1-
843	38.8	4.5	618	14	CNS008B0	AL055149 Drosophill	C 916	38.6	4.4	682	8	CN159561	CN159561 948647 MA
C 844	38.8	4.5	630	8	CO043563	CO043563 UI-M-H00-	C 917	38.6	4.4	687	9	DN118164	DN118164 1117892 M
845	38.8	4.5	632	9	CX413255	CX413255 JGI_XZT29	C 918	38.6	4.4	706	8	CN097844	CN097844 EC2CAAL3C
C 846	38.8	4.5	644	10	DM271858	DM271858 UI-S-GS1-	C 919	38.6	4.4	723	13	DU459833	DU459833 109842106
C 847	38.8	4.5	657	8	CNA60959	CNA60959 UI-M-HB0-	C 920	38.6	4.4	733	10	DT482392	DT482392 WS02519.B
848	38.8	4.5	672	9	CX763526	CX763526 AGENCOURT	C 921	38.6	4.4	745	14	CT418301	CT418301 Sub scrof
C 849	38.8	4.5	699	9	DN888084	DN888084 rag11b06.	C 922	38.6	4.4	777	14	AG600118	AG600118 Mus muscu
C 850	38.8	4.5	702	8	CV200323	CV200323 km02c10.y	C 923	38.6	4.4	827	14	CNS02NEE	AL203999 Tetraodon
851	38.8	4.5	719	14	CT120890	CT120890 Sub scrof	C 924	38.6	4.4	835	1	AJ818009	AJ818009 AJ818009
C 852	38.8	4.5	752	4	EX834633	EX834633 BX834633	C 925	38.6	4.4	866	14	CT222143	CT222143 Sub scrof
C 853	38.8	4.5	766	1	AJ949219	AJ949219 AJ949219	C 926	38.6	4.4	891	1	AM098436	AM098436 AM098436
854	38.8	4.5	770	7	AV757293	AV757293 AV757293	C 927	38.6	4.4	904	13	DU082930	DU082930 271723 To
C 855	38.8	4.5	772	14	CNS03NNT	AL252506 Tetraodon	C 928	38.6	4.4	910	10	DT772698	DT772698 125668677
C 856	38.8	4.5	790	13	CD305220	CD305220 ZMRAF0084	C 929	38.6	4.4	942	10	DT778615	DT778615 125668677
C 857	38.8	4.5	795	10	DM280534	DM280534 UI-S-GU0-	C 930	38.6	4.4	961	10	DM074647	DM074647 VP01_19_N
C 858	38.8	4.5	802	12	CC548502	CC548502 CH240_432	C 931	38.6	4.4	1077	2	BM473293	BM473293 AGENCOURT
C 859	38.8	4.5	817	4	EX747554	EX747554 BX747554	C 932	38.6	4.4	1101	14	CNS00528	AL061987 Drosophill
C 860	38.8	4.5	823	4	CB315012	CB315012 AGENCOURT	C 933	38.6	4.4	1101	14	CNS010CR	AL098805 Drosophill
861	38.8	4.5	857	5	CD171720	CD171720 AGENCOURT	C 934	38.6	4.4	1201	14	CNS0152Z	AL106121 Drosophill
C 862	38.8	4.5	867	12	CG302596	CG302596 CG0F168TH	C 935	38.6	4.4	1332	7	BE875442	BE875442 601489164
C 863	38.8	4.5	896	9	CO882398	CO882398 BovGen10	C 936	38.6	4.4	1338	14	AG396401	AG396401 Mus muscu
C 864	38.8	4.5	905	8	DN568518	DN568518 93882112	C 937	38.6	4.4	1403	10	DM775099	DM775099 Hw_FAT_29
865	38.8	4.5	933	12	CG302606	CG302606 CG0F168TV	C 938	38.6	4.4	2409	6	CR858670	CR858670 Hongo pyg
C 866	38.8	4.5	953	3	BU159214	BU159214 AGENCOURT	C 939	38.6	4.4	5664	6	BC036757	BC036757 Homo sapi
C 867	38.8	4.5	965	3	BQ276670	BQ276670 AGENCOURT	C 940	38.4	4.4	106	8	CN797438	CN797438 DX8P02128
868	38.8	4.5	1007	12	CL139171	CL139171 ISB1-112A	C 941	38.4	4.4	107	8	CN797432	CN797432 DX8P02120
C 869	38.8	4.5	1015	2	BI490178	BI490178 603031949	C 942	38.4	4.4	117	8	CN800596	CN800596 DX8P02767
C 870	38.8	4.5	1021	14	CNS0165E1	AL106644 Drosophill	C 943	38.4	4.4	119	8	CN797074	CN797074 DX8P00768
C 871	38.8	4.5	1101	14	CNS0100X	AL098379 Drosophill	C 944	38.4	4.4	125	8	CN799579	CN799579 DX8P01186
C 872	38.8	4.5	1267	8	CV861738	CV861738 gonad_EST	C 945	38.4	4.4	127	8	CN800517	CN800517 DX8P02647
C 873	38.8	4.5	1406	10	DM779642	DM779642 Hw_Fat_37	C 946	38.4	4.4	130	8	CN796573	CN796573 DX8P00941
874	38.8	4.5	1556	6	BC029685	BC029685 Homo sapi	C 947	38.4	4.4	131	8	CN796329	CN796329 DX8P01385
C 875	38.8	4.5	1591	9	DN688368	DN688368 CXK58-E02	C 948	38.4	4.4	132	1	AI251272	AI251272 QV36H09.x
876	38.8	4.5	1836	6	HSN802705	AL1359596 Homo sapi	C 949	38.4	4.4	132	8	CN797071	CN797071 DX8P00765
877	38.6	4.4	112	2	BJ387232	BJ387232 BJ387232	C 950	38.4	4.4	132	8	CN797135	CN797135 DX8P00846
C 878	38.6	4.4	152	4	C94134	C94134 C94134 Dict	C 951	38.4	4.4	135	8	CN800043	CN800043 DX8P02131
C 879	38.6	4.4	227	4	CB066266	CB066266 PVBE12A02	C 952	38.4	4.4	136	8	CN796446	CN796446 DX8P01011
880	38.6	4.4	299	3	BP704131	BP704131 BP704131	C 953	38.4	4.4	138	8	CN796743	CN796743 DX8P00735
881	38.6	4.4	301	5	CF384267	CF384267 lac04h02.	C 954	38.4	4.4	140	8	CN797047	CN797047 DX8P00735
882	38.6	4.4	330	3	BU760820	BU760820 eae59a04.	C 955	38.4	4.4	141	8	CN796590	CN796590 DX8P01246
883	38.6	4.4	332	1	AL036923	AL036923 DKFP2564B	C 956	38.4	4.4	141	8	CN797055	CN797055 DX8P00747
884	38.6	4.4	334	2	CO184654	CO184654 EC28424.5	C 957	38.4	4.4	143	8	CN797147	CN797147 DX8P00858
885	38.6	4.4	338	2	BM184670	BM184670 fv70h10.y	C 958	38.4	4.4	149	8	CN796719	CN796719 DX8P01278
886	38.6	4.4	343	10	DR874327	DR874327 JGI_CABH9	C 959	38.4	4.4	150	8	CN797091	CN797091 DX8P00787
887	38.6	4.4	347	8	CO895657	CO895657 BovGen_23	C 960	38.4	4.4	152	8	CN797334	CN797334 DX8P01883
888	38.6	4.4	350	4	CAS28397	CAS28397 8072-62 M	C 961	38.4	4.4	152	8	CN801150	CN801150 DX8P00358
889	38.6	4.4	353	9	CX363136	CX363136 JGI_XZT42	C 962	38.4	4.4	155	1	AI252692	AI252692 QV25F02.x
890	38.6	4.4	370	7	AW156431	AW156431 e225b02.y	C 963	38.4	4.4	162	1	AA690006	AA690006 QV25F02.x
C 891	38.6	4.4	383	14	AG372801	AG372801 Mus muscu	C 964	38.4	4.4	165	8	CN797273	CN797273 DX8P01815
892	38.6	4.4	395	8	CN231303	CN231303 WLB061E04	C 965	38.4	4.4	184	2	BM265850	BM265850 FW36F05.y
893	38.6	4.4	435	9	CX478564	CX478564 JGI_XZGS1	C 966	38.4	4.4	184	5	CD465197	CD465197 LeukONI_2
894	38.6	4.4	435	10	DR892593	DR892593 JGI_XZT24	C 967	38.4	4.4	202	8	CN799266	CN799266 DX8P00941
C 895	38.6	4.4	448	10	W94595	W94595 ze03b09.bl	C 968	38.4	4.4	212	7	BE755294	BE755294 209091 MA

C 969	38.4	4.4	222	9	DN919564	MCFTRNAL2	1042	38.4	4.4	617	9	CX395364	CX395364 JGI_XZT27
970	38.4	4.4	235	7	BE058624	anl8e10.y	1043	38.4	4.4	621	8	CX318264	CX318264 JGI_XZT59
C 971	38.4	4.4	248	5	FP044537	QCJ30C09.	C1044	38.4	4.4	626	10	DM280243	DM280243 UI-S-GU0-
972	38.4	4.4	255	3	BQ090910	Ku21h10.y	C1045	38.4	4.4	637	13	CZ098494	CZ098494 OM_Ba010
973	38.4	4.4	267	4	CA802854	sa437b09.	1046	38.4	4.4	639	9	CX394824	CX394824 JGI_XZT27
974	38.4	4.4	271	1	AL837252	AL837252	C1047	38.4	4.4	640	12	CE417423	CE417423 tigr-g88-
975	38.4	4.4	273	2	BG359352	sac23a11.	C1048	38.4	4.4	642	10	DM255031	DM255031 UI-S-GB1-
C 976	38.4	4.4	279	7	AW533068	UI-R-BU0-	C1049	38.4	4.4	644	13	CZ056024	CZ056024 OM_Ba004
977	38.4	4.4	280	5	CK378353	lah95c02.	C1050	38.4	4.4	653	1	A1559640	A1559640 tq58f07.x
978	38.4	4.4	281	7	BF452999	maag4b11.	C1051	38.4	4.4	655	9	DN867232	DN867232 crac26e06.
979	38.4	4.4	284	1	AL837227	AL837227	C1052	38.4	4.4	662	8	CR443717	CR443717 CR443717
980	38.4	4.4	299	2	BI501913	rm06g03.y	1053	38.4	4.4	685	10	DT842869	DT842869 LB00466.C
981	38.4	4.4	299	4	CB701265	AMGNNUC.M	C1054	38.4	4.4	693	3	BM974205	BM974205 UI-CF-EC1
982	38.4	4.4	308	9	DN878787	nae229C10.	1055	38.4	4.4	696	8	CN155261	CN155261 942544 MA
983	38.4	4.4	314	4	CA793832	AGENCOURT	C1056	38.4	4.4	703	10	DM272325	DM272325 UI-S-GS1-
984	38.4	4.4	318	3	BU716755	SJM2AWG09	C1057	38.4	4.4	708	5	CD741850	CD741850 UI-M-A00-
C 985	38.4	4.4	324	1	AI842671	UI-M-A01-	1058	38.4	4.4	709	9	DN237210	DN237210 EST00335
986	38.4	4.4	329	3	BM774043	ra8g10.y	C1059	38.4	4.4	710	10	DM278574	DM278574 UI-S-RH0-
987	38.4	4.4	330	8	CO891122	BovGen_19	C1060	38.4	4.4	714	10	DM257784	DM257784 UI-S-GG0-
C 988	38.4	4.4	341	2	BG869806	602789319	C1061	38.4	4.4	715	13	CZ598794	CZ598794 OM_Ba005
989	38.4	4.4	342	1	AA271298	vb73a07.r	C1062	38.4	4.4	752	12	CC311266	CC311266 TAN32-21P
990	38.4	4.4	347	5	CF968439	lag14h11.	1063	38.4	4.4	777	14	CNS025WB	ALU84612 Tetraodon
C 991	38.4	4.4	349	9	CX456503	JGI_XZG53	1064	38.4	4.4	791	3	BU554551	BU554551 AGENCOURT
C 992	38.4	4.4	352	10	DM279413	UI-S-GU0-	1065	38.4	4.4	802	3	BU851163	BU851163 AGENCOURT
993	38.4	4.4	356	7	AW739766	BR100279	1066	38.4	4.4	805	5	CF288806	CF288806 AGENCOURT
994	38.4	4.4	360	2	BJ680998	BJ680998	1067	38.4	4.4	812	7	BF168820	BF168820 601775145
995	38.4	4.4	363	2	BI383870	BFLG2_002	C1068	38.4	4.4	825	4	DX722920	DX722920 BX722920
996	38.4	4.4	364	5	CD812384	BN10_020P	C1069	38.4	4.4	845	10	AV038977	AV038977 BalbC1191
C 997	38.4	4.4	365	11	AQ043325	CIT-HGP-2	1070	38.4	4.4	845	10	DG869523	DG869523 Oryza sat
998	38.4	4.4	369	5	CD811371	AI975082	1071	38.4	4.4	882	10	DT776163	DT776163 124584470
C 999	38.4	4.4	379	1	AI975082	AI975082	1072	38.4	4.4	884	8	CV069454	CV069454 WPAEhux15
C1000	38.4	4.4	389	7	AW090103	xc91b07.x	C1073	38.4	4.4	890	11	BH159661	BH159661 ENT2D45TF
1001	38.4	4.4	390	5	CK594109	CK594109	1074	38.4	4.4	893	10	DT771306	DT771306 125590156
1002	38.4	4.4	402	4	CB768951	AMGNNUC.N	C1075	38.4	4.4	900	3	BU956349	BU956349 AGENCOURT
1003	38.4	4.4	417	8	CN797495	DK8P02236	C1076	38.4	4.4	903	10	DV051009	DV051009 DAY35_02
1004	38.4	4.4	418	5	CD315172	StrPu621.	1077	38.4	4.4	909	2	BM415521	BM415521 Op20597 M-
C1005	38.4	4.4	421	5	CK422600	AUF_Ipspn	C1078	38.4	4.4	914	9	DN575199	DN575199 90166530
C1006	38.4	4.4	423	2	BF940879	hu60f02.x	C1079	38.4	4.4	914	10	DV072003	DV072003 VP01.11.G
1007	38.4	4.4	425	5	CF804574	lad75f06.	1080	38.4	4.4	929	4	DX461864	DX461864 BX461864
1008	38.4	4.4	426	3	BQ107045	NXLV086.A	1081	38.4	4.4	944	9	DN584995	DN584995 93006597
1009	38.4	4.4	430	9	CX842735	JGI_CAAK1	C1082	38.4	4.4	957	9	DN570114	DN570114 91545629
C1010	38.4	4.4	447	4	BX716746	BX716746	C1083	38.4	4.4	970	10	DV070757	DV070757 VP01_07.P
1011	38.4	4.4	449	9	CX362375	JGI_XZT42	1084	38.4	4.4	975	4	CA460956	CA460956 AGENCOURT
C1012	38.4	4.4	455	9	DN480155	np13_a206	1085	38.4	4.4	981	10	DV056387	DV056387 DL01_18_
1013	38.4	4.4	461	5	CD812243	CD812243	1086	38.4	4.4	982	10	DV056386	DV056386 DL01_18_
1014	38.4	4.4	461	5	CD814226	BN15_022G	1087	38.4	4.4	996	10	DT776671	DT776671 125644169
1015	38.4	4.4	461	5	CD816351	BN15_029F	1088	38.4	4.4	1042	5	CD512912	CD512912 AGENCOURT
1016	38.4	4.4	462	5	CD811870	BN10_019D	1089	38.4	4.4	1093	6	CR859867	CR859867 Pongo pyg
C1017	38.4	4.4	463	5	CD816145	BN15_028L	1090	38.4	4.4	1101	14	CNS00FR3	ALU071143 Drosoephil
1018	38.4	4.4	464	8	CX217408	MNS31478	C1091	38.4	4.4	1101	14	CNS016L1	ALU08896 Drosoephil
C1019	38.4	4.4	465	5	CD812111	BN10_020B	C1092	38.4	4.4	1101	14	CNS017Y1	ALU08676 Drosoephil
1020	38.4	4.4	467	5	CD811978	BN10_019J	C1093	38.4	4.4	1200	1	AJ928743	AJ928743 AJ928743
1021	38.4	4.4	469	10	DR403848	DR403848 CSAH-PNP1	C1094	38.4	4.4	1238	14	AG390565	AG390565 Mus muscu
C1022	38.4	4.4	478	2	BI289170	BI289170 UI-R-DK0-	C1095	38.4	4.4	2247	6	BC089895	BC089895 Rattus no
C1023	38.4	4.4	502	7	AW019444	AW019444 fel1f09.x	1096	38.4	4.4	3900	6	CR860111	CR860111 Pongo pyg
1024	38.4	4.4	504	4	CA369462	CA369462 645920 NC	1097	38.4	4.4	118	8	DT776677	DT776677 Pmpcm_107
1025	38.4	4.4	505	12	CF358394	CF358394 tigr-g88-	1098	38.2	4.4	169	8	CV933359	CV933359 Pmpcm_107
C1026	38.4	4.4	507	5	DF322068	DF322068 HD--13-11	C1099	38.2	4.4	187	4	CB376955	CB376955 Hb02B04.L
1027	38.4	4.4	507	10	DT353071	DT353071 JGI_CABT9	1100	38.2	4.4	207	1	AU053554	AU053554 AU053554
C1028	38.4	4.4	512	9	CB389925	CB389925 JGI_XZT37	1101	38.2	4.4	222	10	DV125365	DV125365 CV03042A1
1029	38.4	4.4	514	8	CN834881	CN834881 AGENCOURT	1102	38.2	4.4	230	5	CF336189	CF336189 JMT--06-C
1030	38.4	4.4	517	10	DR835849	DR835849 LB00432.C	C1103	38.2	4.4	251	1	AJ441590	AJ441590 AJ441590
1031	38.4	4.4	518	9	CX382565	CX382565 JGI_XZT53	C1104	38.2	4.4	251	1	AJ441590	AJ441590 sau22n08.
1032	38.4	4.4	526	9	CA096113	CA096113 JGI_XZT32	1105	38.2	4.4	258	1	ALU83717	ALU83717 AU183717
1033	38.4	4.4	533	3	BU523128	BU523128 AGENCOURT	1106	38.2	4.4	261	4	CB218062	CB218062 NISC nb06
C1034	38.4	4.4	553	4	CA374326	CA374326 648659 NC	1107	38.2	4.4	267	3	BU800887	BU800887 SJF2CX07
C1035	38.4	4.4	564	1	AA817900	AA817900 UI-R-A0-a	1108	38.2	4.4	270	4	CB219030	CB219030 NISC nb12
C1036	38.4	4.4	567	8	CO875846	BovGen_04	1109	38.2	4.4	289	2	B1866594	B1866594 ft58g03.y
1037	38.4	4.4	574	8	CO891009	BovGen_19	1110	38.2	4.4	295	7	BB719628	BB719628 BB719628
1038	38.4	4.4	578	10	DT840068	DT840068 LB00453.C	1111	38.2	4.4	302	9	DN468775	DN468775 USDA-FP-1
1039	38.4	4.4	581	4	CX883466	CX883466 JGI_CAA12	1112	38.2	4.4	305	1	AA740964	AA740964 ob29g09.8
1040	38.4	4.4	596	8	CO880543	CO880543 BovGen_08	C1113	38.2	4.4	320	7	BE808228	BE808228 213382 MA
C1041	38.4	4.4	616	4	BX782118	BX782118 BX782118	1114	38.2	4.4				

1115	38.2	4.4	320	7	BE808230	213384 MA	1188	38.2	4.4	949	13	CL493875	CL493875 SAIL 587
1116	38.2	4.4	328	1	AU261705	AU261705	1189	38.2	4.4	954	11	BH162327	BH162327 ENTRJ37TR
1117	38.2	4.4	337	1	AJ701136	AJ701136	1190	38.2	4.4	973	10	DT781666	DT781666 126398522
1118	38.2	4.4	353	9	DN904454	OR0907.Y	1191	38.2	4.4	998	10	DT783865	DT783865 127410649
1119	38.2	4.4	358	4	CB931550	CB931550	1192	38.2	4.4	1006	14	CNS07A0G	AL436838 T7 end of
1120	38.2	4.4	359	4	CA488793	CA488793	1193	38.2	4.4	1073	10	DV778378	DV778378 Hw Fat 56
1121	38.2	4.4	359	5	CK421307	AUF Ipspn	1194	38.2	4.4	1113	10	DV795359	DV795359 HW LoIn 1
1122	38.2	4.4	365	7	BE682194	180129 MA	1195	38.2	4.4	1396	13	CL641292	CL641292 CH13--8P2
1123	38.2	4.4	369	2	BI343623	BI343623	1196	38.2	4.4	1396	13	CL641292	CL641292 CH13--8P2
1124	38.2	4.4	376	2	EG05496	EG05496	1197	38.2	4.4	118	10	DV077449	DV077449 DLSFmidgu
1125	38.2	4.4	385	7	BF410618	BF410618	1198	38.2	4.4	124	8	CK956016	CK956016 ip45C10.B
1126	38.2	4.4	390	9	DN950902	OST2T 670	1199	38.2	4.4	161	2	BI426118	BI426118 AC070405
1127	38.2	4.4	401	4	CB409793	CB409793	1200	38.2	4.4	162	2	BM544151	BM544151 AGENCOURT
1128	38.2	4.4	405	10	DT456585	GH ON3380	1201	38.2	4.4	182	1	AU095033	AU095033 AU095033
1129	38.2	4.4	407	2	BM534766	BM534766	1202	38.2	4.4	186	8	CO722729	CO722729 MdfR30180
1130	38.2	4.4	414	9	DN483742	DN483742	1203	38.2	4.4	220	7	BE023934	BE023934 em94d01.Y
1131	38.2	4.4	417	9	DN883249	DN883249	1204	38.2	4.4	221	2	BI898852	BI898852 480638 MA
1132	38.2	4.4	422	2	BI834392	BI834392	1205	38.2	4.4	221	9	CF733504	CF733504 AC45C12.Y
1133	38.2	4.4	422	4	CA957581	CA957581	1206	38.2	4.4	240	5	CF303535	CF303535 ABF1--02
1134	38.2	4.4	423	5	CJ317620	CJ317620	1207	38.2	4.4	243	3	BU842760	BU842760 AGENCOURT
1135	38.2	4.4	424	8	CK066361	CK066361	1208	38.2	4.4	265	7	AW432196	AW432196 sh70C09.Y
1136	38.2	4.4	426	8	CN990444	CN990444	1209	38.2	4.4	267	8	CO875936	CO875936 BoyGen 04
1137	38.2	4.4	426	8	CN992046	CN992046	1210	38.2	4.4	270	5	CK050931	CK050931 50043Efic
1138	38.2	4.4	426	10	DT470273	DT470273	1211	38.2	4.4	295	2	BU340235	BU340235 BU340235
1139	38.2	4.4	428	3	BU044457	BU044457	1212	38.2	4.4	298	1	AI249966	AI249966 qx47D01.X
1140	38.2	4.4	439	8	CK033400	CK033400	1213	38.2	4.4	303	2	BM030182	BM030182 488728 MA
1141	38.2	4.4	447	4	BY383776	BY383776	1214	38.2	4.4	306	4	C99456	C99456 C99456 Rice
1142	38.2	4.4	448	10	DV860783	DV860783	1215	38.2	4.4	307	5	CK400031	CK400031 AGENCOURT
1143	38.2	4.4	449	3	BM566470	BM566470	1216	38.2	4.4	310	9	DN135975	DN135975 tam63B05
1144	38.2	4.4	451	3	BQ432030	BQ432030	1217	38.2	4.4	313	9	DN902820	DN902820 naq39R06
1145	38.2	4.4	453	3	BQ475957	platyatom	1218	38.2	4.4	315	9	CK733603	CK733603 OC46f03.Y
1146	38.2	4.4	454	4	BE699159	BE699159	1219	38.2	4.4	321	4	CA803028	CA803028 sau46C03
1147	38.2	4.4	456	5	CF315893	CF315893	1220	38.2	4.4	322	1	AI302128	AI302128 qn19f10.X
1148	38.2	4.4	477	4	C93690	C93690	1221	38.2	4.4	328	7	BU564312	BU564312 AGENCOURT
1149	38.2	4.4	479	9	DN885984	DN885984	1222	38.2	4.4	328	7	BF076909	BF076909 226675 MA
1150	38.2	4.4	481	4	CA515631	CA515631	1223	38.2	4.4	328	12	CC809305	CC809305 ZMMB8C04B
1151	38.2	4.4	486	8	CO923606	CO923606	1224	38.2	4.4	329	4	BF702082	BF702082 BX702082
1152	38.2	4.4	497	10	DM010461	DM010461	1225	38.2	4.4	332	5	CF382719	CF382719 lac90905
1153	38.2	4.4	503	9	CK410043	CK410043	1226	38.2	4.4	335	7	AW945168	AW945168 ETS61361
1154	38.2	4.4	527	4	BS524738	BS524738	1227	38.2	4.4	335	9	AW945168	AW945168 ETS61361
1155	38.2	4.4	546	9	CK749807	CK749807	1228	38.2	4.4	352	3	BQ424539	BQ424539 AGENCOURT
1156	38.2	4.4	563	3	BM734291	BM734291	1229	38.2	4.4	360	8	CO204707	CO204707 WS0061.B2
1157	38.2	4.4	571	5	CD727102	CD727102	1230	38.2	4.4	369	5	CF926795	CF926795 laf41h01
1158	38.2	4.4	574	1	AM137799	AM137799	1231	38.2	4.4	375	9	DN114045	DN114045 1113377 M
1159	38.2	4.4	586	1	AI462326	AI462326	1232	38.2	4.4	376	9	DN113691	DN113691 1112993 M
1160	38.2	4.4	603	9	DR011150	DR011150	1233	38.2	4.4	379	9	DN585645	DN585645 93869372
1161	38.2	4.4	622	10	DR011150	DR011150	1234	38.2	4.4	384	8	CO894344	CO894344 Boven 22
1162	38.2	4.4	634	9	CK439952	CK439952	1235	38.2	4.4	402	3	BM933517	BM933517 UI-M-B21
1163	38.2	4.4	639	8	CN985806	CN985806	1236	38.2	4.4	402	5	CF329852	CF329852 NACL--05
1164	38.2	4.4	644	1	AJ813744	AJ813744	1237	38.2	4.4	411	4	CB802438	CB802438 AMGNNUC:M
1165	38.2	4.4	649	10	DT783479	DT783479	1238	38.2	4.4	412	8	CK123933	CK123933 1323838 N
1166	38.2	4.4	660	2	DM078411	DM078411	1239	38.2	4.4	416	1	AL387990	AL387990 MEBC48A02
1167	38.2	4.4	682	3	BQ200171	BQ200171	1240	38.2	4.4	420	5	CF357670	CF357670 rm94C01.Y
1168	38.2	4.4	690	3	BQ538199	BQ538199	1241	38.2	4.4	429	8	CNS76973	CNS76973 r553g11.X
1169	38.2	4.4	692	10	DT494336	DT494336	1242	38.2	4.4	433	5	CK144522	CK144522 3530 1.11
1170	38.2	4.4	698	8	CV259339	CV259339	1243	38.2	4.4	442	5	CF319079	CF319079 CJ319079
1171	38.2	4.4	699	9	DR132934	DR132934	1244	38.2	4.4	444	5	CF357686	CF357686 rm94d06.Y
1172	38.2	4.4	713	1	AU030034	AU030034	1245	38.2	4.4	454	8	CN194447	CN194447 r94f06.Y
1173	38.2	4.4	722	9	DR025415	DR025415	1246	38.2	4.4	458	8	CN164935	CN164935 995320 MA
1174	38.2	4.4	727	9	AGN11025	AGN11025	1247	38.2	4.4	462	3	BP214064	BP214064 BP214064
1175	38.2	4.4	761	14	AG303406	AG303406	1248	38.2	4.4	471	3	BP681334	BP681334 BP681334
1176	38.2	4.4	784	14	AG537625	AG537625	1249	38.2	4.4	489	1	AJ701118	AJ701118 AJ701118
1177	38.2	4.4	804	3	BU937914	BU937914	1250	38.2	4.4	495	7	AW294744	AW294744 UI-H-BW0-
1178	38.2	4.4	807	3	BU958859	BU958859	1251	38.2	4.4	495	9	CX512934	CX512934 JGI XZG57
1179	38.2	4.4	842	10	DM259657	DM259657	1252	38.2	4.4	496	10	DT722280	DT722280 LB01333.CR
1180	38.2	4.4	856	7	BE964493	BE964493	1253	38.2	4.4	496	10	BP764256	BP764256 BP764256
1181	38.2	4.4	862	5	CF934053	CF934053	1254	38.2	4.4	504	3	AK207505	AK207505 HS 3249 B
1182	38.2	4.4	868	14	CN907DOU	CN907DOU	1255	38.2	4.4	511	11	CK421152	CK421152 AUF Ipspn
1183	38.2	4.4	886	4	AX759012	AX759012	1256	38.2	4.4	512	5	AV609838	AV609838 Sna_gcrof
1184	38.2	4.4	888	10	DR732583	DR732583	1257	38.2	4.4	520	8	CV549922	CV549922 T9EST2yr3
1185	38.2	4.4	900	10	DM020631	DM020631	1258	38.2	4.4	521	8	CN798395	CN798395 D4P01587
1186	38.2	4.4	926	14	AG399219	AG399219	1259	38.2	4.4	523	10	DT851769	DT851769 LB001493.C
1187	38.2	4.4	948	7	BF141360	BF141360	1260	38.2	4.4	527	9	CX485896	CX485896 JGI XZG35
										529	10	DV947787	DV947787 SB03009A1

1261	38	4.4	530	3	BM942318	UI-N-BZ1-	1334	37.8	4.3	229	8	CV492424	CV492424
1262	38	4.4	536	5	CF801537	rj60e11.y	1335	37.8	4.3	234	8	CX158892	CX158892
1263	38	4.4	544	3	BP935210	BP935210	1336	37.8	4.3	238	8	CO895257	CO895257
1264	38	4.4	547	10	DT849094	LB00485.C	1337	37.8	4.3	239	3	BUB51712	BUB51712
1265	38	4.4	567	8	CO804992	AGENCOURT	1338	37.8	4.3	240	1	AI678857	AI678857
1266	38	4.4	573	5	CK618908	mk17b09.y	1339	37.8	4.3	254	5	CF330391	CF330391
1267	38	4.4	579	8	CO3037547	1350462.N	1340	37.8	4.3	261	10	DV867244	DV867244
1268	38	4.4	582	9	DN873497	nad26910.	1341	37.8	4.3	263	1	AA711043	AA711043
1269	38	4.4	631	3	BU063494	Fgr_3.D01	1342	37.8	4.3	296	1	AU033171	AU033171
1270	38	4.4	632	5	CK461066	931402.MA	1343	37.8	4.3	302	2	BI021679	BI021679
1271	38	4.4	634	10	DT836009	LB00433.C	1344	37.8	4.3	305	7	BE022424	BE022424
1272	38	4.4	635	9	DN146170	4842.A10	1345	37.8	4.3	335	4	CB930816	CB930816
1273	38	4.4	636	9	CX391240	JGI_XZT38	1346	37.8	4.3	339	7	AW705520	AW705520
1274	38	4.4	640	11	BH186548	025_H16-	1347	37.8	4.3	341	3	BO932932	BO932932
1275	38	4.4	640	14	CNS07R05	AL623495.T3	1348	37.8	4.3	350	5	CF546249	CF546249
1276	38	4.4	641	3	BQ266512	NISC.flf13	1349	37.8	4.3	353	5	CF317206	CF317206
1277	38	4.4	652	1	AV692691	AV692691	1350	37.8	4.3	356	5	CK381884	CK381884
1278	38	4.4	653	9	CK968726	HESCA.30	1351	37.8	4.3	359	1	AA270231	AA270231
1279	38	4.4	660	2	BU584084	BJ684084-	1352	37.8	4.3	360	1	AL726038	AL726038
1280	38	4.4	663	5	CF728119	UI-N-HB0-	1353	37.8	4.3	380	9	CX345991	CX345991
1281	38	4.4	674	3	BP762184	BP762184	1354	37.8	4.3	382	8	CV999881	CV999881
1282	38	4.4	679	9	DN883796	DR556850.naf17f02.	1355	37.8	4.3	389	8	CV962771	CV962771
1283	38	4.4	679	10	DR556850	WS0329.C2	1356	37.8	4.3	392	5	CK380619	CK380619
1284	38	4.4	697	3	BO502834	MI-P-NA-a	1357	37.8	4.3	403	1	AU261558	AU261558
1285	38	4.4	704	5	CF552627	67-102016	1358	37.8	4.3	429	5	CJ315106	CJ315106
1286	38	4.4	712	1	AV713580	AV713580	1359	37.8	4.3	430	3	BN941167	BN941167
1287	38	4.4	715	14	AG371878	Mus.muscu	1360	37.8	4.3	436	9	CX369376	CX369376
1288	38	4.4	716	3	BU620283	UI-H-FH1-	1361	37.8	4.3	436	9	CX329663	CX329663
1289	38	4.4	717	14	DX064627	KB-B072C1	1362	37.8	4.3	439	9	CX396957	CX396957
1290	38	4.4	728	4	BM745710	BM745710	1363	37.8	4.3	445	8	CN540860	CN540860
1291	38	4.4	733	14	AG415916	Mus.muscu	1364	37.8	4.3	455	10	DR898845	DR898845
1292	38	4.4	737	2	BG288558	602388025	1365	37.8	4.3	473	1	AL041562	AL041562
1293	38	4.4	741	9	CK579485	TTE000224	1366	37.8	4.3	487	5	CD415292	CD415292
1294	38	4.4	750	4	CA502810	UI-CF-FN0	1367	37.8	4.3	493	4	CB969776	CB969776
1295	38	4.4	766	8	CR567068	CR567068	1368	37.8	4.3	508	9	CX373566	CX373566
1296	38	4.4	776	9	CX584960	TTE000353	1369	37.8	4.3	510	8	CV895245	CV895245
1297	38	4.4	795	9	DR138548	DR138548	1370	37.8	4.3	512	8	CX318063	CX318063
1298	38	4.4	828	5	CD356330	AGENCOURT	1371	37.8	4.3	512	10	DT843414	DT843414
1299	38	4.4	853	13	DU023910	DU023910.384.Toma	1372	37.8	4.3	514	7	AW568434	AW568434
1300	38	4.4	855	10	DT773495	DT773495.125583859	1373	37.8	4.3	529	5	CF518389	CF518389
1301	38	4.4	864	5	CO763353	brain.EST	1374	37.8	4.3	538	4	C92760	C92760
1302	38	4.4	865	5	CK198814	FGAS00730	1375	37.8	4.3	545	8	CO303048	CO303048
1303	38	4.4	878	3	BU850652	AGENCOURT	1376	37.8	4.3	560	8	CO080800	CO080800
1304	38	4.4	880	5	CK158829	FGAS03979	1377	37.8	4.3	561	8	CO810335	CO810335
1305	38	4.4	888	7	BB900885	BB900885	1378	37.8	4.3	566	4	CB202696	CB202696
1306	38	4.4	892	4	CB230927	AGENCOURT	1379	37.8	4.3	576	7	AW644204	AW644204
1307	38	4.4	903	5	CK160110	FGAS04165	1380	37.8	4.3	593	9	BE557061	BE557061
1308	38	4.4	909	14	CNS00JTL	AL076720.Drosophi	1381	37.8	4.3	602	7	BE557061	BE557061
1309	38	4.4	931	13	C2999128	C2999128.188689.To	1382	37.8	4.3	614	9	DN368200	DN368200
1310	38	4.4	934	3	BU588245	AGENCOURT	1383	37.8	4.3	618	11	BH310026	BH310026
1311	38	4.4	940	9	DN570209	DN570209.93857559	1384	37.8	4.3	619	3	BQ525629	BQ525629
1312	38	4.4	944	8	CO766179	CO766179.spleen.ES	1385	37.8	4.3	619	10	DV124988	DV124988
1313	38	4.4	951	10	DT771303	DT771303.125255677	1386	37.8	4.3	623	8	CV972225	CV972225
1314	38	4.4	958	13	CL508148	CL508148.SAIL.792	1387	37.8	4.3	634	9	CK346242	CK346242
1315	38	4.4	966	4	CB204438	CB204438.AGENCOURT-	1388	37.8	4.3	637	8	CO810335	CO810335
1316	38	4.4	970	8	CO762897	CO762897.brain.EST	1389	37.8	4.3	637	9	CX398018	CX398018
1317	38	4.4	975	3	BQ718516	BQ718516.AGENCOURT	1390	37.8	4.3	637	9	DN304397	DN304397
1318	38	4.4	979	10	DT782503	DT782503.126455302	1391	37.8	4.3	647	10	DT360633	DT360633
1319	38	4.4	987	10	DV074753	DV074753.DAY20.18	1392	37.8	4.3	649	10	DT359981	DT359981
1320	38	4.4	991	14	CNS00JTM8	AL077118.Drosophi	1393	37.8	4.3	656	8	CK334289	CK334289
1321	38	4.4	995	4	CB194716	CB194716.AGENCOURT	1394	37.8	4.3	661	4	BM707648	BM707648
1322	38	4.4	998	14	AG388659	AG388659.Mus.muscu	1395	37.8	4.3	661	10	DT345373	DT345373
1323	38	4.4	1014	1	AU284724	AU284724.VP01.19.N	1396	37.8	4.3	662	4	EX708485	EX708485
1324	38	4.4	1019	10	DV074648	DV074648.VP01.19.N	1397	37.8	4.3	665	9	CK804665	CK804665
1325	38	4.4	1096	13	CL472179	CL472179.SAIL.173b	1398	37.8	4.3	666	4	EX707566	EX707566
1326	38	4.4	1109	12	CC933402	CC933402.ZMWBc054	1399	37.8	4.3	669	5	CF405301	CF405301
1327	38	4.4	1160	9	DR151047	DR151047.49259351	1400	37.8	4.3	672	3	BQ799076	BQ799076
1328	38	4.4	1345	10	DV781218	DV781218.Hw.FAT_29	1401	37.8	4.3	678	4	EX723552	EX723552
1329	38	4.4	1331	6	CR749601	CR749601.Homo.sapi	1402	37.8	4.3	686	4	EX708510	EX708510
1330	37.8	4.3	165	2	BI941711	BI941711.sc86f03.y	1403	37.8	4.3	714	4	EX691298	EX691298
1331	37.8	4.3	184	8	CK025427	CK025427.Md1v4-404	1404	37.8	4.3	719	8	CK997976	CK997976
1332	37.8	4.3	211	1	AL697999	AL697999.DKF2p686M	1405	37.8	4.3	729	9	DN313720	DN313720
1333	37.8	4.3	211	8	CX124919	CX124919.1324772.N	1406	37.8	4.3	735	2	BM384416	BM384416

C1407	37.8	37.8	4.3	742	10	DW252250	UI-S-GBO-	DW252250	UI-S-GBO-	1480	37.6	4.3	301	1	A1348932	A1348932	ts98n09.x
1408	37.8	37.8	4.3	745	2	BG289608	602381575	BG289608	602381575	1481	37.6	4.3	307	1	A1349017	A1349017	ts99a11.x
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C1413	37.8	37.8	4.3	770	9	DN866938	nac24908	DN866938	nac24908	1486	37.6	4.3	320	3	BQ958612	BQ958612	AGENCOURT
C1414	37.8	37.8	4.3	783	4	BX730524	BX730524	BX730524	BX730524	1487	37.6	4.3	325	9	DN136063	DN136063	tsm64804
C1415	37.8	37.8	4.3	797	4	BK779860	BK779860	BK779860	BK779860	1488	37.6	4.3	327	8	CN612752	CN612752	C88EST00
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1417	37.8	37.8	4.3	807	14	CNS0128R	Drosophila	AL101253	Drosophila	1490	37.6	4.3	338	7	BE681634	BE681634	179364_MA
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C1420	37.8	37.8	4.3	818	10	DT066980	AGENCOURT	DT066980	AGENCOURT	1493	37.6	4.3	345	3	BM965655	BM965655	ko15b08.y
1421	37.8	37.8	4.3	824	8	DN157340	946039_MA	DN157340	946039_MA	C1494	37.6	4.3	351	1	AI451546	AI451546	mu46f05.x
1422	37.8	37.8	4.3	832	3	BUB58775	AGENCOURT	BUB58775	AGENCOURT	1495	37.6	4.3	352	2	BI848734	BI848734	471254_MA
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1424	37.8	37.8	4.3	854	14	AG484151	Mus muscu	AG484151	Mus muscu	1497	37.6	4.3	358	7	BF582663	BF582663	602094058
1425	37.8	37.8	4.3	865	14	CNS02087	Tetraodon	AL175264	Tetraodon	C1498	37.6	4.3	367	1	AI613270	AI613270	ty35d11.x
C1426	37.8	37.8	4.3	885	10	DT771624	125654981	DT771624	125654981	C1499	37.6	4.3	376	7	BE982327	BE982327	UI-M-CG0p
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1428	37.8	37.8	4.3	902	14	AG420319	Mus muscu	AG420319	Mus muscu								
1429	37.8	37.8	4.3	905	14	CNS008KH	Drosophila	AL077798	Drosophila								
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1459	37.6	37.6	4.3	237	8	CV496004	73678.1_C	CV496004	73678.1_C								
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ALIGNMENTS

RESULT 1	748 bp	mRNA	linear	EST 12-FEB-2003
CB242167/c	UI-CF-FNO-aggd-f-19-0-UI.s1	UI-CF-FNO Homo sapiens	cdna clone	
LOCUS	UI-CF-FNO-aggd-f-19-0-UI 3', mRNA sequence.			
DEFINITION	CB242167			
ACCESSION	CB242167.1	GI:283633811		
VERSION	EST.			
KEYWORDS	Homo sapiens (human)			
SOURCE	Homo sapiens			
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.			
REFERENCE	1 (bases 1 to 748)			
AUTHORS	Bonaldo, M.F., Lennon, G. and Soares, M.B.			
TITLE	Normalization and subtraction: two approaches to facilitate gene discovery			
JOURNAL	Genome Res. 6 (9), 791-806 (1996)			
PUBMED	8889548			
COMMENT	Contact: McCray, PB University of Iowa 2024 University of Iowa Med Labs, Iowa City, IA 52242, USA Tel: 319 356 4866 Fax: 319 356 7171 Email: paul-mccray@uiowa.edu Tissue Procurement: Dr. M. J. Welsh, University of Iowa cDNA Library preparation: Dr. M. Bento Soares, University of Iowa cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa DNA Sequencing by: Dr. M. Bento Soares, University of Iowa Clone Distribution: Researchers may obtain clones from Research Genetics (www.resgen.com) or from Open Biosystems (www.openbiosystems.com). The following repetitive elements were found in this cDNA sequence: 1-38, >AT rich#Low_complexity (matched complement) Seq primer: M13 FORWARD POLYA=Yes.			
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	/tissue_type="Human Lung Epithelial cells"			
	/lab_host="DH10B (Life Technologies)"			
	/clone_lib="UI-CF-FNO"			
	/note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a			

modified polylinker; Site 1: EcoR I; Site 2: Not I;
UI-CF-FNO is a subcloned cDNA library derived from two
normalized Human lung epithelial cell libraries (EN1 and
DU1). The library was subcloned according to
Bonaldi, Lennon and Soares, Genome Research, 6:791-806,
1996. For additional information, contact:
bento-soares@uiowa.edu
TAG_TISSUE=Human Lung Epithelial Cell Lines untreated LPS
6hr to LPS 24h
TAG_LIB=UI-CF-FNO
TAG_SEQ=CTGCTCAGGT"

[illegible]

RESULT 2
BM982101/c
LOCUS

DEFINITION	ACCESSION VERSION	KEYWORDS	SOURCE ORGANISM	REFERENCE AUTHORS TITLE	JOURNAL PUBMED COMMENT
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FEATURES

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ORIGIN

Query Match
Best Local
Matches 709

Qy	157	AGTTCTAAATCTCTTCCCTCCTCCTGTTGCTGCCACTAATGCTGATGCTCATGGTCTCTCTA	216
Db	712	AAAGTCTAAATCTCTTCCCTCCTCCTG-TGCTGGCACATAATGCTGAT-TCAATGGTCTCTCTA	655

UI-CF-EN1-acr-i-08-0-UI.s1 UI-CF-EN1 Homo sapiens CDNA clone
 UI-CF-EN1-acr-i-08-0-UI.3', mRNA sequence.
 BM982101
 BM982101.1 GI:19605260
 EST.
 Homo sapiens (human)
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homnidae; Homo.
 1 (bases 1 to 715)
 Bonaldo,M.F., Lennon,G. and Soares,M.B.
 Normalization and subtraction: two approaches to facilitate gene
 discovery
 Genome Res. 6 (9), 791-806 (1996)
 8889548
 Contact: McCray, PB
 McCray Lab
 University of Iowa
 2024 University of Iowa Med Labs, Iowa City, IA 52242, USA
 Tel: 319 356 4866
 Fax: 319 356 7171
 Email: paul-mccray@iowa.edu
 Tissue Procurement: Dr. M. J. Welsh, University of Iowa
 cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
 cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Researchers may obtain clones from Research
 Genetics (www.resgen.com) or from Open Biosystems
 (www.openbiosystems.com).
 The following repetitive elements were found in this cDNA
 sequence: 1-38, >AT-rich#Low_complexity (matched complement)
 Seq primer: M13 FORWARD
 POLYA=Yes.

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Location/Qualifiers
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/clone="UI-CF-EN1-acr-i-08-01-UI"
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Cells"
/dev_stage="Adult"
/lab_host="DH10B (life Technologies) (T1 phage resistant)"
/clone_lib="UI-CF-EN1"
/note="Organ: Lung; Vector: p7T3-Pac (Pharmacia) with a
modified polylinker; Site 1: Ecor I; Site 2: Not I;
UI-CF-EN1 is a normalized cDNA library containing the
following tissue(s): Primary lung Cystic Fibrosis
Epithelial cells. The library was constructed according to
Bonaldi, Lennon and Soares, Genome Research, 6:791-806,
1996. First strand cDNA synthesis was primed with an
oligo-dT primer containing a Not I site. Double stranded
cDNA was ligated to an Ecor I adaptor, digested with Not
I, and cloned directionally into p7T3-Pac vector. The
oligonucleotide used to prime the synthesis of
first-strand cDNA contains a library tag sequence that is
located between the Not I site and the (dT)18 tail. The
sequence tag for this library is CTGCTCAGGT.
TAG TISSUE=Human Lung Epithelial Cell Lines untreated LPS
6hr to LPS 24h
TAG LIB=UI-CF-EN1
TAG_SEQ=CTGCTCAGGT"

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Query Match 78.8%; Score 685.8; DB 3; Length 715;
Best Local Similarity 99.3%; Pred. No. 1e-174;
Matches 709; Conservative 0; Mismatches 3; Indels 2; Gaps 2

Qy	157	AGTTCTAAATCTCTTCCCTCCTCCTGTTGCTGCCACTAATGCTGATGTCATGGTCTCTCTA	216
Dy	712	AAAGTCTAAATCTCTTCCCTCCTCCTG-TGCTGGCACCTAATGCTGAT-TCAATGGTCTCTCTA	655


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Db 594 GGTCTCAGGAAGCGCGCCAGGAATGTGAGTGCAAGATTGGTCTCTGAGAGCCCGAGAA 535
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QY 397 GCAATGTGAAGAAAACAGACACCAAGGACCAACAGAAAGCCAAACAAGCATTTCCAGAG 456
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QY 577 CAGACACTCTTCTTCCCACTCTCTCCACTGTACCCACCCCTAAATCATTTCCAGT 636
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QY 637 GCTCTCAAAAAGCATGTTTTCAAGATCAATTTGTTGTTGTTGTTCTCTCTAGTGTCTTT 696
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QY 697 CTCTGCTGACTGTAGCCTGTGCTCCCTTACCCAGGCTTAGGCTTAATACCTGAA 756
Db 174 CTCTGCTGACTGTAGCCTGTGCTCCCTTACCCAGGCTTAGGCTTAATACCTGAA 115
QY 757 GATTCAGGAACTGTAGCTTCTAGCTAGTGTCTTAACCTTAATGCAATCAGGAA 816
Db 114 GATTCAGGAACTGTAGCTTCTAGCTAGTGTCTTAACCTTAATGCAATCAGGAA 55
QY 817 GTAGCAACAGAGTCAATAATATTTTAAATGTCAAAAAAAGGAAAAA 870
Db 54 GTAGCAACAGAGTCAATAATATTTTAAATGTCAAAAAAAGGAAAAA 1

RESULT 3
BM978124/c
LOCUS
DEFINITION
  UI-CF-EC1-aeb-a-23-0-UI.s1 UI-CF-EC1 Homo sapiens cDNA clone
  UI-CF-EC1-aeb-a-22-0-UI 3', mRNA sequence.
ACCESSION
  BM978124
VERSION
  BM978124.1 GI:19597232
KEYWORDS
  EST.
SOURCE
  Homo sapiens (human)
  ORGANISM
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
    Hominidae; Homo.
  1 (bases 1 to 753)
  Bonaldo,M.F., Lennon,G. and Soares,M.B.
  Normalization and subtraction: two approaches to facilitate gene
  discovery
JOURNAL
  Genome Res. 6 (9), 791-806 (1996)
PUBMED
  8889548
COMMENT
  Contact: McCray, PB
  McCray Lab
  University of Iowa
  2024 University of Iowa Med Labs, Iowa City, IA 52242, USA
  Tel: 319 356 4866
  Fax: 319 356 7171
  Email: paul-mccray@uiowa.edu
  Tissue Procurement: Dr. M. J. Welsh, University of Iowa
  cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
```

```
FEATURES
    source
    Location/Qualifiers
      1..753
      /organism="Homo sapiens"
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      /clone="UI-CF-EC1-aeb-a-22-0-UI"
      /tissue_type="Lung"
      /dev_stage="Adult and Fetal"
      /lab_host="DH10B (Life Technologies) (T1 phage resistant)"
      /clone_lib="UI-CF-EC1"
      /note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a
      modified polylinker; Site 1: EcoR I; Site 2: Not I;
      UI-CF-EC1 is a normalized cDNA library containing the
      following tissue(s): Normal lung from adult and from fetal
      day 64, day 87, week 19 and week 42. The library was
      constructed according to Bonaldo, Lennon and Soares,
      Genome Research, 6:791-806, 1996. First strand cDNA
      synthesis was primed with an oligo-dT primer containing a
      Not I site. Double stranded cDNA was ligated to an EcoR I
      adaptor, digested with Not I, and cloned directionally
      into pT7T3-Pac vector. The oligonucleotide used to prime
      the synthesis of first-strand cDNA contains a library tag
      sequence that is located between the Not I site and the
      (dT)18 tail. The sequence tag for this library is
      AAGTGTTCAC.
      TAG TISSUE=Normal Lung Epithelial Cells Tissue nos 369-371
      and 380-383
      TAG_LIB=UI-CF-EC1
      TAG_SEQ=AAGTGTTCAC"
ORIGIN
    Query Match 78.5%; Score 682.8; DB 3; Length 753;
    Best Local Similarity 97.1%; Pred. No. 6.7e-174;
    Matches 733; Conservative 0; Mismatches 3; Indels 19; Gaps 3;
    QY 133 CAGCTGCACCCGACAGTTGGATGAAAGTTCTAATCTCTTCCCTCTCTCTGTTGCTGCCAC 192
    Db 753 CAGCTGCACCCGACAGTTGGATGAAAG-TCTAATCTCTTCCCTCTCTCTGTTGCTGCCAC 696
    QY 193 TAAATGCTGATGCCATGGTCTCTAGCAGCTGAATCCAGGGTTCGCGAGGCGCACAGG 252
    Db 695 TAAATGCTGATGCCATGGTCTCTAGCAGCTGAATCCAGGGTTCGCGAGGCGCACAGG 636
    QY 253 ACCGAGGCCAGGCTTCTAGGAGATGGCTCCAGNAGGCGGCCAAGAATGTGAGTGCAA-- 310
    Db 635 ACCGAGGCCAGGCTTNTAGGAGATGGCTCCAGNAGGCGGCCAAGAATGTGAGTGCAAAG 576
    QY 311 -----AGATTGGTTCTGAGAGCCCGAGAGAAAAAATTCATGACAGTGTC 355
    Db 575 CAATGCTGTTGTTCCAGATTGGTTCTGAGAGCCCGCGAGAGAAATTCATGACAGTGTC 516
    QY 356 TGGGCTGCCAAAGAGCAGTGCCTCTGATCATTTTCAAGGGGCAATGTGAAGAAAACAAG 415
    Db 515 TGGGCTGCCAAAGAGCAGTGCCTCTGATCATTTTCAAGGGGCAATGTGAAGAAAACAAG 456
    QY 416 ACACCAAGGCCACCAAGAAAGCCAAAGCAATTCAGAGGCTCTGAGCGCCCAATTTCTCAA 475
    Db 455 ACACCAAGGCCACCAAGAAAGCCAAAGCAATTCAGAGGCTCTGAGCGCCCAATTTCTCAA 396
    QY 476 ACAATGTCAGCTAAGAGCTTTTGTCTGCTGCTTTGTAGGAGCTCTGAGCGCCCACTCTTC 535
    Db 395 ACAATGTCAGCTAAGAGCTTTTGTCTGCTTTGTAGGAGCTCTGAGCGCCCACTCTTC 336
    QY 536 AATTAAACATTTCTCAGCCCAAGAGACAGTGCACACCTTACCAGACACTCTTTCTTCCC 595
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cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.reagen.com) or from Open Biosystems
(www.openbiosystems.com).
Seq primer: M13 FORWARD
POLYA=Yes.

PUBMED	16341674
COMMENT	Contact:

Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Soeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr
Plate: 22 row: H column: 10
High quality sequence stop: 677.

FEATURES

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1. 677
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="S14K402-22-H10"
/cell_line="K402"
/lab_host="Top10F,"
/clone_l1b="S14K402"
/notes="Organ: Stomach; Vector: pTZ18RP1; Site1: EcoRI;
Site2: NotI; The poly (A)+ RNA was dephosphorylated with
bacterial alkaline phosphatase (BAP) and then decapped
with tobacco acid pyrophosphatase (TAP). The decapped
inact mRNA was ligated with DNA-RNA linker including EcoRI
I site by treatment of T4 RNA ligase and the first strand
cDNA was synthesized from oligo dt-selected mRNA by
priming with dt-tailed vector. The dt-tailed vector was
adjusted to have about 60nt. The cDNA vector was
circularized with E. coli DNA ligase after digestion of
EcoRI which site is also included in vector. An RNA strand
converted to a DNA strand by Okayama-Berg method. The
obtained cDNA vectors were used for transformation of
competent cells E. coli Top10F, by electroporation method.
The cDNA libraries constructed by this method are
full-length enriched cDNA library."

```

ORIGIN

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Query Match      77.8%; Score 677; DB 3; Length 677;
Best Local Similarity 100.0%; Pred. No. 2.5e-172;
Matches 677; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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61	QY	CTGACCTGAGTCATCCCGAGGATCAGGAGCCTCCAGCAGGGAACCTTTCATTATATCT	120
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121	QY	TCAAGCAACTTACAGCTGCACCGACAGTTCGCGATGAAAGTTCTAACTCTTCCCTCCTCC	180
61	DB	TCAAGCAACTTACAGCTGCACCGACAGTTCGCGATGAAAGTTCTAACTCTTCCCTCCTCC	120
181	QY	TGTTGTGTCACCTAATGCTGATGTCCATGTGCTCTAGCAGCCTGAATCCAGGGGTGCGCA	240
121	DB	TGTTGTGTCACCTAATGCTGATGTCCATGTGCTCTAGCAGCCTGAATCCAGGGGTGCGCA	180
241	QY	GAGGCCACAGGACCGAGCCAGGCTCTTAGGAGATGGCTCCAGGAGGCGGCCCAAGAAT	300
181	DB	GAGGCCACAGGACCGAGGCCAGGCTCTTAGGAGATGGCTCCAGGAGGCGGCCCAAGAAT	240
301	QY	GTGAGTGCAAAGATTGGTTCTCAGAGCCCGGAGAGAAAATTCATGACAGTGTCTGGGC	360
241	DB	GTGAGTGCAAAGATTGGTTCTCAGAGCCCGGAGAGAAAATTCATGACAGTGTCTGGGC	300
361	QY	TGCCAAAGAAGCAGTGCCCTCTGTGATCATTTCAAGGGCAATGTGAAGAAAACAAGACACC	420
301	DB	TGCCAAAGAAGCAGTGCCCTCTGTGATCATTTCAAGGGCAATGTGAAGAAAACAAGACACC	360
421	QY	AAAGGCACACAGAAAGCCAAAACAAGCATTTCCAGAGCTGCGACGAATTTCTCAAAACAAT	480
361	DB	AAAGGCACACAGAAAGCCAAAACAAGCATTTCCAGAGCTGCGACGAATTTCTCAAAACAAT	420
481	QY	GTGAGCTAAGAAGCTTTGCTCTGCTTTGTAGGAGCTCTGAGGCGCCCACTCTTCCCAATTA	540
421	DB	GTGAGCTAAGAAGCTTTGCTCTGCTTTGTAGGAGCTCTGAGGCGCCCACTCTTCCCAATTA	480

Qy	541	AACATTCTCAGCCAAAGAAGACAGTGAGGACACCTTACGAGACACTCTTTCTTCTCCACCTTC	600
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Qy	601	ACTCTCCCACTGTATACCAACCAACCCCTAAATCATTTCCAGTGCTCTCAAAAAGCATGTTTTTCAA	660
Db	541	ACTCTCCCACTGTATACCAACCAACCCCTAAATCATTTCCAGTGCTCTCAAAAAGCATGTTTTTCAA	600
Qy	661	GATCATTTTGTGTGTGTGCTCTCTCTAGTGTCTTCTTCTCGTCAAGTCTTAGCCCTGTGCC	720
Db	601	GATCATTTTGTGTGTGTGCTCTCTCTAGTGTCTTCTTCTCTCGTCAAGTCTTAGCCCTGTGCC	660
Qy	721	CTCCCTTACCCAGGCT	737
Db	661	CTCCCTTACCCAGGCT	677

RESULT 6
BT 770944

BI1770344	BI1770944	820 bp	linear	EST 25-SEP-2000
LOCUS	6030597639f1	Homo sapiens	cdna	
DEFINITION	NIH_MGC_122	Homo sapiens	clone IMAGE:5209073	5',
			mRNA sequence.	

ACCESSION BI770944
VERSION BI770944.1
KEYWORDS EST. GI:15762522

SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homidae; Homininae; Homininae; Homo.

1 (bases 1 to 820)
NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.

Contact: Robert G. Lachy, PhD
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: Life Technology

CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I M A G E Consortium

CDNA Library Arrayed by: the I.M.A.G.E.B.
DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>

Plate: L1AM11524 row: j column: 18
High quality sequence stop: 772.

FEATURES

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/clone_lib="NIH_MGC_122"
/note="Organ: pooled lung and spleen; vector: pCMV-SPORT6;"

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Site 1: NotI; Site 2: EcoRV (destroyed); RNA source anonymous pool of 24 week female lung, 16 week female

anonymous pool of 21 week female sang/16 week female spleen, and 20-22 week male spleens. Library is oligo-dt primed, and directionally cloned (EcoRV site is destroyed).

primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.4 kb, insert size range 1.2 kb. Library is normalized and enriched for

range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber

(Invitrogen). Research Genetics tracking code 026. Note: this is a NIH_MGC Library."

ORIGIN

Query Match	77.7%	Score 675.6;	DB 2;	Length 820;
Best Local Similarity	94.2%	Pred. No. 6,2e-172;		

Matches 769; Conservative 0; Mismatches 34; Indels 13; Gaps 6; Best Local Similarity 54.2%; P-Val. NO. 0.25-1/2;

QY 65 CCTGAGTCATCCCGAGGGATCAGGAGCTCCAGCAGGGAACTTCCATTATATTTCTTCAA 124

Db 1 CCTGAGTCATCCCCA - GGATCAGGAGCCTCCAGCAGGGAACCTTCCATTATATCTTTCAA 59

Qy	125	GCAACTTACAGCTGCACCGACAGTTGCGATGAAAGTTCTTAATCTCTTCCCTCCTCTGTT	184
Db	60	GCAACTTACAGCTGCACCGACAGTTGCGATGAAAGTTCTTAATCTCTTCCCTCCTCTGTT	119
Qy	185	GCTGCCACTAATGCTGATGTCATGTCCTCTAGCAGCCTGAATCCAGGGGTCGCAGAGG	244
Db	120	GCTGCCACTAATGCTGATGTCATGTCCTCTAGCAGCCTGAATCCA-GGGTCCGAGAGG	178
Qy	245	CCACAGGACCGAGCGCCAGGCTTCTAGGAGATGGCTCCAGGAAGCGCGCAAGATGTGA	304
Db	179	CCACAGGACCGAGCGCCAGGCTTCTAGGAGATGGCTCCAGGAAGCGCGCAAGATGTGA	238
Qy	305	GTGCAAGATTGGTTCTCTG-AGAGCCCGAGAGAAATTTATGACAGTGTCTGGGCTGC	363
Db	239	GTGCAAGATTGGTTCTCTGCTGGCGCCGCCAAGAAATTTATGACAGTGTCTGGGCTGC	298
Qy	364	CAAGAAGCAGTGCCTCTGATCAATTTCAAGGGCAATGTGAAGAAACAGACACCAA	423
Db	299	CAAGAAGCAGTGCCTCTGATCAATTTCAAGGGCAATGTGAAGAAACAGACACCAA	358
Qy	424	GGCACACAGAAGCAACCAAGCAATTCAGAGCCTGCCAGCAATTTCTCAAACAATGTC	483
Db	359	GGCACACAGAAGCAACCAAGCAATTCAGAGCCTGCCAGCAATTTCTCAAACAATGTC	418
Qy	484	AGCTAAGAAGCTTGTCTGCTTGTAGGAGCTCTGAGCGGCCACTCTTCCAATTAAC	543
Db	419	AGCTAAGAAGCTTGTCTGCTTGTAGGAGCTCTGAGCGGCCACTCTTCCAATTAAC	478
Qy	544	ATTCTCAGCCAGAGACAGTGAGCACACCTACAGACACTCTTCTGCCACCTCACT	603
Db	479	ATTCTCAGCCAGAGACAGTGAGCACACCTACAGACACTCTTCTGCCACCTCACT	538
Qy	604	CTCCCACTGTACCCACCCCTAAATCAATCCAGTGTCTCAAAAGCATGTTTTCAAGAT	663
Db	539	CTCCCACTGTACCCACCCCTAAATCAATCCAGTGTCTCAAAAGCATGTTTTCAAGAT	598
Qy	664	CATTTTGTGTTGCTCTCTCTAGTGTCTTCTCTCTGTCAGTCTTAGCCTGTGCCCTC	723
Db	599	CA-ATTGTTGGTGTCTCTCTAGTGTCTTCTCTCTGTCAGTCTTAGCCTGTGCCCTC	657
Qy	724	CCCTTACCAGGCTTAGGCTTAATTAACCTGAAAGATTCAGGAACTAGCTTCTTAGC	783
Db	658	CCCTTACCAGGCTTAGGCTTAATTAACCTGAAAGATTCAGGAACTAGCTTCTTAGC	717
Qy	784	TAGTGTCAAT-----TAACCTTAAATGCAATCAGGAAAGTAGCAACAGAACTCAA-	834
Db	718	TAGTGTCAATTTAAGCCCTTAAATTTGCCACTCAGGAACACGTTAGGCAACAGAACTCAAT	777
Qy	835	TAAATATTTTAAATGTCAAAAAAMAAAAA 870	
Db	778	TAAATATTTTAAATGTCACCAACCAACCAACGAA 813	
RESULT 7			
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LOCUS			
DEFINITION			
BX102380 Soares ovary tumor NbHOT Homo sapiens cdna clone			
IMAGp998H051817 ; IMAGE:740020, mRNA sequence.			
BX102380			
BX102380.1 GI:27831743			
EST.			
Homo sapiens (human)			
ORGANISM			
Homo sapiens			
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;			
Homnidae; Homo.			
1 (bases 1 to 671)			
REFERENCE			
AUTHORS			
Ebert,L., Heil,O., Hennig,S., Neubert,P., Partsch,E., Peters,M.,			
Radelof,U., Schneider,D. and Korn,B.			
Human Unigeneset - RZPD3			
TITLE			
JOURNAL			
Unpublished (2003)			
COMMENT			
Contact: Ina Rolfs			
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH			

Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany			
RZPD; IMAGp998H051817.			
RZPDLIB; I.M.A.G.E. cdna Clone Collection;			
Human Unigeneset - RZPD3 (RZPDLIB No.972)			
http://www.rzpd.de/CloneCards/cgi-			
bin/showlib.pl.cgi?response?libNo=972 Contact: Ina Rolfs			
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH			
Heubnerweg 6, D-14059 Berlin, Germany			
Tel: +49 30 32639 101			
Fax: +49 30 32639 111			
www.rzpd.de			
This clone is available royalty-free from RZPD;			
contact RZPD (clone@rzpd.de) for further information. Seq primer:			
M13r, Primer sequence: TTTCACACAGAAACAGCTATGAC.			
Location/Qualifiers			
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modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st			
strand cdna was primed with a Not I - oligo(dT) primer [5'			
TGTTACCAATCTGAATGGAGCGCGCGGTTTTTTTTTTTTTTT 3'],			
double-stranded cdna was size selected, ligated to Eco RI			
adapters (Pharmacia), digested with Not I and cloned into			
the Not I and Eco RI sites of a modified pT7T3 vector			
(Pharmacia). Library constructed by Bento Soares and			
M.Fatima Bonaldo. "			
ORIGIN			
Query Match 77.1%; Score 671; DB 4; Length 671;			
Best Local Similarity 100.0%; Pred. No. 1e-170;			
Matches 671; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
Qy	1	CTCGCCCTCAAAATGGGAACGCTGGCGTGGGACTAAAGCATAGACACAGGCTGAGTATC	60
Db	1	CTCGCCCTCAAAATGGGAACGCTGGCGTGGGACTAAAGCATAGACACAGGCTGAGTATC	60
Qy	61	CTGACCTGAGTCATCCCAGGGATCAGGAGCCTCAGCAGGGAACCTTCCATTATTTCT	120
Db	61	CTGACCTGAGTCATCCCAGGGATCAGGAGCCTCAGCAGGGAACCTTCCATTATTTCT	120
Qy	121	TCAGCAACTTACAGCTGCACCGCAGTTGGGATGAAAGTTCTTAATCTCTTCCCTCTCTCC	180
Db	121	TCAGCAACTTACAGCTGCACCGCAGTTGGGATGAAAGTTCTTAATCTCTTCCCTCTCTCC	180
Qy	181	TGTTGCTGCCACTAATGCTGATGTCATGTCCTCTAGCAGCCTGAATCCAGGGTTCGCCA	240
Db	181	TGTTGCTGCCACTAATGCTGATGTCATGTCCTCTAGCAGCCTGAATCCAGGGTTCGCCA	240
Qy	241	GAGGCCACAGGACCGAGGCCAGGCTTCTAGAGATGCTCCAGGAAGCGGCCCAAGAT	300
Db	241	GAGGCCACAGGACCGAGGCCAGGCTTCTAGAGATGCTCCAGGAAGCGGCCCAAGAT	300
Qy	301	GTGAGTCCAAAGATTGGTTCTCTGAGAGCCCGAGGAAGAAATTCATGACAGTGTCTGGGC	360
Db	301	GTGAGTCCAAAGATTGGTTCTCTGAGAGCCCGAGGAAGAAATTCATGACAGTGTCTGGGC	360
Qy	361	TGCCAAAGAAGCAGTGGCCCTGTGATCAATTTCAAGGGCAATGTGAAGAAAAACAACACC	420
Db	361	TGCCAAAGAAGCAGTGGCCCTGTGATCAATTTCAAGGGCAATGTGAAGAAAAACAACACC	420
Qy	421	AAAGGCCACACAGAAAGCCAAACAGCATTCAGAGCCTGCCAGCAATTTCTCAACAT	480
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Db 481 GTCAGCTAAGAGCTTTGGCTCTGCCTTTGTAGGAGCTCTGAGCGCCCACTCTTCCAAATTA 540
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Qy 601 ACTCTCCCACTGTACCCACCCCTTAATCATTTCCAGTGTCTCTCAAAAGCATGTTTTCAA 660
Db 601 ACTCTCCCACTGTACCCACCCCTTAATCATTTCCAGTGTCTCTCAAAAGCATGTTTTCAA 660
Qy 661 GATCATTTTGT 671
Db 661 GATCATTTTGT 671

RESULT 8
BM831028
LOCUS
DEFINITION
K-EST0104808 S14K402s1 Homo sapiens cDNA clone S14K402s1-18-A11 5',
mRNA sequence.
ACCESSION
BM831028
VERSION
BM831028.1 GI:19187437
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE
AUTHORS
Oh, J.H., Yang, J.O., Hahn, Y., Kim, M.R., Byun, S.S., Jeon, Y.J.,
Kim, J.M., Song, K.S., Noh, S.M., Kim, S., Yoo, H.S., Kim, Y.S. and
Kim, N.S.
Transcriptome analysis of human gastric cancer
Mamm. Genome 16 (12), 942-954 (2005)
16341674

TITLE
JOURNAL
PUBMED
COMMENT
Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Boeun-dong Yusong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongseung@mail.kribb.re.kr
Plate: 18 row: A column: 11
High quality sequence stop: 666.
Location/Qualifiers
1. 666

FEATURES
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="S14K402s1-18-A11"
/cell_line="K402"
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/clone_lib="S14K402s1"
/notes="Organ: Stomach; Vector: pTZ19RP1; Site 1: EcoRI;
Site 2: NotI; The poly (A)+ RNA was dephosphorylated with
bacterial alkaline phosphatase (BAP) and then decapped
with tabacco acid pyrophosphatase (TAP). The decapped
intact mRNA was ligated with DNA-RNA linker including EcoR
I site by treatment of T4 RNA ligase and the first strand
cDNA was synthesized from oligo dt-selected mRNA by
priming with dt-tailed vector. The dt-tailed vector was
adjusted to have about 60nt. The cDNA vector was
circularized with E. coli DNA ligase after digestion of
EcoRI which site is also included in vector. An RNA strand
converted to a DNA strand by Okayama-Berg method. The
obtained cDNA vectors were used for transformation of
competent cells E. coli Top10f' by electroporation method.
The cDNA libraries constructed by this method are
full-length enriched cDNA library. After analyzing and
sequencing about 2,000 ~ 3,000 colonies in original cDNA
library, the abundant cDNAs were selected and amplified by
PCR reaction using vector region primer including T7
promotor as 5' primer and N(dt)14 as 3' primer. The PCR

products were used as template for synthesis of
biotinylated single stranded RNA by in vitro transcription
reaction. The synthesized RNA probes were hybridized with
antisense single stranded cDNAs prepared from original
library and incubated with avidin-gel. After removing
DNA-RNA hybrids by centrifuge, the subtracted cDNA
libraries were constructed by transformation of the
remaining DNA into competent cells E. coli Top10f' with
electroporation method."

ORIGIN

Query Match 76.6%; Score 666; DB 3; Length 666;
Best Local Similarity 100.0%; Pred. No. 2.4e-169;
Matches 666; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 61 CTGACCTGAGTCATCCCCAGGGATCAGGAGCCTCCAGCAGGGAACCTTCCATTATATTTCT 120
Db 1 CTGACCTGAGTCATCCCCAGGGATCAGGAGCCTCCAGCAGGGAACCTTCCATTATATTTCT 60
Qy 121 TCAAGCAACTTACAGCTGCACCGACAGTTCGATGAAGTTCTAAATCTCTTCCCTCTCC 180
Db 61 TCAAGCAACTTACAGCTGCACCGACAGTTCGATGAAGTTCTAAATCTCTTCCCTCTCC 120
Qy 181 TGTGTGTCACCTAATGCTGATGTCCATGCTCTTAGCAGCCTGAATCCAGGGGTGCCCA 240
Db 121 TGTGTGTCACCTAATGCTGATGTCCATGCTCTTAGCAGCCTGAATCCAGGGGTGCCCA 180
Qy 241 GAGGCCACAGGACCGAGCCAGGCTTCTAGGAGATGGTCCAGGAGGCGGCAAGAAT 300
Db 181 GAGGCCACAGGACCGAGCCAGGCTTCTAGGAGATGGTCCAGGAGGCGGCAAGAAT 240
Qy 301 GTGAGTGCAAAAGATTGGTTCTTGAGAGCCCGAGAGAAAATTCATCAGAGTGTCTGGGC 360
Db 241 GTGAGTGCAAAAGATTGGTTCTTGAGAGCCCGAGAGAAAATTCATCAGAGTGTCTGGGC 300
Qy 361 TGCCAAAGAGCAGTGCCCTCTGTGATCATTTCAAGGGCAATGTGAAGAAAACAAGACACC 420
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Qy 421 AAAGGCCACACAGAAAGCCAAACAGCATTCCAGAGCCTCCAGCAATTTCTCAACAAT 480
Db 361 AAAGGCCACACAGAAAGCCAAACAGCATTCCAGAGCCTCCAGCAATTTCTCAACAAT 420
Qy 481 GTCAGCTAAGAGCTTTGGCTCTGCTCTGTAGAGCTCTGAGCGCCCACTTCCCAATTA 540
Db 421 GTCAGCTAAGAGCTTTGGCTCTGCTCTGTAGAGCTCTGAGCGCCCACTTCCCAATTA 480
Qy 541 AACATTCTCAGCCCAAGAGACAGTGAACAACCTACAGACACTCTTCTTCTCCCACTTC 600
Db 481 AACATTCTCAGCCCAAGAGACAGTGAACAACCTACAGACACTCTTCTTCTCCCACTTC 540
Qy 601 ACTCTCCCACTGTACCCACCCCTTAATCATTTCCAGTGTCTCTCAAAAGCATGTTTTCAA 660
Db 541 ACTCTCCCACTGTACCCACCCCTTAATCATTTCCAGTGTCTCTCAAAAGCATGTTTTCAA 600
Qy 661 GATCATTTTGTGTTGGTCTCTCTAGTGTCTTCTCTCTCGTCAGTCTTAGCTGTGCC 720
Db 601 GATCATTTTGTGTTGGTCTCTCTAGTGTCTTCTCTCTCGTCAGTCTTAGCTGTGCC 660
Qy 721 CTCCCC 726
Db 661 CTCCCC 666

RESULT 9
BM854000
LOCUS
DEFINITION
K-EST0136291 S14K402 Homo sapiens cDNA clone S14K402-37-E04 5',
mRNA sequence.
ACCESSION
BM854000
VERSION
BM854000.1 GI:19210399
KEYWORDS
Homo sapiens (human)
EST.
BM854000 664 bp mRNA linear EST 06-MAR-2002

expression library"
/note="Organ: Mammary gland (cancer tissue); Vector:
pCMV6-XL5; Site 1: EcoRI; Site 2: XhoI/Sall compatible and
ligatio; Oligo-dT primed reverse transcription optimized
for large and GC rich mRNA transcripts, cDNA size
selection, optimized ligation for large inserts into
mammalian expression vector, random clones selected for
end sequence verification of full-length genes"

ORIGIN

Query Match 71.5%; Score 622; DB 9; Length 628;
Best Local Similarity 100.0%; Pred. No. 2.1e-157;
Matches 622; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 29 GGACTAAAGCATAGACACAGGCTGAGTATCTGACCTGAGTCATCCCGAGGATCAGG 88
DB 7 GGACTAAAGCATAGACACAGGCTGAGTATCTGACCTGAGTCATCCCGAGGATCAGG 66
QY 89 AGCCTCCAGCAGGGAACCTTCCATTATATTTCTTCAAGCAACTTTACAGCTGCACCGACAGT 148
DB 67 AGCCTCCAGCAGGGAACCTTCCATTATATTTCTTCAAGCAACTTTACAGCTGCACCGACAGT 126
QY 149 TGGATGAAGATTTCTAATCTCTTCCCTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 208
DB 127 TGGATGAAGATTTCTAATCTCTTCCCTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 186
QY 209 GGTCTCTAGCAGCTGAATCCAGGGGTGCGCAGAGGCCACAGGACCGAGGCCAGGCTTC 268
DB 187 GGTCTCTAGCAGCTGAATCCAGGGGTGCGCAGAGGCCACAGGACCGAGGCCAGGCTTC 246
QY 269 TAGGAGATGCTCTCAGGAAGCGCGCCAAAGATGTGAGTGCAAGATTTGGTTCTTGAGAGC 328
DB 247 TAGGAGATGCTCTCAGGAAGCGCGCCAAAGATGTGAGTGCAAGATTTGGTTCTTGAGAGC 306
QY 329 CCCGAGAAGAAATTCATGACAGTGTCTGGGCTGCCAAGAGAGAGTGTGCTGATCA 388
DB 307 CCCGAGAAGAAATTCATGACAGTGTCTGGGCTGCCAAGAGAGAGTGTGCTGATCA 366
QY 389 TTTCAGGGCAATGTGAAGAAACACACACACCAAGGCCACACAGAAAGCCAAACAGCA 448
DB 367 TTTCAGGGCAATGTGAAGAAACACACACACCAAGGCCACACAGAAAGCCAAACAGCA 426
QY 449 TTCCAGAGCTGCGCAGCAATTTCTCAAAACATGTGAGTGAAGAGTGTGCTGCTGCTTT 508
DB 427 TTCCAGAGCTGCGCAGCAATTTCTCAAAACATGTGAGTGAAGAGTGTGCTGCTGCTTT 486
QY 509 GTAGAGCTGTAGGCCCACTCTTCCAAATTAACATTTTCAGCCCAAGAGACAGTGAGC 568
DB 487 GTAGAGCTGTAGGCCCACTCTTCCAAATTAACATTTTCAGCCCAAGAGACAGTGAGC 546
QY 569 ACACCTACAGACACTTCTTCTCCCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 628
DB 547 ACACCTACAGACACTTCTTCTTCTCCCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 606
QY 629 ATTCCAGTGTCTCAAAAAGCA 650
DB 607 ATTCCAGTGTCTCAAAAAGCA 628

RESULT 11
DN998245
LOCUS
DEFINITION
DN998245 Human breast cancer tissue, large insert, pCMV expression
library Homo sapiens cDNA clone TC124609 5', similar to Homo sapiens
DNC (UNQ473), mRNA sequence.
ACCESSION
VERSION
DN998245.1 GI:66258072
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

1 (bases 1 to 628)
Birkett, C., Cho, J., Gau, Y., Hamer, R., Kelly, S., Kovacs, K., Liu, L.,
Liu, X., Porter, J., Sachs, A., Shu, Y., Sun, Z., Wong, J., Wu, M.,
Zhang, X., Jay, G. and He, W.
High-throughput cloning of full-length human cDNAs directly from
cDNA libraries optimized for large and rare transcripts
Unpublished (2005)
Contact: Kovacs, KF
High Throughput cDNA Cloning
Origene Technologies, Inc. (www.origene.com)
6 Taft Court, Suite 100, Rockville, MD 20850, USA
Tel: 301 340 3188
Fax: 301 340 8606
Email: cDNA@origene.com
This EST submission is part of an on-going human full-length
cloning project at Origene Technologies, Inc.
Please contact Origene for access.
Origene Technologies, Inc.
6 Taft Ct. Suite 100
Rockville, MD 20850
Tel: (301) 340-3188
http://www.origene.com
Seq primer: pCMV6 5prime forward vector primer, Origene
Technologies Inc.
Location/Qualifiers
1. 628
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="TC124609"
/tissue type="Breast cancer"
/clone lib="Human breast cancer tissue, large insert, pCMV
expression library"
/notes="Organ: Mammary gland (cancer tissue); Vector:
pCMV6-XL5; Site 1: EcoRI; Site 2: XhoI/Sall compatible and
ligatio; Oligo-dT primed reverse transcription optimized
for large and GC rich mRNA transcripts, cDNA size
selection, optimized ligation for large inserts into
mammalian expression vector, random clones selected for
end sequence verification of full-length genes"

FEATURES
source

ORIGIN

Query Match 71.4%; Score 621.4; DB 9; Length 628;
Best Local Similarity 99.8%; Pred. No. 3.1e-157;
Matches 622; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 36 AGCATAGACACAGGCTGAGTATCTGACCTGAGTCATCCCGAGGATCAGGAGCTCC 95
DB 6 AGCATAGACACAGGCTGAGTATCTGACCTGAGTCATCCCGAGGATCAGGAGCTCC 65
QY 96 AGCAGGGACCTTCCATTATTTCTTCAAGCAACTTTACAGCTGCACCGACAGTTGGATG 155
DB 66 AGCAGGGACCTTCCATTATTTCTTCAAGCAACTTTACAGCTGCACCGACAGTTGGATG 125
QY 156 AAAGTTCTAATCTCTTCCCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 215
DB 126 AAAGTTCTAATCTCTTCCCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 185
QY 216 AGCAGCTGAATCCAGGGTTCGACAGGCCACAGAGCCAGAGCCAGGCTTTAGAGAG 275
DB 186 AGCAGCTGAATCCAGGGTTCGACAGGCCACAGAGCCAGAGCCAGGCTTTAGAGAG 245
QY 276 TGGCTCCAGAGAGGGGCCCAAGATGTGATGCAAGATTTGGTTCTTGAGAGCCCCGAGA 335
DB 246 TGGCTCCAGAGAGGGGCCCAAGATGTGATGCAAGATTTGGTTCTTGAGAGCCCCGAGA 305
QY 336 AGAAATTCATGACAGTGTCTGGGCTGCCAAGAGACAGTGCCTCTGTATCATTTCAAG 395
DB 306 AGAAATTCATGACAGTGTCTGGGCTGCCAAGAGACAGTGCCTCTGTATCATTTCAAG 365
QY 396 GGCATGTGAAGAAACAAAGACACCAAGAGGCCACCAAGAGGCCAAGCAATTCAGA 455
DB 366 GGCATGTGAAGAAACAAAGACACCAAGAGGCCACCAAGAGGCCAAGCAATTCAGA 425


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QY 456 GCCTGCCAGCAATTTCTCAAAACATGTGCTAGCTAAGAGCTTTGCTCTGCTTTGTAGGAG 515
DB 426 GCCTGCCAGCAATTTCTCAAAACATGTGCTAGCTAAGAGCTTTGCTCTGCTTTGTAGGAG 485
QY 516 CTCCTGAGGGCCACATCTTCCCAATTAACAATCTCTAGCCCAAGAGACAGTGAGCACACCTA 575
DB 486 CTCCTGAGGGCCACATCTTCCCAATTAACAATCTCTAGCCCAAGAGACAGTGAGCACACCTA 545
QY 576 CCAGACACTCTTCTTCTCCACCTCACTCTCCACTGTACCCACCCCTAAATCATTTCCAG 635
DB 546 CCAGACACTCTTCTTCTCCACCTCACTCTCCACTGTACCCACCCCTAAATCATTTCCAG 605
QY 636 TGCTCTCAAAAAGCATGTTTTTC 658
DB 606 TGCTCTCAAAAAGCATGTTTTTC 628

RESULT 12
CD688783 631 bp mRNA linear EST 25-JUN-2003
LOCUS EST5305 human nasopharynx Homo sapiens cDNA, mRNA sequence.
DEFINITION CD688783
ACCESSION CD688783
VERSION CD688783.1 GI:32207896
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 631)
AUTHORS Liu,X.-Q., Zhou,Y., Zhang,L.-J., Xu,H., Chen,H.-K., Pan,Z.-G. and
Zeng,Y.-X.
TITLE Transcriptional Gene Expression Profile of Human Nasopharynx
JOURNAL Unpublished (2003)
COMMENT Contact: Yixin Zeng
Cancer Center
Sun Yat-sen University
651 Dongfeng Road East, Guangzhou 510060, China
Tel: 86-1380-9770-743
Fax: 86-20-8775-4506
Email: yxzeng@zsus.edu.cn.

FEATURES
source
1..631
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/tissue_type="normal nasopharynx"
/clone_lib="human nasopharynx"
/note="ESTs generated from a normal nasopharynx cDNA
library from southern Chinese"

ORIGIN
Query Match 69.9%; Score 607.8; DB 5; Length 631;
Best Local Similarity 99.7%; Pred. No. 1.5e-153;
Matches 609; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 37 GCATGACCACACAGGCTGAGTATCTCTGACCTGAGTCATCCCCAGGATCAGGAGCTCCA 96
DB 21 GCATGACCACACAGGCTGAGTATCTCTGACCTGAGTCATCCCCAGGATCAGGAGCTCCA 80
QY 97 GCAGGGAACCTCCATATATATTTCTTCAAGCAACTTACAGCTGCACCGACAGTTGGATGA 156
DB 81 GCAGGGAACCTCCATATATATTTCTTCAAGCAACTTACAGCTGCACCGACAGTTGGATGA 140
QY 157 AGTTCTAATCTTCCCTCTCTCTGCTGCCAATGCTGATGTCATGCTCTCTA 216
DB 141 AGTTCTAATCTTCTCCCTCTCTCTGCTGCCAATGCTGATGTCATGCTCTCTA 200
QY 217 GCAGGCTGAATCCAGGGGTGCGCAGAGGCCACAGGGACCGAGGCCAGGCTTCTAGGAGAT 276
DB 201 GCAGGCTGAATCCAGGGGTGCGCAGAGGCCACAGGGACCGAGGCCAGGCTTCTAGGAGAT 260
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```
QY 277 GGCTCCAGGAGCGCGCAAGATGTGAGTCAAGATTGGTTCTGTGAGAGCCCGAGAA 336
DB 261 GGCTCCAGGAGCGCGCAAGATGTGAGTCAAGATTGGTTCTGTGAGAGCCCGAGAA 320
QY 337 GAAATATCATCAGACAGTGTCTGGGCTGCCAAAGAGACAGTGCCCTGTGATCATTTCAAGG 396
DB 321 GAAATATCATCAGACAGTGTCTGGGCTGCCAAAGAGACAGTGCCCTGTGATCATTTCAAGG 380
QY 397 GCAATGTGAAGAAACAAGACACCAAGGCGACCAAGAAAGCCAAAAGAAGCATTTCCAGAG 456
DB 381 GCAATGTGAAGAAACAAGACACCAAGGCGACCAAGAAAGCCAAAAGAAGCATTTCCAGAG 440
QY 457 CCTGCCAGCAATTTCTCAACAATGTGAGCTAAGAGCTTTGCTGCTTTGTAGGAGC 516
DB 441 CCTGCCAGCAATTTCTCAACAATGTGAGCTAAGAGCTTTGCTGCTTTGTAGGAGC 500
QY 517 TCTGAGGGCCCACTCTTCCCAATTAACAATTTCTGAGCCCAAGAGACAGTGAGCACACCTAC 576
DB 501 TCTGAGGGCCCACTCTTCCCAATTAACAATTTCTGAGCCCAAGAGACAGTGAGCACACCTAC 560
QY 577 CAGACACTCTTCTTCTCCACCTCACTCTCCACTGTACCCACCCCTAAATCATTTCCAGT 636
DB 561 CAGACACTCTTCTTCTCCACCTCACTCTCCACTGTACCCACCCCTAAATCATTTCCAGT 620
QY 637 GCTCTCAAAA 647
DB 621 GCTCTCAAAA 631

RESULT 13
BM746867 628 bp mRNA linear EST 04-MAR-2002
LOCUS K-EST0021326 S6SNU62081 Homo sapiens cDNA clone S6SNU62081-4-A11
DEFINITION 5', mRNA sequence.
ACCESSION BM746867
VERSION BM746867.1 GI:19076451
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 628)
AUTHORS Oh,J.H., Yang,J.O., Hahn,Y., Kim,M.R., Byun,S.S., Jeon,Y.J.,
Kim,J.M., Song,K.S., Noh,S.M., Kim,S., Yoo,H.S., Kim,Y.S. and
Kim,N.S.
TITLE Transcriptome analysis of human gastric cancer
JOURNAL Mamm. Genome 16 (12), 942-954 (2005)
PUBMED 16341674
COMMENT Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr
Plate: 4 row: A column: 11
High quality sequence stop: 628.
Location/Qualifiers
1..628
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="S6SNU62081-4-A11"
/sex="F"
/tissue_type="Ascites"
/cell_type="Scattering floating"
/lab_lines="SNU-620"
/lab_host="Top10F"
/clone_lib="S6SNU62081"
/note="Organ: Stomach; Vector: pCNS; Site_1: EcoRI;
Site 2: NotI; The poly (A) + RNA was dephosphorylated with
bacterial alkaline phosphatase (BAP) and then deapped
```


with tobacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including EcoR I site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dT-selected mRNA by priming with dT-tailed vector. The dT-tailed vector was adjusted to have about 60nt. The cDNA vector was circularized with E. coli DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coli Top10p by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library. After analyzing and sequencing about 2,000 ~ 3,000 colonies in original cDNA library, the abundant cDNAs were selected and amplified by PCR reaction using vector region primer including T7 promoter as 5' primer and N(dT)14 as 3' primer. The PCR products were used as template for synthesis of biotinylated single stranded RNA by in vitro transcription reaction. The synthesized RNA probes were hybridized with antisense single stranded cDNAs prepared from original library and incubated with avidin-gel. After removing DNA-RNA hybrids by centrifuge, the subtracted cDNA libraries were constructed by transformation of the remaining DNA into competent cells E. coli Top10p with electroporation method."

ORIGIN

Query Match 69.8%; Score 607.2; DB 3; Length 628;
Best Local Similarity 98.6%; Pred. No. 2.2e-153;
Matches 612; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 36 AGCATAGACACACGAGCTGAGTATCTGACGTGATCTCCCGAGGATCAGGAGCTCC 95
DB 1 AGCATAGACACACGAGCTGAGTATCTGACGTGATCTCCCGAGGATCAGGAGCTCC 60
QY 96 AGCAGGGAACCTTCCATTATTTCTTCAAGCACTTACAGCTCCACCGACAGTTGGGATG 155
DB 61 AGCAGGGAACCTTCCATTATTTCTTCAAGCACTTACAGCTCCACCGACAGTTGGGATG 120
QY 156 AAAGTTCTATCTTCTCCCTCTCTCTGTTGCTGCCACTAATGCTGATGCTCATGTTCTCT 215
DB 121 AAAGTTCTATCTTCTTCTCCCTCTCTCTGTTGCTGCCACTAATGCTGATGCTCATGTTCTCT 180
QY 216 AGCAGCTGATATCCAGGGTGGCAGAGGCCACAGGACCGAGGCGAGGCTTCTAGGAGA 275
DB 181 AGCAGCTGATATCCAGGGTGGCAGAGGCCACAGGACCGAGGCGAGGCTTCTAGGAGA 240
QY 276 TGGCTCCAGGAGCGGCCAAGATCTGAGTCAAGAGTTGGTTCTGAGGCGCCGAGA 335
DB 241 TGGCTCCAGGAGCGGCCAAGATCTGAGTCAAGAGTTGGTTCTGAGGCGCCGAGA 300
QY 336 AGAAATTCATGACAGTGTCTGGGCTGCCAAGAAGCAGTGCCCTGTGATCATTTCAAG 395
DB 301 AGAAATTCATGACAGTGTCTGGGCTGCCAAGAAGCAGTGCCCTGTGATCATTTCAAG 360
QY 396 GGCATGTGAAGAAAACAAGACACCAAGGACCAACAGAAAGCAACAGCATTCAGAA 455
DB 361 GGCATGTGAAGAAAACAAGACACCAAGGACCAACAGAAAGCAACAGCATTCAGAA 420
QY 456 GCCTGCAGCAATTTCTCAACATGTCAGTCAAGAGCTTGTCTGCTGCTTTGTAGGAG 515
DB 421 GCCTGCAGCAATTTCTCAACATGTCAGTCAAGAGCTTGTCTGCTGCTTTGTAGGAG 480
QY 516 CTCTGAGCGCCACTCTTCCAAATTAACATTTCTCAGCCAGAGAGACAGTGAGCACACCTA 575
DB 481 CTCTGAGCGCCACTCTTCCAAATTAACATTTCTCAGCCAGAGAGACAGTGAGCACACCTA 540
QY 576 CCAGACACTCTTCTTCCACCTCTACTCTCCACTGTACCCACCCCTAAATCATTTCCAG 635
DB 541 CCAGACACTCTTCTTCCACCTCTACTCTCCAAATGTACCCACCCCTAAATCATTTCCAG 600
QY 636 TGCTCTCAAAAAGCATGTTTT 656

Db 601 TGCTCTCAAAAGCCTGTTTT 621

RESULT 14
BU682452/c
LOCUS

DEFINITION

UI-CF-EC1-acf-e-16-0-UI.s1 UI-CF-EC1 Homo sapiens cDNA clone

UI-CF-EC1-acf-e-16-0-UI 3', mRNA sequence.

BU682452 592 bp mRNA linear EST 07-OCT-2002

VERSION BU682452.1 GI:23533364

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 592)

AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.

TITLE Normalization and subtraction: two approaches to facilitate gene

JOURNAL discovery

PUBMED Genome Res. 6 (9), 791-806 (1996)

COMMENT 8889548

Contact: McCray, PB

McCray Lab

University of Iowa

2024 University of Iowa Med Labs, Iowa City, IA 52242, USA

Tel: 319 356 4866

Fax: 319 356 7171

Email: paul-mccray@uiowa.edu

Tissue Procurement: Dr. M. J. Welsh, University of Iowa

cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

Cloning Distribution: Researchers may obtain clones from Research

Genetics (www.resgen.com) or from Open Biosystems

(www.openbiosystems.com).

Seq primer: M13 FORWARD

POLYA=Yes.

Location/Qualifiers

1..592

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

UI-CF-EC1-acf-e-16-0-UI.s1 UI-CF-EC1 Homo sapiens cDNA clone

UI-CF-EC1-acf-e-16-0-UI 3', mRNA sequence.

BU682452 592 bp mRNA linear EST 07-OCT-2002

VERSION BU682452.1 GI:23533364

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 592)

AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.

TITLE Normalization and subtraction: two approaches to facilitate gene

JOURNAL discovery

PUBMED Genome Res. 6 (9), 791-806 (1996)

COMMENT 8889548

Contact: McCray, PB

McCray Lab

University of Iowa

2024 University of Iowa Med Labs, Iowa City, IA 52242, USA

Tel: 319 356 4866

Fax: 319 356 7171

Email: paul-mccray@uiowa.edu

Tissue Procurement: Dr. M. J. Welsh, University of Iowa

cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

Cloning Distribution: Researchers may obtain clones from Research

Genetics (www.resgen.com) or from Open Biosystems

(www.openbiosystems.com).

Seq primer: M13 FORWARD

POLYA=Yes.

Location/Qualifiers

1..592

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="UI-CF-EC1-acf-e-16-0-UI"

/tissue_type="Lung"

/dev_stage="Adult and Fetal"

/lab_host="UI-CF-EC1"

UI-CF-EC1-acf-e-16-0-UI.s1 UI-CF-EC1 Homo sapiens cDNA clone

UI-CF-EC1-acf-e-16-0-UI 3', mRNA sequence.

BU682452 592 bp mRNA linear EST 07-OCT-2002

VERSION BU682452.1 GI:23533364

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 592)

AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.

TITLE Normalization and subtraction: two approaches to facilitate gene

JOURNAL discovery

PUBMED Genome Res. 6 (9), 791-806 (1996)

COMMENT 8889548

Contact: McCray, PB

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2024 University of Iowa Med Labs, Iowa City, IA 52242, USA

Tel: 319 356 4866

Fax: 319 356 7171

Email: paul-mccray@uiowa.edu

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(www.openbiosystems.com).

Seq primer: M13 FORWARD

POLYA=Yes.

Location/Qualifiers

1..592

/organism="Homo sapiens"

/mol_type="mRNA"

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/clone="UI-CF-EC1-acf-e-16-0-UI"

/tissue_type="Lung"

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/lab_host="UI-CF-EC1"

UI-CF-EC1-acf-e-16-0-UI.s1 UI-CF-EC1 Homo sapiens cDNA clone

UI-CF-EC1-acf-e-16-0-UI 3', mRNA sequence.

BU682452 592 bp mRNA linear EST 07-OCT-2002

VERSION BU682452.1 GI:23533364

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 592)

AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.

TITLE Normalization and subtraction: two approaches to facilitate gene

JOURNAL discovery

PUBMED Genome Res. 6 (9), 791-806 (1996)

COMMENT 8889548

Contact: McCray, PB

McCray Lab

University of Iowa

2024 University of Iowa Med Labs, Iowa City, IA 52242, USA

Tel: 319 356 4866

Fax: 319 356 7171

Email: paul-mccray@uiowa.edu

Tissue Procurement: Dr. M. J. Welsh, University of Iowa

cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

Cloning Distribution: Researchers may obtain clones from Research

Genetics (www.resgen.com) or from Open Biosystems

(www.openbiosystems.com).

Seq primer: M13 FORWARD

POLYA=Yes.

Location/Qualifiers

1..592

/organism="Homo sapiens"

/mol_type="mRNA"

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/clone="UI-CF-EC1-acf-e-16-0-UI"

/tissue_type="Lung"

/dev_stage="Adult and Fetal"

/lab_host="UI-CF-EC1"

UI-CF-EC1-acf-e-16-0-UI.s1 UI-CF-EC1 Homo sapiens cDNA clone

UI-CF-EC1-acf-e-16-0-UI 3', mRNA sequence.

BU682452 592 bp mRNA linear EST 07-OCT-2002

VERSION BU682452.1 GI:23533364

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 592)

AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.

TITLE Normalization and subtraction: two approaches to facilitate gene

JOURNAL discovery

PUBMED Genome Res. 6 (9), 791-806 (1996)

COMMENT 8889548

Contact: McCray, PB

McCray Lab

University of Iowa

2024 University of Iowa Med Labs, Iowa City, IA 52242, USA

Tel: 319 356 4866

Fax: 319 356 7171

Email: paul-mccray@uiowa.edu

Tissue Procurement: Dr. M. J. Welsh, University of Iowa

cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

Cloning Distribution: Researchers may obtain clones from Research

Genetics (www.resgen.com) or from Open Biosystems

(www.openbiosystems.com).

Seq primer: M13 FORWARD

POLYA=Yes.

Location/Qualifiers

1..592

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="UI-CF-EC1-acf-e-16-0-UI"

/tissue_type="Lung"

/dev_stage="Adult and Fetal"

/lab_host="UI-CF-EC1"

UI-CF-EC1-acf-e-16-0-UI.s1 UI-CF-EC1 Homo sapiens cDNA clone

UI-CF-EC1-acf-e-16-0-UI 3', mRNA sequence.

BU682452 592 bp mRNA linear EST 07-OCT-2002

VERSION BU682452.1 GI:23533364

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 592)

AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.

TITLE Normalization and subtraction: two approaches to facilitate gene

JOURNAL discovery

PUBMED Genome Res. 6 (9), 791-806 (1996)

COMMENT 8889548

Contact: McCray, PB

McCray Lab

University of Iowa

2024 University of Iowa Med Labs, Iowa City, IA 52242, USA

Tel: 319 356 4866

Fax: 319 356 7171

Email: paul-mccray@uiowa.edu

Tissue Procurement: Dr. M. J. Welsh, University of Iowa

cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

Cloning Distribution: Researchers may obtain clones from Research

Genetics (www.resgen.com) or from Open Biosystems

(www.openbiosystems.com).

Seq primer: M13 FORWARD

POLYA=Yes.

Location/Qualifiers

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UI-CF-EC1-acf-e-16-0-UI.s1 UI-CF-EC1 Homo sapiens cDNA clone

UI-CF-EC1-acf-e-16-0-UI 3', mRNA sequence.

BU682452 592 bp mRNA linear EST 07-OCT-2002

VERSION BU682452.1 GI:23533364

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 592)

AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.

TITLE Normalization and subtraction: two approaches to facilitate gene

JOURNAL discovery

PUBMED Genome Res. 6 (9), 791-806 (1996)

COMMENT 8889548

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McCray Lab

University of Iowa

2024 University of Iowa Med Labs, Iowa City, IA 52242, USA

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Email: paul-mccray@uiowa.edu

Tissue Procurement: Dr. M. J. Welsh, University of Iowa

cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

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Genetics (www.resgen.com) or from Open Biosystems

(www.openbiosystems.com).

Seq primer: M13 FORWARD

POLYA=Yes.

Location/Qualifiers

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/organism="Homo sapiens"

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VERSION DB236758.1 GI:83225873
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 589)
AUTHORS Kimura,K., Wakamatsu,A., Suzuki,Y., Ota,T., Nishikawa,T.,
Yamashita,R., Yamamoto,J., Sekine,M., Teuritani,K., Wakaguri,H.,
Ishii,S., Sugiyama,T., Saito,K., Isono,Y., Irie,R., Kishida,N.,
Yoneyama,T., Otsuka,R., Kanda,K., Yokoi,T., Kondo,H., Wagatsuma,M.,
Murakawa,K., Ishida,S., Iehibashi,T., Takahashi-Fujii,A.,
Tanase,T., Nagai,K., Kikuchi,H., Nakai,K., Isogai,T. and Sugano,S.
Diversification of Transcriptional Modulation: Large-scale
Identification and Characterization of Putative Alternative
Promoters of Human Genes
Genome Res. 16 (1), 55-65 (2006)
16344560
Contact: Takao Isogai
FLJ Project (HRI Team)
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```

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NEDO human cDNA project (New Energy and Industrial Technology
Developmental Organization, Japan); cDNA library construction:
Helix Research Institute (HRI); 5'-end one pass sequencing: HRI,
Research Association for Biotechnology (RAB) and Biotechnology
Center, National Institute of Technology and Evaluation; 3'-end one
pass sequencing: RAB.

FEATURES

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GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

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Listing first 1500 summaries

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756	856.6	98.5	1171	7	US-10-237-435-4
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4	App				Sequence 4, App
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C 867	39.4	4.5	1401	16	US-11-096-568A-4469	Sequence 4469, Ap	C 942	38	4.4	420	8	US-10-021-323-10189	Sequence 10189, A
C 868	39.2	4.5	309	9	US-10-374-930-45013	Sequence 45013, A	C 943	38	4.4	524	4	US-09-925-065A-500749	Sequence 500749,
C 869	39.2	4.5	337	9	US-10-674-124A-22631	Sequence 22631, A	C 944	38	4.4	524	5	US-09-925-065A-500749	Sequence 500749,
C 870	39.2	4.5	571	8	US-10-021-323-7115	Sequence 7115, Ap	945	38	4.4	1034	9	US-10-425-115-171187	Sequence 171187,
C 871	39.2	4.5	587	8	US-10-021-323-15513	Sequence 15513, A	946	38	4.4	1474	8	US-10-818-809-1	Sequence 1, Appli
C 872	39.2	4.5	1873	6	US-10-175-523-37	Sequence 37, Appl	C 947	38	4.4	1533	9	US-10-723-860-7968	Sequence 7968, Ap
C 873	39.2	4.5	1873	13	US-10-723-860-6238	Sequence 6238, Ap	C 948	38	4.4	5164	8	US-10-433-793-152	Sequence 152, App
C 874	39.2	4.5	1873	9	US-11-099-266-37	Sequence 37, Appl	C 949	38	4.4	6319	10	US-10-311-455-1615	Sequence 1615, Ap
C 875	39.2	4.5	5321	8	US-10-257-165-15	Sequence 15, Appl	C 950	38	4.4	294575	10	US-10-737-082-127	Sequence 127, App
C 876	39.2	4.5	5321	8	US-10-240-589C-3	Sequence 3, Appli	C 951	38	4.4	294575	10	US-10-765-790-127	Sequence 127, App
C 877	39	4.5	548	9	US-10-425-115-61583	Sequence 61583, A	C 952	38	4.4	431287	8	US-10-322-281-48	Sequence 48, Appl
C 878	39	4.5	587	9	US-10-425-115-110066	Sequence 110066,	953	37.8	4.3	344	3	US-09-764-891-1788	Sequence 1788, Ap
C 879	39	4.5	600	16	US-11-136-527-7310	Sequence 7310, Ap	954	37.8	4.3	641	8	US-10-424-599-77576	Sequence 77576, A
C 880	39	4.5	1790	7	US-10-170-385-462	Sequence 462, App	955	37.8	4.3	654	12	US-10-301-480-568184	Sequence 568184,
C 881	39	4.5	2118	16	US-11-136-527-3214	Sequence 3214, Ap	956	37.8	4.3	654	12	US-10-301-480-568187	Sequence 568187,
C 882	39	4.5	2211	16	US-11-232-440-36	Sequence 36, Appl	957	37.8	4.3	654	12	US-10-301-480-1181593	Sequence 1181593,
C 883	39	4.5	2249	9	US-10-723-860-6384	Sequence 6384, Ap	958	37.8	4.3	654	12	US-10-301-480-1181596	Sequence 1181596,
C 884	38.8	4.5	413	3	US-09-918-995-17652	Sequence 17652, A	C 959	37.6	4.3	332	9	US-10-357-930-56482	Sequence 56482, A
C 885	38.8	4.5	546	8	US-10-021-323-4518	Sequence 4518, Ap	C 960	37.6	4.3	450	8	US-10-021-323-4616	Sequence 4616, Ap
C 886	38.8	4.5	551	8	US-10-424-599-132498	Sequence 132498,	C 961	37.6	4.3	506	9	US-10-425-115-60121	Sequence 60121, Ap
C 887	38.8	4.5	862	7	US-10-264-043-359	Sequence 359, App	C 962	37.6	4.3	521	8	US-10-424-599-50022	Sequence 50022, A
C 888	38.8	4.5	1042	10	US-10-750-185-57597	Sequence 57597, A	C 963	37.6	4.3	560	8	US-10-021-323-3016	Sequence 3016, Ap
C 889	38.8	4.5	1042	10	US-10-750-623-57597	Sequence 57597, A	C 964	37.6	4.3	579	8	US-10-021-323-6397	Sequence 6397, Ap
C 890	38.8	4.5	2814	4	US-09-925-065A-58402	Sequence 58402, A	C 965	37.6	4.3	8649	8	US-10-221-613-117	Sequence 117, App
C 891	38.8	4.5	2814	5	US-09-925-065A-58402	Sequence 58402, A	C 966	37.6	4.3	8649	8	US-10-221-613-117	Sequence 51, Appl
C 892	38.8	4.5	2814	12	US-10-301-480-159640	Sequence 159640,	C 967	37.6	4.3	16132	10	US-10-504-601-21	Sequence 21, Appl
C 893	38.8	4.5	2814	12	US-10-301-480-773049	Sequence 773049,	968	37.4	4.3	158	3	US-09-768-827-50	Sequence 50, Appl
C 894	38.6	4.4	332	9	US-10-723-860-353	Sequence 353, App	969	37.4	4.3	416	3	US-09-918-995-17909	Sequence 17909, A
C 895	38.6	4.4	332	10	US-10-756-149-379	Sequence 379, App	C 970	37.4	4.3	439	3	US-03-764-891-1336	Sequence 1336, Ap
C 896	38.6	4.4	1083	9	US-10-723-860-5056	Sequence 5056, Ap	C 971	37.4	4.3	500	9	US-10-425-115-5045	Sequence 5045, Ap
C 897	38.6	4.4	2125	3	US-09-880-107-2412	Sequence 2412, Ap	C 972	37.4	4.3	579	9	US-10-425-115-140518	Sequence 140518,
C 898	38.6	4.4	2125	8	US-10-706-791-20	Sequence 20, Appl	C 973	37.4	4.3	638	9	US-10-425-115-94457	Sequence 94457, A
C 899	38.6	4.4	6609	7	US-10-311-455-1856	Sequence 1856, Ap	974	37.4	4.3	932	9	US-10-425-115-105074	Sequence 105074,
C 900	38.4	4.4	417	9	US-10-425-115-209	Sequence 209, App	C 975	37.4	4.3	8111	6	US-10-172-086-55	Sequence 55, Appl
C 901	38.4	4.4	424	6	US-10-198-846-2329	Sequence 2329, Ap	C 976	37.4	4.3	8111	9	US-10-311-507-85	Sequence 85, Appl
C 902	38.4	4.4	488	9	US-10-425-115-108291	Sequence 108291,	C 977	37.4	4.3	8111	9	US-10-480-846-55	Sequence 55, Appl
C 903	38.4	4.4	499	8	US-10-021-323-1716	Sequence 1716, Ap	C 978	37.4	4.3	14950	7	US-10-311-455-1230	Sequence 1230, Ap
C 904	38.4	4.4	565	4	US-09-925-065A-500019	Sequence 500019,	979	37.4	4.3	80226	13	US-11-097-143-25216	Sequence 25216, A
C 905	38.4	4.4	565	4	US-09-925-065A-500020	Sequence 500020,	C 980	37.4	4.3	111836	8	US-10-322-281-51	Sequence 51, Appl
C 906	38.4	4.4	565	5	US-09-925-065A-500019	Sequence 500019,	C 981	37.2	4.3	426	3	US-09-960-352-13817	Sequence 13817, A
C 907	38.4	4.4	565	5	US-09-925-065A-500020	Sequence 500020,	C 982	37.2	4.3	565	8	US-10-021-323-11255	Sequence 11125, A
C 908	38.4	4.4	649	8	US-10-424-599-16518	Sequence 16518, A	C 983	37.2	4.3	607	9	US-10-425-115-57557	Sequence 57557, A
C 909	38.4	4.4	1072	6	US-10-021-811-57	Sequence 57, Appl	C 984	37.2	4.3	1172	16	US-11-136-527-808	Sequence 808, App
C 910	38.4	4.4	1072	8	US-10-659-869-57	Sequence 57, Appl	985	37.2	4.3	1172	16	US-11-136-527-808	Sequence 4904, App
C 911	38.4	4.4	1954	9	US-10-723-860-7576	Sequence 7576, Ap	C 986	37.2	4.3	2274	9	US-10-425-115-169213	Sequence 169213,
C 912	38.4	4.4	2890	10	US-10-487-078-147	Sequence 147, App	C 987	37.2	4.3	2549	3	US-09-764-898-82	Sequence 82, Appl
C 913	38.4	4.4	2890	10	US-10-487-078-147	Sequence 147, App	C 988	37.2	4.3	2911	7	US-10-264-049-283	Sequence 283, App
C 914	38.4	4.4	1595	7	US-10-311-455-1570	Sequence 1570, Ap	C 989	37.2	4.3	6577	8	US-10-311-455-1329	Sequence 1329, App
C 915	38.4	4.4	1595	7	US-10-240-453-269	Sequence 269, App	C 990	37.2	4.3	6577	8	US-10-221-613-181	Sequence 181, App
C 916	38.4	4.4	3673778	7	US-10-312-841-1	Sequence 1, Appli	C 991	37.2	4.3	240825	3	US-09-790-289-1	Sequence 1, Appli
C 917	38.4	4.4	277	3	US-09-764-877-22	Sequence 22, Appl	C 992	37.2	4.3	240825	8	US-10-468-582-1	Sequence 1, Appli
C 918	38.2	4.4	277	3	US-10-242-515-22	Sequence 22, Appl	C 993	37.2	4.3	240825	8	US-10-468-582-1	Sequence 1, Appli
C 919	38.2	4.4	277	7	US-10-242-515-22	Sequence 22, Appl	C 994	37.2	4.3	240825	8	US-10-468-582-1	Sequence 1, Appli

c 993	37.2	4.3	240825	13	US-11-028-971-1	Sequence 1, Appl1	1066	36.6	4.2	7781	7	US-10-311-455-1142	Sequence 1142, Ap
c 994	37	4.3	137	10	US-10-631-467-1322	Sequence 1322, Ap	c1067	36.6	4.2	16439	17	US-10-311-455-860	Sequence 860, App
c 995	37	4.3	240	8	US-10-437-963-102161	Sequence 102161, Ap	c1068	36.6	4.2	96583	15	US-11-117-187-203	Sequence 203, App
c 996	37	4.3	231	8	US-10-621-901-1971	Sequence 1971, Ap	1069	36.4	4.2	201	16	US-11-124-367A-8285	Sequence 8285, Ap
c 997	37	4.3	409	3	US-09-918-995-36415	Sequence 36415, A	1070	36.4	4.2	201	16	US-11-124-367A-8286	Sequence 8286, Ap
c 998	37	4.3	444	7	US-10-422-355-263	Sequence 263, App	c1071	36.4	4.2	201	16	US-11-124-367A-10925	Sequence 10925, A
c 999	37	4.3	507	9	US-10-425-115-113680	Sequence 113680, A	c1072	36.4	4.2	201	16	US-11-124-367A-12635	Sequence 12635, A
c 1000	37	4.3	516	8	US-10-021-323-16996	Sequence 16996, A	1073	36.4	4.2	261	8	US-10-242-535A-8796	Sequence 8796, A
c 1001	37	4.3	580	8	US-10-424-599-111106	Sequence 111106, A	c1074	36.4	4.2	261	8	US-10-085-783A-8796	Sequence 8796, Ap
c 1002	37	4.3	619	12	US-10-301-480-33171	Sequence 33171, A	c1075	36.4	4.2	286	9	US-10-425-115-31235	Sequence 11235, A
c 1003	37	4.3	619	12	US-10-301-480-645580	Sequence 645580, A	1076	36.4	4.2	395	9	US-10-425-115-134040	Sequence 134040, A
c 1004	37	4.3	657	8	US-10-424-599-89835	Sequence 89835, A	c1077	36.4	4.2	423	8	US-10-437-963-59850	Sequence 59850, A
c 1005	37	4.3	1059	8	US-10-424-599-112556	Sequence 112556, A	c1078	36.4	4.2	424	3	US-09-814-353-2211	Sequence 2211, Ap
c 1006	37	4.3	1130	9	US-10-425-115-132399	Sequence 132399, A	c1079	36.4	4.2	424	3	US-09-814-353-8551	Sequence 8551, Ap
c 1007	37	4.3	1316	9	US-10-425-115-109626	Sequence 109626, A	1080	36.4	4.2	441	9	US-10-425-115-95129	Sequence 95129, A
c 1008	37	4.3	1400	16	US-11-136-527-7203	Sequence 7203, Ap	1081	36.4	4.2	459	8	US-10-437-963-6545	Sequence 6545, Ap
c 1009	37	4.3	1856	10	US-10-750-185-53997	Sequence 53997, A	1082	36.4	4.2	577	4	US-09-925-065A-339698	Sequence 339698, A
c 1010	37	4.3	1856	10	US-10-750-623-53997	Sequence 53997, A	1083	36.4	4.2	577	4	US-09-925-065A-339698	Sequence 339698, A
c 1011	37	4.3	1967	16	US-11-136-527-3107	Sequence 3107, Ap	1084	36.4	4.2	578	3	US-09-745-288-95	Sequence 95, Appl
c 1012	37	4.3	2282	8	US-10-424-599-39005	Sequence 39005, A	1085	36.4	4.2	578	3	US-09-825-301-30	Sequence 30, Appl
c 1013	37	4.3	3393	7	US-10-311-455-144	Sequence 144, App	1086	36.4	4.2	578	7	US-10-033-527-30	Sequence 30, Appl
c 1014	37	4.3	5397	7	US-10-311-455-2178	Sequence 2178, Ap	1087	36.4	4.2	578	8	US-10-453-919-95	Sequence 95, Appl
c 1015	37	4.3	6136	8	US-10-257-166-123	Sequence 123, App	1088	36.4	4.2	582	12	US-10-301-480-412715	Sequence 412715, A
c 1016	37	4.3	8234	7	US-10-311-455-1632	Sequence 1632, Ap	1089	36.4	4.2	582	12	US-10-301-480-1026124	Sequence 1026124, A
c 1017	37	4.3	10039	7	US-10-311-455-2015	Sequence 2015, Ap	c1090	36.4	4.2	607	4	US-09-925-065A-91145	Sequence 91145, A
c 1018	36.8	4.2	201	16	US-11-124-367A-8282	Sequence 8282, Ap	c1091	36.4	4.2	607	5	US-09-925-065A-91145	Sequence 91145, A
c 1019	36.8	4.2	282	9	US-10-357-930-47794	Sequence 47794, A	c1092	36.4	4.2	607	12	US-10-301-480-192386	Sequence 192386, A
c 1020	36.8	4.2	360	9	US-10-357-930-59073	Sequence 59073, A	c1093	36.4	4.2	607	12	US-10-301-480-805795	Sequence 805795, A
c 1021	36.8	4.2	367	9	US-10-425-115-171575	Sequence 171575, A	c1094	36.4	4.2	624	6	US-10-066-543-491	Sequence 491, App
c 1022	36.8	4.2	370	9	US-10-357-930-7949	Sequence 7949, Ap	1095	36.4	4.2	627	6	US-10-198-846-8297	Sequence 8297, App
c 1023	36.8	4.2	391	9	US-10-723-860-3748	Sequence 3748, Ap	1096	36.4	4.2	662	12	US-10-301-480-534274	Sequence 534274, A
c 1024	36.8	4.2	391	9	US-10-756-149-3657	Sequence 3657, Ap	1097	36.4	4.2	662	12	US-10-301-480-1147683	Sequence 1147683, A
c 1025	36.8	4.2	407	9	US-10-425-115-86072	Sequence 86072, A	c1098	36.4	4.2	758	9	US-10-425-115-42510	Sequence 42510, A
c 1026	36.8	4.2	445	3	US-09-814-353-17408	Sequence 17408, A	1099	36.4	4.2	826	7	US-10-266-829-35	Sequence 35, Appl
c 1027	36.8	4.2	483	8	US-10-021-323-13466	Sequence 13466, A	1100	36.4	4.2	826	10	US-10-878-523-35	Sequence 35, Appl
c 1028	36.8	4.2	598	8	US-10-767-701-24993	Sequence 24993, A	1101	36.4	4.2	880	9	US-10-425-115-161875	Sequence 161875, A
c 1029	36.8	4.2	631	9	US-10-363-345A-11729	Sequence 11729, A	1102	36.4	4.2	924	8	US-10-424-599-69395	Sequence 69395, A
c 1030	36.8	4.2	631	9	US-10-363-345A-11730	Sequence 11730, A	1103	36.4	4.2	952	9	US-10-425-115-65097	Sequence 65097, A
c 1031	36.8	4.2	631	10	US-10-363-483A-11729	Sequence 11729, A	1104	36.4	4.2	977	9	US-10-425-115-19711	Sequence 19711, A
c 1032	36.8	4.2	631	10	US-10-363-483A-11730	Sequence 11730, A	1105	36.4	4.2	1129	9	US-10-425-115-88252	Sequence 88252, A
c 1033	36.8	4.2	638	5	US-09-925-065A-766318	Sequence 766318, A	1106	36.4	4.2	1301	9	US-10-425-115-179473	Sequence 179473, A
c 1034	36.8	4.2	638	5	US-09-925-065A-766318	Sequence 766318, A	1107	36.4	4.2	1301	9	US-10-264-237-570	Sequence 570, App
c 1035	36.8	4.2	838	6	US-10-027-632-142219	Sequence 142219, A	1108	36.4	4.2	1515	9	US-10-425-115-66881	Sequence 66881, A
c 1036	36.8	4.2	838	7	US-10-027-632-142219	Sequence 142219, A	1109	36.4	4.2	1515	10	US-10-750-185-31803	Sequence 31803, A
c 1037	36.8	4.2	1290	7	US-10-321-204-8	Sequence 8, Appl1	c1110	36.4	4.2	1675	10	US-10-750-623-31803	Sequence 31803, A
c 1038	36.8	4.2	1305	12	US-10-301-480-32738	Sequence 32738, A	1111	36.4	4.2	2304	6	US-10-198-846-13978	Sequence 13978, A
c 1039	36.8	4.2	1305	12	US-10-301-480-646147	Sequence 646147, A	1112	36.4	4.2	2479	10	US-10-789-378-51	Sequence 51, Appl
c 1040	36.8	4.2	1333	8	US-10-424-599-59340	Sequence 59340, A	1113	36.4	4.2	2479	10	US-10-955-054A-50	Sequence 50, Appl
c 1041	36.8	4.2	1400	13	US-11-060-756-1074	Sequence 1074, Ap	c1114	36.4	4.2	2865	8	US-10-221-714A-42	Sequence 42, Appl
c 1042	36.8	4.2	1400	13	US-11-060-756-5346	Sequence 5346, Ap	1115	36.4	4.2	3009	8	US-10-424-599-132002	Sequence 132002, A
c 1043	36.8	4.2	1697	3	US-09-862-027-7	Sequence 7, Appl1	c1116	36.4	4.2	8305	7	US-10-311-455-1541	Sequence 1541, Ap
c 1044	36.8	4.2	1697	10	US-10-989-228-7	Sequence 9, Appl1	1117	36.4	4.2	12010	9	US-10-723-860-5515	Sequence 5515, Ap
c 1045	36.8	4.2	2100	9	US-10-788-792-94	Sequence 94, Appl	c1118	36.4	4.2	12010	9	US-10-723-860-5559	Sequence 5559, Ap
c 1046	36.8	4.2	2111	6	US-10-198-846-13921	Sequence 13921, A	c1119	36.4	4.2	169865	11	US-10-330-773-32	Sequence 32, Appl
c 1047	36.8	4.2	3217	6	US-10-027-632-114758	Sequence 114758, A	1120	36.2	4.2	238	9	US-10-357-930-60315	Sequence 60315, A
c 1048	36.8	4.2	3217	7	US-10-027-632-114758	Sequence 114758, A	c1121	36.2	4.2	282	8	US-10-021-323-14775	Sequence 14775, A
c 1049	36.8	4.2	5511	7	US-10-311-455-1844	Sequence 1844, Ap	c1122	36.2	4.2	328	8	US-10-021-323-7832	Sequence 7832, Ap
c 1050	36.8	4.2	14112	8	US-10-311-455-1416	Sequence 1416, Ap	c1123	36.2	4.2	358	3	US-09-960-352-5559	Sequence 5559, Ap
c 1051	36.8	4.2	14112	8	US-10-221-714A-200	Sequence 200, App	c1124	36.2	4.2	410	8	US-10-424-599-83877	Sequence 83877, A
c 1052	36.8	4.2	14112	8	US-10-433-793-10	Sequence 10, Appl	c1125	36.2	4.2	423	9	US-10-425-115-96492	Sequence 96492, A
c 1053	36.8	4.2	57889	11	US-10-330-773-1	Sequence 1, Appl1	1126	36.2	4.2	439	3	US-09-922-293-1138	Sequence 1138, Ap
c 1054	36.8	4.2	254396	11	US-10-330-773-534	Sequence 534, App	1127	36.2	4.2	507	8	US-10-424-599-96388	Sequence 96388, A
c 1055	36.6	4.2	265	9	US-10-357-930-48840	Sequence 48840, A	c1128	36.2	4.2	521	9	US-10-425-115-81195	Sequence 81195, A
c 1056	36.6	4.2	458	9	US-10-425-115-107782	Sequence 107782, A	c1129	36.2	4.2	558	9	US-10-425-115-112505	Sequence 112505, A
c 1057	36.6	4.2	588	6	US-10-027-632-70592	Sequence 70592, A	c1130	36.2	4.2	600	10	US-10-972-079-68289	Sequence 68289, A
c 1058	36.6	4.2	588	6	US-10-027-632-71173	Sequence 71173, A	c1131	36.2	4.2	616	8	US-10-424-599-101283	Sequence 101283, A
c 1059	36.6	4.2	588	6	US-10-027-632-312205	Sequence 312205, A	c1132	36.2	4.2	673	10	US-10-764-420-1723	Sequence 1723, Ap
c 1060	36.6	4.2	588	7	US-10-027-632-70592	Sequence 70592, A	1133	36.2	4.2	989	12	US-10-301-480-557831	Sequence 557831, A
c 1061	36.6	4.2	588	7	US-10-027-632-71173	Sequence 71173, A	c1134	36.2	4.2	989	12	US-10-301-480-1171240	Sequence 1171240, A
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122	34.8	4.0	399	3	US-09-621-976-8976	Sequence 8976, Ap	c 195	33.8	3.9	552	3	US-09-270-767-8781	Sequence 8781, Ap
123	34.8	4.0	612	3	US-09-385-982-280	Sequence 280, App	c 196	33.8	3.9	552	3	US-09-270-767-24063	Sequence 24063, A
124	34.8	4.0	805	3	US-09-809-545A-70	Sequence 70, Appl	c 197	33.8	3.9	711	3	US-09-621-976-17854	Sequence 17854, A
125	34.8	4.0	977	3	US-09-484-970B-137	Sequence 137, App	c 198	33.8	3.9	837	4	US-09-297-648-4026	Sequence 4026, Ap
126	34.8	4.0	2066	3	US-09-205-258-105	Sequence 105, App	c 199	33.8	3.9	943	3	US-09-149-476-35	Sequence 35, Appl
127	34.8	4.0	2066	3	US-10-004-860-105	Sequence 105, App	c 200	33.8	3.9	1925	3	US-09-148-545-128	Sequence 128, App
128	34.6	4.0	307	3	US-09-621-976-16246	Sequence 16246, A	c 201	33.8	3.9	1925	3	US-09-621-011-128	Sequence 128, App
129	34.6	4.0	601	3	US-09-949-016-146956	Sequence 146956, A	c 202	33.8	3.9	2379	4	US-10-036-041-71	Sequence 71, Appl
130	34.6	4.0	997	3	US-09-907-794A-376	Sequence 376, App	c 203	33.8	3.9	3060	3	US-09-991-181-504	Sequence 504, App
131	34.6	4.0	997	3	US-09-905-125A-376	Sequence 376, App	c 204	33.8	3.9	3060	3	US-09-990-444-504	Sequence 504, App
132	34.6	4.0	997	3	US-09-902-775A-376	Sequence 376, App	c 205	33.8	3.9	3060	3	US-09-997-333-504	Sequence 504, App
133	34.6	4.0	997	3	US-09-906-700-376	Sequence 376, App	c 206	33.8	3.9	3060	3	US-09-992-598-504	Sequence 504, App
134	34.6	4.0	997	3	US-09-903-603A-376	Sequence 376, App	c 207	33.8	3.9	3060	4	US-09-989-735-504	Sequence 504, App
135	34.6	4.0	997	3	US-09-904-920A-376	Sequence 376, App	c 208	33.8	3.9	3060	5	US-09-989-726-504	Sequence 504, App
136	34.6	4.0	997	3	US-09-909-064-376	Sequence 376, App	c 209	33.8	3.9	3060	5	US-09-997-514-504	Sequence 504, App
137	34.6	4.0	997	3	US-09-905-381A-376	Sequence 376, App	c 210	33.8	3.9	3060	5	US-09-989-728-504	Sequence 504, App
138	34.6	4.0	997	3	US-09-906-618-376	Sequence 376, App	c 211	33.8	3.9	3060	5	US-09-997-349-504	Sequence 504, App
139	34.6	4.0	997	3	US-09-906-646-376	Sequence 376, App	c 212	33.8	3.9	3060	5	US-09-997-653-504	Sequence 504, App
140	34.6	4.0	997	3	US-09-904-462-376	Sequence 376, App	c 213	33.8	3.9	3060	5	US-09-989-232A-504	Sequence 504, App
141	34.6	4.0	997	3	US-09-902-736A-376	Sequence 376, App	c 214	33.8	3.9	5852	2	US-07-867-106-2	Sequence 2, Appl
142	34.6	4.0	997	3	US-09-906-722A-376	Sequence 376, App	c 215	33.8	3.9	7724	3	US-10-314-739A-1	Sequence 1, Appl
143	34.6	4.0	997	4	US-09-905-449-376	Sequence 376, App	c 216	33.8	3.9	7724	3	US-08-486-049-1	Sequence 1, Appl
144	34.6	4.0	997	4	US-09-903-562B-376	Sequence 376, App	c 217	33.8	3.9	9058	3	US-09-653-285-9	Sequence 9, Appl
145	34.6	4.0	997	4	US-09-903-562B-376	Sequence 376, App	c 218	33.8	3.9	9058	3	US-09-653-285-9	Sequence 9, Appl
146	34.6	4.0	997	4	US-09-907-841-376	Sequence 376, App	c 219	33.8	3.9	17353	3	US-09-949-016-13437	Sequence 13437, A
147	34.6	4.0	1414	3	US-09-501-115-5	Sequence 5, Appl	c 220	33.8	3.9	19124	2	US-08-487-846B-13	Sequence 13, Appl
148	34.6	4.0	1414	3	US-10-357-886-5	Sequence 5, Appl	c 221	33.8	3.9	33227	3	US-09-949-016-14108	Sequence 14108, A
149	34.6	4.0	253345	3	US-09-949-016-12656	Sequence 12656, A	c 222	33.8	3.9	174170	3	US-09-949-016-14810	Sequence 14810, A
150	34.6	4.0	253364	3	US-09-949-016-13639	Sequence 13639, A	c 223	33.8	3.9	174170	3	US-09-949-016-14811	Sequence 14811, A
151	34.6	4.0	267482	3	US-09-949-002-659	Sequence 659, App	c 224	33.8	3.9	174318	3	US-09-949-016-11880	Sequence 11880, A
152	34.6	4.0	267505	3	US-09-949-002-783	Sequence 783, App	c 225	33.8	3.9	174318	3	US-09-949-016-14812	Sequence 14812, A
153	34.6	4.0	374159	3	US-09-949-016-15868	Sequence 15868, A	c 226	33.8	3.9	174318	3	US-09-949-016-14813	Sequence 14813, A
154	34.4	4.0	600	2	US-08-187-186A-1	Sequence 1, Appl	c 227	33.8	3.9	227979	3	US-09-949-016-11842	Sequence 11842, A
155	34.4	4.0	600	2	US-08-442-497C-1	Sequence 1, Appl	c 228	33.8	3.9	784019	3	US-09-949-016-14033	Sequence 14033, A
156	34.4	4.0	600	3	US-09-333-033-1	Sequence 1, Appl	c 229	33.8	3.9	828152	3	US-09-949-016-12777	Sequence 12777, A
157	34.4	4.0	600	3	US-10-004-832-1	Sequence 1, Appl	c 230	33.6	3.9	358	2	US-08-721-488-9	Sequence 9, Appl
158	34.4	4.0	600	7	PCT-US94-05186-1	Sequence 1, Appl	c 231	33.6	3.9	601	3	US-09-949-016-120219	Sequence 120219, A
159	34.4	4.0	692	3	US-09-328-111-285	Sequence 285, App	c 232	33.6	3.9	611	3	US-09-205-258-109	Sequence 109, App
160	34.4	4.0	1792	3	US-08-747-221B-18	Sequence 18, Appl	c 233	33.6	3.9	611	3	US-10-004-860-109	Sequence 109, App
161	34.4	4.0	1792	3	US-08-747-221B-20	Sequence 20, Appl	c 234	33.6	3.9	931	3	US-09-482-273-31	Sequence 31, Appl
162	34.4	4.0	1792	3	US-09-005-051-18	Sequence 20, Appl	c 235	33.6	3.9	1191	2	US-08-671-320-14	Sequence 14, Appl
163	34.4	4.0	1792	3	US-09-005-051-20	Sequence 20, Appl	c 236	33.6	3.9	1191	2	US-08-868-577-14	Sequence 14, Appl
164	34.4	4.0	1792	3	US-09-403-943F-18	Sequence 18, Appl	c 237	33.6	3.9	1196	3	US-09-207-914-14	Sequence 2, Appl
165	34.4	4.0	1792	3	US-09-403-943F-20	Sequence 20, Appl	c 238	33.6	3.9	1196	3	US-09-065-040-2	Sequence 2, Appl
166	34.4	4.0	2668	3	US-09-370-838-156	Sequence 156, App	c 239	33.6	3.9	1210	3	US-09-244-805-45	Sequence 45, Appl
167	34.4	4.0	2668	3	US-09-854-133-156	Sequence 156, App	c 240	33.6	3.9	1230	3	US-09-244-805-6	Sequence 6, Appl
168	34.2	3.9	519	3	US-09-328-111-415	Sequence 415, App	c 241	33.6	3.9	2002	3	US-09-819-993-1	Sequence 1, Appl
169	34.2	3.9	990	3	US-09-800-728-79	Sequence 79, Appl	c 242	33.6	3.9	2002	3	US-10-193-295-1	Sequence 1, Appl

243	33.6	3.9	2002	3	US-10-622-516-1	Sequence 1, Appl1	c 316	33.2	3.8	17331	3	US-09-949-016-14503	Sequence 14503, A
244	33.6	3.9	2123	3	US-09-724-864-18	Sequence 18, Appl1	c 317	33.2	3.8	23849	3	US-09-949-016-13813	Sequence 13813, A
245	33.6	3.9	2498	3	US-07-943-843-3	Sequence 3, Appl1	c 318	33.2	3.8	24040	3	US-09-949-016-12118	Sequence 12118, A
246	33.6	3.9	2498	2	US-08-347-003-3	Sequence 3, Appl1	c 319	33.2	3.8	42053	3	US-09-949-016-15924	Sequence 15924, A
247	33.6	3.9	2504	2	US-08-946-412-1	Sequence 1, Appl1	c 320	33.2	3.8	69263	3	US-09-949-016-12594	Sequence 12594, A
248	33.6	3.9	2714	3	US-09-949-016-1021	Sequence 1021, Ap	c 321	33.2	3.8	69709	3	US-09-949-016-16036	Sequence 16036, A
249	33.6	3.9	2789	3	US-09-136-282-3	Sequence 3, Appl1	c 322	33.2	3.8	77036	3	US-09-949-016-16156	Sequence 16156, A
250	33.6	3.9	2789	3	US-09-505-744-3	Sequence 3, Appl1	c 323	33.2	3.8	101558	3	US-09-949-016-12243	Sequence 12243, A
251	33.6	3.9	6896	3	US-09-573-080A-422	Sequence 422, App	c 324	33.2	3.8	151256	3	US-09-949-016-12674	Sequence 12674, A
252	33.6	3.9	6896	5	US-09-854-867-422	Sequence 422, App	c 325	33.2	3.8	151261	3	US-09-949-016-13242	Sequence 13242, A
253	33.6	3.9	8220	2	US-08-568-459A-11	Sequence 11, Appl	c 326	33.2	3.8	235064	3	US-09-949-016-15390	Sequence 15390, A
254	33.6	3.9	8220	2	US-08-487-826B-11	Sequence 11, Appl	c 327	33	3.8	194	3	US-09-621-976-9596	Sequence 9596, Ap
255	33.6	3.9	8220	3	US-09-210-288-11	Sequence 11, Appl	c 328	33	3.8	247	2	US-08-691-641-4	Sequence 4, Appl1
256	33.6	3.9	8220	3	US-10-153-273-11	Sequence 11, Appl	c 329	33	3.8	275	3	US-09-328-111-385	Sequence 385, App
257	33.6	3.9	54945	3	US-09-967-669-10	Sequence 10, Appl	c 330	33	3.8	300	3	US-09-621-976-16227	Sequence 16227, A
258	33.6	3.9	65485	3	US-09-949-016-12303	Sequence 13757, A	c 331	33	3.8	323	3	US-09-621-976-10374	Sequence 10374, A
259	33.6	3.9	65552	3	US-09-949-016-12303	Sequence 12303, A	c 332	33	3.8	347	3	US-09-621-976-16136	Sequence 16136, A
260	33.6	3.9	83938	3	US-09-949-016-16068	Sequence 16068, A	c 333	33	3.8	444	3	US-08-688-988-44	Sequence 44, Appl
261	33.6	3.9	219964	3	US-09-949-016-15086	Sequence 15086, A	c 334	33	3.8	457	3	US-09-385-982-15	Sequence 15, Appl
262	33.6	3.9	227750	3	US-09-949-016-17175	Sequence 17175, A	c 335	33	3.8	505	3	US-09-621-976-15639	Sequence 15639, A
263	33.4	3.8	140	2	US-08-628-417-5	Sequence 5, Appl1	c 336	33	3.8	601	3	US-09-949-016-203410	Sequence 203410,
264	33.4	3.8	147	3	US-09-621-976-10383	Sequence 10383, A	c 337	33	3.8	601	3	US-09-949-016-203411	Sequence 203411,
265	33.4	3.8	191	3	US-09-621-976-10184	Sequence 10184, A	c 338	33	3.8	601	3	US-09-949-016-203412	Sequence 203412,
266	33.4	3.8	240	2	US-08-628-417-6	Sequence 6, Appl1	c 339	33	3.8	607	3	US-09-809-545A-19	Sequence 19, Appl
267	33.4	3.8	348	3	US-09-621-976-16137	Sequence 16137, A	c 340	33	3.8	700	3	US-09-735-271-1096	Sequence 1096, Ap
268	33.4	3.8	601	3	US-09-949-016-58445	Sequence 58445, A	c 341	33	3.8	1049	3	US-09-800-729-67	Sequence 67, Appl
269	33.4	3.8	1074	3	US-09-248-335-67	Sequence 67, Appl	c 342	33	3.8	1249	3	US-09-461-325-128	Sequence 128, App
270	33.4	3.8	1100	3	US-07-861-458C-4	Sequence 4, Appl1	c 343	33	3.8	1249	3	US-10-012-543-128	Sequence 128, App
271	33.4	3.8	1114	3	US-09-152-060-4	Sequence 41, Appl	c 344	33	3.8	1249	3	US-10-115-123-128	Sequence 128, App
272	33.4	3.8	1114	3	US-09-852-797-41	Sequence 41, Appl	c 345	33	3.8	1260	3	US-09-461-323-93	Sequence 93, Appl
273	33.4	3.8	1114	3	US-09-853-161-41	Sequence 41, Appl	c 346	33	3.8	1260	3	US-10-012-543-93	Sequence 93, Appl
274	33.4	3.8	1114	3	US-10-058-993-41	Sequence 41, Appl	c 347	33	3.8	1260	3	US-10-115-123-93	Sequence 93, Appl
275	33.4	3.8	1129	3	US-09-227-357-40	Sequence 40, Appl	c 348	33	3.8	1401	4	US-09-605-703B-543	Sequence 543, App
276	33.4	3.8	1129	3	US-09-973-278-80	Sequence 80, Appl	c 349	33	3.8	1738	2	US-08-379-482A-2	Sequence 2, Appl1
277	33.4	3.8	1141	3	US-09-806-708B-22	Sequence 22, Appl	c 350	33	3.8	2158	2	US-07-602-608-1	Sequence 1, Appl1
278	33.4	3.8	1461	3	US-08-722-126A-4	Sequence 4, Appl1	c 351	33	3.8	2158	2	US-08-261-578-1	Sequence 1, Appl1
279	33.4	3.8	1461	7	PCT-US95-04258-4	Sequence 4, Appl1	c 352	33	3.8	3299	3	US-09-800-729-68	Sequence 68, Appl
280	33.4	3.8	1468	3	US-09-205-258-142	Sequence 142, App	c 353	33	3.8	3581	2	US-08-738-349-1	Sequence 1, Appl1
281	33.4	3.8	1468	3	US-10-004-860-142	Sequence 142, App	c 354	33	3.8	50217	3	US-09-949-016-16067	Sequence 16067, A
282	33.4	3.8	1540	3	US-08-977-001-2	Sequence 2, Appl1	c 355	33	3.8	76962	3	US-09-949-016-17482	Sequence 17482, A
283	33.4	3.8	1606	3	US-09-820-004-1	Sequence 1, Appl1	c 356	33	3.8	390416	3	US-09-949-016-16923	Sequence 16923, A
284	33.4	3.8	2043	3	US-09-614-912-171	Sequence 171, App	c 357	32.8	3.8	250	3	US-09-621-976-18363	Sequence 18363, A
285	33.4	3.8	3593	3	US-09-645-069-22	Sequence 22, Appl	c 358	32.8	3.8	386	3	US-10-131-827-8646	Sequence 8646, Ap
286	33.4	3.8	3593	3	US-09-644-934-10	Sequence 10, Appl	c 359	32.8	3.8	386	5	US-10-131-831-8646	Sequence 8646, Ap
287	33.4	3.8	3593	5	US-10-115-609-22	Sequence 22, Appl	c 360	32.8	3.8	445	3	US-09-247-155-53	Sequence 53, Appl
288	33.4	3.8	18999	3	US-09-949-002-703	Sequence 703, App	c 361	32.8	3.8	445	3	US-09-903-190-53	Sequence 53, Appl
289	33.4	3.8	26225	5	US-09-584-429-448	Sequence 448, App	c 362	32.8	3.8	601	3	US-09-949-016-27649	Sequence 27649, A
290	33.4	3.8	27271	3	US-09-949-002-622	Sequence 622, App	c 363	32.8	3.8	601	3	US-09-949-016-158180	Sequence 158180,
291	33.4	3.8	130724	3	US-09-949-016-13753	Sequence 13753, A	c 364	32.8	3.8	601	3	US-09-949-016-199729	Sequence 199729,
292	33.4	3.8	580073	3	US-08-545-528D-1	Sequence 1, Appl1	c 365	32.8	3.8	903	7	PCT-US95-06406A-21	Sequence 21, Appl
293	33.2	3.8	364	3	US-09-621-976-17202	Sequence 17202, A	c 366	32.8	3.8	963	3	US-09-328-352-400	Sequence 400, App
294	33.2	3.8	601	3	US-09-949-016-27650	Sequence 27650, A	c 367	32.8	3.8	1117	3	US-09-247-373B-33	Sequence 33, Appl
295	33.2	3.8	601	3	US-09-949-016-34608	Sequence 34608, A	c 368	32.8	3.8	1189	3	US-09-716-123-46	Sequence 46, Appl
296	33.2	3.8	601	3	US-09-949-016-70844	Sequence 70844, A	c 369	32.8	3.8	1212	3	US-09-182-145-34	Sequence 34, Appl
297	33.2	3.8	601	3	US-09-949-016-70845	Sequence 70845, A	c 370	32.8	3.8	1212	3	US-09-182-145-35	Sequence 35, Appl
298	33.2	3.8	601	3	US-09-949-016-70846	Sequence 70846, A	c 371	32.8	3.8	1333	5	US-09-537-654-5	Sequence 5, Appl1
299	33.2	3.8	601	3	US-09-949-016-120218	Sequence 120218, A	c 372	32.8	3.8	1333	5	US-10-818-809-5	Sequence 5, Appl1
300	33.2	3.8	601	3	US-09-949-016-148785	Sequence 148785, A	c 373	32.8	3.8	1733	3	US-09-073-569-1	Sequence 1, Appl1
301	33.2	3.8	601	3	US-09-949-016-152844	Sequence 152844, A	c 374	32.8	3.8	1872	3	US-09-801-052-1	Sequence 1, Appl1
302	33.2	3.8	601	3	US-09-949-016-158181	Sequence 158181, A	c 375	32.8	3.8	1872	3	US-10-636-579-1	Sequence 1, Appl1
303	33.2	3.8	611	3	US-09-385-983-66	Sequence 66, Appl	c 376	32.8	3.8	1872	3	US-10-636-579-1	Sequence 1, Appl1
304	33.2	3.8	1195	4	US-09-297-648-3131	Sequence 3131, Ap	c 377	32.8	3.8	1895	3	US-09-444-336-7	Sequence 7, Appl1
305	33.2	3.8	1195	4	US-09-297-648-3132	Sequence 3132, Ap	c 378	32.8	3.8	1895	3	US-10-093-045-7	Sequence 7, Appl1
306	33.2	3.8	1419	3	US-09-270-767-30857	Sequence 30857, A	c 379	32.8	3.8	1895	3	US-10-093-246-7	Sequence 7, Appl1
307	33.2	3.8	1467	3	US-09-949-016-2761	Sequence 2761, App	c 380	32.8	3.8	1914	5	US-09-690-454-34	Sequence 34, Appl
308	33.2	3.8	1738	3	US-09-918-909A-27	Sequence 27, Appl	c 381	32.8	3.8	1914	5	US-10-062-831-34	Sequence 34, Appl
309	33.2	3.8	2005	2	US-07-916-901-5	Sequence 5, Appl1	c 382	32.8	3.8	1986	3	US-08-687-590-57	Sequence 57, Appl
310	33.2	3.8	2311	3	US-09-800-729-66	Sequence 66, Appl	c 383	32.8	3.8	2625	3	US-09-270-767-10080	Sequence 10080, A
311	33.2	3.8	2394	3	US-09-800-729-33	Sequence 33, Appl	c 384	32.8	3.8	2686	3	US-09-228-986-3	Sequence 3, Appl1
312	33.2	3.8	3585	3	US-09-270-767-14479	Sequence 14479, A	c 385	32.8	3.8	2886	3	US-10-101-464A-3	Sequence 3, Appl1
313	33.2	3.8	3701	3	US-09-220-132-57	Sequence 57, Appl	c 386	32.8	3.8	3275	3	US-09-370-838-151	Sequence 151, App
314	33.2	3.8	16505	3	US-09-949-016-11962	Sequence 11962, A	c 387	32.8	3.8	3275	3	US-09-854-133-151	Sequence 151, App
315	33.2	3.8	16506	3	US-09-949-016-13836	Sequence 13836, A	c 388	32.8	3.8	4086	3	US-09-702-705-1801	Sequence 1801, Ap

389	32.8	3.8	4086	3	US-09-736-457-1801	Sequence 1801, Ap	462	32.6	3.7	1878	3	US-09-465-558-39	Sequence 39, Appl
390	32.8	3.8	4086	3	US-09-671-325-1801	Sequence 1801, Ap	463	32.6	3.7	1883	3	US-10-012-231A-145	Sequence 145, App
391	32.8	3.8	4086	3	US-10-017-754-1801	Sequence 1801, Ap	464	32.6	3.7	1883	3	US-10-015-368A-145	Sequence 145, App
392	32.8	3.8	12001	2	US-08-458-568A-11	Sequence 11, Appl	465	32.6	3.7	1883	3	US-10-006-768A-145	Sequence 145, App
393	32.8	3.8	152331	3	US-09-128-155-16	Sequence 16, Appl	466	32.6	3.7	1883	3	US-10-015-671A-145	Sequence 145, App
394	32.8	3.8	183202	3	US-09-949-016-13614	Sequence 13614, A	467	32.6	3.7	1883	3	US-10-015-393A-145	Sequence 145, App
395	32.8	3.8	37182	3	US-09-949-016-17371	Sequence 17371, A	468	32.6	3.7	1883	3	US-10-011-833A-145	Sequence 145, App
396	32.8	3.8	373694	3	US-09-949-016-12062	Sequence 12062, A	469	32.6	3.7	1883	3	US-10-006-041A-145	Sequence 145, App
397	32.8	3.8	393753	3	US-09-949-016-14573	Sequence 14573, A	470	32.6	3.7	1883	3	US-10-012-064A-145	Sequence 145, App
398	32.8	3.8	393753	3	US-09-949-016-14573	Sequence 14574, A	471	32.6	3.7	1883	4	US-10-015-392A-145	Sequence 145, App
399	32.8	3.8	818128	3	US-09-949-016-14546	Sequence 14546, A	472	32.6	3.7	1883	5	US-10-011-795B-145	Sequence 145, App
400	32.8	3.8	818128	3	US-09-949-016-14547	Sequence 14547, A	473	32.6	3.7	1883	5	US-10-015-386A-145	Sequence 145, App
401	32.8	3.8	818128	3	US-09-949-016-14548	Sequence 14548, A	474	32.6	3.7	1883	5	US-10-012-121A-145	Sequence 145, App
402	32.8	3.8	818128	3	US-09-949-016-14549	Sequence 14549, A	475	32.6	3.7	1883	5	US-10-006-485A-145	Sequence 145, App
403	32.8	3.8	818128	3	US-09-949-016-14550	Sequence 14550, A	476	32.6	3.7	1883	5	US-10-006-746A-145	Sequence 145, App
404	32.8	3.8	818128	3	US-09-949-016-14551	Sequence 14551, A	477	32.6	3.7	1883	5	US-10-012-752A-145	Sequence 145, App
405	32.8	3.8	818128	3	US-09-949-016-14552	Sequence 14552, A	478	32.6	3.7	1883	5	US-10-017-253A-145	Sequence 145, App
406	32.8	3.8	818128	3	US-09-949-016-14553	Sequence 14553, A	479	32.6	3.7	1883	5	US-10-015-519A-145	Sequence 145, App
407	32.8	3.8	818128	3	US-09-949-016-14554	Sequence 14554, A	480	32.6	3.7	1883	5	US-10-015-715A-145	Sequence 145, App
408	32.8	3.8	818128	3	US-09-949-016-14555	Sequence 14555, A	481	32.6	3.7	1883	5	US-10-007-236A-145	Sequence 145, App
409	32.8	3.8	818128	3	US-09-949-016-14556	Sequence 14556, A	482	32.6	3.7	1920	3	US-10-214-269-17	Sequence 17, Appl
410	32.8	3.8	818128	3	US-09-949-016-14557	Sequence 14557, A	483	32.6	3.7	2026	3	US-09-690-454-30	Sequence 30, Appl
411	32.8	3.8	818128	3	US-09-949-016-14558	Sequence 14558, A	484	32.6	3.7	2026	5	US-10-062-831-30	Sequence 30, Appl
412	32.8	3.8	818128	3	US-09-949-016-14559	Sequence 14559, A	485	32.6	3.7	2525	3	US-09-229-583A-1	Sequence 1, Appl
413	32.8	3.8	818128	3	US-09-949-016-14560	Sequence 14560, A	486	32.6	3.7	2525	3	US-10-187-904-1	Sequence 1, Appl
414	32.8	3.8	818128	3	US-09-949-016-14561	Sequence 14561, A	487	32.6	3.7	2550	10	5258287-23	Patent No. 5258287
415	32.8	3.8	818128	3	US-09-949-016-14562	Sequence 14562, A	488	32.6	3.7	2671	10	5168051-9	Patent No. 5168051
416	32.8	3.8	818128	3	US-09-949-016-14563	Sequence 14563, A	489	32.6	3.7	4946	3	US-10-148-806-1	Sequence 1, Appl
417	32.8	3.8	818128	3	US-09-949-016-14564	Sequence 14564, A	490	32.6	3.7	4950	3	US-09-949-016-1805	Sequence 1805, Ap
418	32.8	3.8	818128	3	US-09-949-016-14565	Sequence 14565, A	491	32.6	3.7	4950	3	US-09-949-016-1806	Sequence 1806, Ap
419	32.8	3.8	818128	3	US-09-949-016-14566	Sequence 14566, A	492	32.6	3.7	6388	3	US-09-573-080A-179	Sequence 179, App
420	32.8	3.8	818128	3	US-09-949-016-14567	Sequence 14567, A	493	32.6	3.7	6388	5	US-09-854-867-179	Sequence 179, App
421	32.8	3.8	1082144	4	US-09-531-420-211	Sequence 211, Appl	494	32.6	3.7	6877	2	US-08-347-340-1	Sequence 1, Appl
422	32.8	3.8	1664976	3	US-08-916-121B-1	Sequence 1, Appl	495	32.6	3.7	20608	3	US-09-949-016-16595	Sequence 16595, A
423	32.6	3.7	258	3	US-09-692-570-1	Sequence 1, Appl	496	32.6	3.7	37925	3	US-09-984-429-701	Sequence 701, App
424	32.6	3.7	271	3	US-09-621-976-15353	Sequence 15353, A	497	32.6	3.7	111235	3	US-09-949-016-15328	Sequence 15328, A
425	32.6	3.7	299	3	US-09-621-976-10380	Sequence 10380, A	498	32.6	3.7	114183	3	US-09-949-002-849	Sequence 849, App
426	32.6	3.7	384	3	US-10-131-827-8187	Sequence 8187, Ap	499	32.6	3.7	115814	3	US-09-949-016-16205	Sequence 16205, A
427	32.6	3.7	384	5	US-10-131-831-8187	Sequence 8187, Ap	500	32.6	3.7	127546	3	US-09-949-002-624	Sequence 624, App
428	32.6	3.7	412	3	US-09-270-767-2370	Sequence 2370, Ap	501	32.6	3.7	636591	3	US-09-949-016-11808	Sequence 11808, A
429	32.6	3.7	412	3	US-09-270-767-18252	Sequence 18252, A	502	32.6	3.7	636591	3	US-09-949-016-13388	Sequence 13388, A
430	32.6	3.7	601	3	US-09-949-016-159666	Sequence 159666, A	503	32.6	3.7	1230025	3	US-09-198-452A-1	Sequence 1, Appl
431	32.6	3.7	882	2	US-08-908-965C-9	Sequence 9, Appl	504	32.6	3.7	1230230	3	US-09-438-185A-1	Sequence 1, Appl
432	32.6	3.7	1172	2	US-07-945-288-9	Sequence 9, Appl	505	32.4	3.7	132	3	US-09-621-976-13468	Sequence 13468, A
433	32.6	3.7	1172	2	US-08-462-831-9	Sequence 9, Appl	506	32.4	3.7	188	3	US-09-621-976-10364	Sequence 10364, A
434	32.6	3.7	1172	2	US-08-461-809-9	Sequence 9, Appl	507	32.4	3.7	221	3	US-09-621-976-15416	Sequence 15416, A
435	32.6	3.7	1172	2	US-08-461-441-9	Sequence 9, Appl	508	32.4	3.7	231	3	US-09-248-796A-12356	Sequence 12356, A
436	32.6	3.7	1172	3	PCT-US93-08518-9	Sequence 9, Appl	509	32.4	3.7	250	3	US-09-621-976-17371	Sequence 17371, A
437	32.6	3.7	1273	3	US-09-270-767-14731	Sequence 14731, A	510	32.4	3.7	415	4	US-09-880-107-3593	Sequence 3593, Ap
438	32.6	3.7	1412	3	US-09-614-912-197	Sequence 197, App	511	32.4	3.7	484	3	US-09-270-767-3048	Sequence 3048, Ap
439	32.6	3.7	1662	3	US-09-668-097A-13	Sequence 13, Appl	512	32.4	3.7	484	3	US-09-270-767-18330	Sequence 18330, A
440	32.6	3.7	1674	3	US-09-991-181-300	Sequence 300, App	513	32.4	3.7	572	3	US-09-696-169A-12	Sequence 12, Appl
441	32.6	3.7	1674	3	US-09-990-444-300	Sequence 300, App	514	32.4	3.7	601	3	US-09-949-016-70924	Sequence 70924, A
442	32.6	3.7	1674	3	US-09-997-333-300	Sequence 300, App	515	32.4	3.7	601	3	US-09-949-016-70925	Sequence 70925, A
443	32.6	3.7	1674	3	US-09-992-588-300	Sequence 300, App	516	32.4	3.7	631	3	US-08-817-913-6	Sequence 6, Appl
444	32.6	3.7	1674	4	US-09-989-735-300	Sequence 300, App	517	32.4	3.7	674	3	US-08-817-913-7	Sequence 7, Appl
445	32.6	3.7	1674	5	US-09-989-726-300	Sequence 300, App	518	32.4	3.7	687	3	US-08-817-913-8	Sequence 8, Appl
446	32.6	3.7	1674	5	US-09-997-514-300	Sequence 300, App	519	32.4	3.7	693	3	US-08-817-913-9	Sequence 9, Appl
447	32.6	3.7	1674	5	US-09-989-728-300	Sequence 300, App	520	32.4	3.7	758	3	US-08-817-913-10	Sequence 10, Appl
448	32.6	3.7	1674	5	US-09-997-349-300	Sequence 300, App	521	32.4	3.7	855	3	US-08-817-913-11	Sequence 11, Appl
449	32.6	3.7	1674	5	US-09-997-653-300	Sequence 300, App	522	32.4	3.7	859	3	US-08-817-913-12	Sequence 12, Appl
450	32.6	3.7	1674	5	US-09-989-293A-300	Sequence 300, App	523	32.4	3.7	991	3	US-08-924-747-25	Sequence 25, Appl
451	32.6	3.7	1736	3	US-09-182-816-22	Sequence 22, Appl	524	32.4	3.7	991	3	US-09-247-373B-25	Sequence 25, Appl
452	32.6	3.7	1736	3	US-09-182-816-22	Sequence 24, Appl	525	32.4	3.7	991	3	US-09-286-715-25	Sequence 25, Appl
453	32.6	3.7	1736	3	US-09-471-528-24	Sequence 24, Appl	526	32.4	3.7	1151	3	US-09-270-767-12633	Sequence 12633, A
454	32.6	3.7	1736	3	US-09-471-528-24	Sequence 24, Appl	527	32.4	3.7	1201	3	US-09-461-325-36	Sequence 36, Appl
455	32.6	3.7	1736	3	US-09-634-530-22	Sequence 22, Appl	528	32.4	3.7	1201	3	US-10-012-542-36	Sequence 36, Appl
456	32.6	3.7	1736	3	US-09-634-530-24	Sequence 24, Appl	529	32.4	3.7	1201	3	US-10-115-123-36	Sequence 13, Appl
457	32.6	3.7	1740	3	US-09-709-103-45	Sequence 45, Appl	530	32.4	3.7	1214	3	US-08-817-913-13	Sequence 14, Appl
458	32.6	3.7	1740	3	US-09-439-410A-45	Sequence 45, Appl	531	32.4	3.7	1232	3	US-08-817-913-14	Sequence 15, Appl
459	32.6	3.7	1782	3	US-09-069-023-37	Sequence 37, Appl	532	32.4	3.7	1352	3	US-08-817-913-15	Sequence 15, Appl
460	32.6	3.7	1801	3	US-09-709-103-3	Sequence 3, Appl	533	32.4	3.7	1411	3	US-09-904-615-38	Sequence 38, Appl
461	32.6	3.7	1801	3	US-09-439-410A-3	Sequence 3, Appl	534	32.4	3.7	1411	3	US-10-054-988-38	Sequence 38, Appl

535	32.4	3.7	1641	2	US-08-300-303A-8	Sequence 8, Appl1	608	32.2	3.7	6755	3	US-08-931-999-4	Sequence 4, Appl1
536	32.4	3.7	1641	3	US-08-988-197-8	Sequence 8, Appl1	C 609	32.2	3.7	10053	3	US-09-949-016-17485	Sequence 17485, A
537	32.4	3.7	1641	3	US-10-385-072-8	Sequence 8, Appl1	C 610	32.2	3.7	13335	3	US-09-949-016-13162	Sequence 13162, A
538	32.4	3.7	1734	3	US-08-817-913-16	Sequence 16, Appl1	C 611	32.2	3.7	32099	3	US-09-949-016-16562	Sequence 16562, A
539	32.4	3.7	1753	3	US-09-870-356-53	Sequence 53, Appl1	C 612	32.2	3.7	33206	4	US-09-880-107-2380	Sequence 2380, Ap
540	32.4	3.7	1795	3	US-09-646-561-16	Sequence 16, Appl1	C 613	32.2	3.7	50000	3	US-09-662-254B-23	Sequence 23, Appl1
541	32.4	3.7	1795	3	US-09-646-561-18	Sequence 18, Appl1	614	32.2	3.7	89716	3	US-09-949-016-11900	Sequence 11900, A
542	32.4	3.7	1920	3	US-08-817-913-17	Sequence 17, Appl1	615	32.2	3.7	100877	3	US-09-949-016-1376	Sequence 1376, A
543	32.4	3.7	2079	3	US-09-489-847-25	Sequence 25, Appl1	C 616	32.2	3.7	113100	3	US-09-949-016-12945	Sequence 12245, A
544	32.4	3.7	2579	3	US-09-949-016-2494	Sequence 2494, Ap	C 617	32.2	3.7	114842	3	US-09-949-016-14993	Sequence 14993, A
545	32.4	3.7	2621	3	US-09-949-016-1072	Sequence 1072, Ap	C 618	32.2	3.7	120609	3	US-09-949-016-13315	Sequence 13915, A
546	32.4	3.7	3975	3	US-09-270-767-3	Sequence 3, Appl1	619	32.2	3.7	135667	3	US-09-949-016-15051	Sequence 15051, A
547	32.4	3.7	4466	3	US-09-410-551B-20	Sequence 20, Appl1	C 620	32.2	3.7	149971	3	US-09-949-016-13590	Sequence 13590, A
548	32.4	3.7	4466	3	US-09-940-316B-20	Sequence 20, Appl1	621	32.2	3.7	152486	3	US-09-949-016-12869	Sequence 12869, A
549	32.4	3.7	4478	3	US-09-410-551B-16	Sequence 16, Appl1	622	32.2	3.7	177251	3	US-09-949-016-15941	Sequence 15841, A
550	32.4	3.7	4478	3	US-09-940-316B-16	Sequence 16, Appl1	623	32.2	3.7	256171	3	US-09-949-016-12822	Sequence 12822, A
551	32.4	3.7	4547	3	US-09-410-551B-22	Sequence 22, Appl1	C 624	32.2	3.7	256176	3	US-09-949-016-15524	Sequence 15524, A
552	32.4	3.7	4547	3	US-09-940-316B-22	Sequence 22, Appl1	625	32.2	3.7	260247	3	US-09-949-016-13358	Sequence 13358, A
553	32.4	3.7	4571	3	US-09-940-316B-18	Sequence 18, Appl1	626	32	3.7	81	3	US-09-270-767-27621	Sequence 27621, A
554	32.4	3.7	4571	3	US-09-940-316B-18	Sequence 18, Appl1	627	32	3.7	268	3	US-09-621-976-73	Sequence 73, Appl1
555	32.4	3.7	11151	5	US-09-984-429-496	Sequence 496, App	628	32	3.7	405	3	US-09-513-999C-14389	Sequence 14389, A
556	32.4	3.7	14176	2	US-08-307-499-1	Sequence 1, Appl1	629	32	3.7	424	3	US-09-621-976-11043	Sequence 11043, A
557	32.4	3.7	14176	2	US-08-307-499-14	Sequence 14, Appl1	C 630	32	3.7	480	3	US-10-131-827-8192	Sequence 8192, Ap
558	32.4	3.7	14176	3	US-09-299-268-1	Sequence 1, Appl1	C 631	32	3.7	480	5	US-10-131-831-8192	Sequence 8192, Ap
559	32.4	3.7	14176	3	US-09-299-268-14	Sequence 14, Appl1	632	32	3.7	552	3	US-09-461-325-111	Sequence 111, App
560	32.4	3.7	34185	3	US-09-545-481-3	Sequence 3, Appl1	633	32	3.7	552	3	US-10-012-542-111	Sequence 111, App
561	32.4	3.7	77536	3	US-09-410-551B-1	Sequence 1, Appl1	634	32	3.7	552	3	US-10-115-123-111	Sequence 111, App
562	32.4	3.7	77536	3	US-09-410-551B-1	Sequence 1, Appl1	635	32	3.7	554	3	US-09-696-169A-14	Sequence 14, Appl1
563	32.4	3.7	105189	3	US-09-949-016-13029	Sequence 13029, A	636	32	3.7	748	2	US-08-361-467B-3	Sequence 3, Appl1
564	32.4	3.7	139049	3	US-09-949-016-17030	Sequence 17030, A	637	32	3.7	748	2	US-08-484-332C-3	Sequence 3, Appl1
565	32.4	3.7	276681	3	US-09-949-016-13840	Sequence 13840, A	638	32	3.7	766	3	US-10-125-258-1	Sequence 1, Appl1
566	32.4	3.7	1830121	3	US-09-557-884-1	Sequence 1, Appl1	639	32	3.7	824	3	US-10-144-929-29	Sequence 29, Appl1
567	32.4	3.7	1830121	3	US-09-643-990A-1	Sequence 1, Appl1	640	32	3.7	873	3	US-09-270-767-6426	Sequence 6426, Ap
568	32.4	3.7	1830121	3	US-10-158-865-1	Sequence 1, Appl1	641	32	3.7	873	3	US-09-270-767-21708	Sequence 21708, A
569	32.2	3.7	147	3	US-09-621-976-10254	Sequence 10254, A	642	32	3.7	890	3	US-09-152-060-16	Sequence 16, Appl1
570	32.2	3.7	396	3	US-09-640-173-16	Sequence 16, Appl1	643	32	3.7	890	3	US-09-852-797-16	Sequence 16, Appl1
571	32.2	3.7	396	3	US-09-713-550-16	Sequence 16, Appl1	644	32	3.7	890	3	US-09-853-161-16	Sequence 16, Appl1
572	32.2	3.7	396	3	US-09-825-294-16	Sequence 16, Appl1	645	32	3.7	890	3	US-10-058-993-16	Sequence 16, Appl1
573	32.2	3.7	396	3	US-09-970-966-16	Sequence 16, Appl1	646	32	3.7	1016	3	US-09-999-833A-96	Sequence 96, Appl1
574	32.2	3.7	601	3	US-09-949-016-20883	Sequence 20883, A	647	32	3.7	1016	3	US-10-020-445A-96	Sequence 96, Appl1
575	32.2	3.7	601	3	US-09-949-016-55342	Sequence 55342, A	648	32	3.7	1016	4	US-09-978-189-96	Sequence 96, Appl1
576	32.2	3.7	601	3	US-09-949-016-170626	Sequence 170626, A	649	32	3.7	1016	4	US-10-017-085A-96	Sequence 96, Appl1
577	32.2	3.7	687	3	US-09-907-907A-38	Sequence 38, Appl1	650	32	3.7	1016	5	US-10-145-129A-96	Sequence 96, Appl1
578	32.2	3.7	695	3	US-10-401-038-2	Sequence 2, Appl1	651	32	3.7	1016	5	US-10-013-929A-96	Sequence 96, Appl1
579	32.2	3.7	822	2	US-07-644-372-1	Sequence 1, Appl1	C 652	32	3.7	1016	5	US-10-013-917A-96	Sequence 96, Appl1
580	32.2	3.7	1011	3	US-09-662-254B-74	Sequence 74, Appl1	653	32	3.7	1039	3	US-09-902-540-1280	Sequence 1280, Ap
581	32.2	3.7	1048	3	US-09-489-847-38	Sequence 38, Appl1	654	32	3.7	1051	3	US-09-270-767-11946	Sequence 11946, A
582	32.2	3.7	1059	3	US-09-205-258-74	Sequence 74, Appl1	655	32	3.7	1104	4	US-09-297-648-3396	Sequence 3396, Ap
583	32.2	3.7	1059	3	US-10-004-660-74	Sequence 74, Appl1	656	32	3.7	1126	3	US-09-489-847-60	Sequence 60, Appl1
584	32.2	3.7	1315	3	US-09-721-822A-10	Sequence 10, Appl1	657	32	3.7	1141	3	US-09-806-708B-22	Sequence 22, Appl1
585	32.2	3.7	1518	3	US-09-614-912-191	Sequence 191, App	658	32	3.7	1296	3	US-09-461-325-29	Sequence 29, Appl1
586	32.2	3.7	1834	3	US-09-927-738-26	Sequence 26, Appl1	659	32	3.7	1296	3	US-10-012-542-29	Sequence 29, Appl1
587	32.2	3.7	2114	3	US-09-602-472A-5	Sequence 5, Appl1	660	32	3.7	1296	3	US-10-115-123-29	Sequence 29, Appl1
588	32.2	3.7	2406	2	US-08-687-702-2	Sequence 2, Appl1	661	32	3.7	1400	3	US-09-774-490-5	Sequence 5, Appl1
589	32.2	3.7	2525	3	US-09-865-171-39	Sequence 39, Appl1	662	32	3.7	1404	4	US-09-880-107-3399	Sequence 3399, Ap
590	32.2	3.7	2525	3	US-09-234-393-39	Sequence 39, Appl1	663	32	3.7	1515	4	US-09-880-107-3396	Sequence 3396, Ap
591	32.2	3.7	2665	3	US-08-971-089-5	Sequence 5, Appl1	664	32	3.7	1570	3	US-10-012-231A-291	Sequence 291, App
592	32.2	3.7	2665	3	US-10-117-604A-5	Sequence 5, Appl1	665	32	3.7	1570	3	US-10-015-389A-291	Sequence 291, App
593	32.2	3.7	2852	3	US-09-027-137-2	Sequence 2, Appl1	666	32	3.7	1570	3	US-10-006-768A-291	Sequence 291, App
594	32.2	3.7	2852	3	US-09-344-441-2	Sequence 2, Appl1	667	32	3.7	1570	3	US-10-015-671A-291	Sequence 291, App
595	32.2	3.7	3116	3	US-09-311-021-187	Sequence 187, App	668	32	3.7	1570	3	US-10-015-393A-291	Sequence 291, App
596	32.2	3.7	3124	3	US-09-734-030-1	Sequence 1, Appl1	669	32	3.7	1570	3	US-10-011-833A-291	Sequence 291, App
597	32.2	3.7	3124	3	US-10-153-921-1	Sequence 1, Appl1	670	32	3.7	1570	3	US-10-006-041A-291	Sequence 291, App
598	32.2	3.7	3124	3	US-10-669-689-1	Sequence 1, Appl1	671	32	3.7	1570	3	US-10-012-064A-291	Sequence 291, App
599	32.2	3.7	5275	2	US-08-485-588-1	Sequence 1, Appl1	672	32	3.7	1570	4	US-10-015-392A-291	Sequence 291, App
600	32.2	3.7	5275	2	US-08-484-565-1	Sequence 1, Appl1	673	32	3.7	1570	5	US-10-011-795B-291	Sequence 291, App
601	32.2	3.7	5275	2	US-08-480-751-1	Sequence 1, Appl1	674	32	3.7	1570	5	US-10-015-386A-291	Sequence 291, App
602	32.2	3.7	5275	2	US-08-943-986-1	Sequence 1, Appl1	675	32	3.7	1570	5	US-10-012-121A-291	Sequence 291, App
603	32.2	3.7	5275	3	US-08-353-784-1	Sequence 1, Appl1	676	32	3.7	1570	5	US-10-006-485A-291	Sequence 291, App
604	32.2	3.7	5275	3	US-08-484-719B-1	Sequence 1, Appl1	677	32	3.7	1570	5	US-10-006-746A-291	Sequence 291, App
605	32.2	3.7	5275	3	US-08-484-159-1	Sequence 1, Appl1	678	32	3.7	1570	5	US-10-012-752A-291	Sequence 291, App
606	32.2	3.7	6409	3	US-09-967-908A-1	Sequence 1, Appl1	679	32	3.7	1570	5	US-10-017-253A-291	Sequence 291, App
607	32.2	3.7	6409	3	US-10-159-151-1	Sequence 1, Appl1	680	32	3.7	1570	5	US-10-015-519A-291	Sequence 291, App

681	32	3.7	1570	5	US-10-015-715A-291	Sequence 291, Appl	C 754	31.8	3.7	62327	3	US-09-949-016-16809	Sequence 16809, A
682	32	3.7	1570	5	US-10-007-236A-291	Sequence 291, Appl	C 755	31.8	3.7	67755	3	US-03-949-016-13703	Sequence 13703, A
683	32	3.7	1734	3	US-10-012-231A-51	Sequence 51, Appl	756	31.8	3.7	79122	4	US-03-531-120-200	Sequence 200, Appl
684	32	3.7	1734	3	US-10-015-389A-51	Sequence 51, Appl	757	31.8	3.7	79163	3	US-09-949-016-12273	Sequence 12273, A
685	32	3.7	1734	3	US-10-006-768A-51	Sequence 51, Appl	758	31.8	3.7	131379	3	US-09-949-016-16050	Sequence 16050, A
686	32	3.7	1734	3	US-10-015-671A-51	Sequence 51, Appl	759	31.8	3.7	168104	3	US-09-949-016-12026	Sequence 12026, A
687	32	3.7	1734	3	US-10-015-393A-51	Sequence 51, Appl	760	31.8	3.7	168105	3	US-09-949-016-16554	Sequence 16554, A
688	32	3.7	1734	3	US-10-011-833A-51	Sequence 51, Appl	761	31.8	3.7	314798	3	US-09-949-016-13539	Sequence 13539, A
689	32	3.7	1734	3	US-10-006-041A-51	Sequence 51, Appl	C 762	31.8	3.7	314798	3	US-09-949-016-13539	Sequence 13539, A
690	32	3.7	1734	3	US-10-012-064A-51	Sequence 51, Appl	763	31.8	3.7	390890	3	US-09-949-016-14720	Sequence 14720, A
691	32	3.7	1734	4	US-10-015-392A-51	Sequence 51, Appl	764	31.6	3.6	212	3	US-09-621-976-1325	Sequence 1325, Ap
692	32	3.7	1734	5	US-10-011-795B-51	Sequence 51, Appl	765	31.6	3.6	215	3	US-09-621-976-15321	Sequence 15321, A
693	32	3.7	1734	5	US-10-015-386A-51	Sequence 51, Appl	C 766	31.6	3.6	253	3	US-08-520-678A-25	Sequence 25, Appl
694	32	3.7	1734	5	US-10-012-121A-51	Sequence 51, Appl	C 767	31.6	3.6	253	3	US-08-897-126-25	Sequence 25, Appl
695	32	3.7	1734	5	US-10-006-485A-51	Sequence 51, Appl	C 768	31.6	3.6	253	3	US-10-158-314B-25	Sequence 25, Appl
696	32	3.7	1734	5	US-10-006-746A-51	Sequence 51, Appl	C 769	31.6	3.6	257	2	US-08-520-678A-24	Sequence 24, Appl
697	32	3.7	1734	5	US-10-012-752A-51	Sequence 51, Appl	C 770	31.6	3.6	257	3	US-08-897-126-24	Sequence 24, Appl
698	32	3.7	1734	5	US-10-017-253A-51	Sequence 51, Appl	C 771	31.6	3.6	257	3	US-10-158-314B-24	Sequence 24, Appl
699	32	3.7	1734	5	US-10-015-519A-51	Sequence 51, Appl	772	31.6	3.6	319	2	US-07-593-657-14	Sequence 14, Appl
700	32	3.7	1734	5	US-10-015-715A-51	Sequence 51, Appl	C 773	31.6	3.6	450	3	US-10-131-827-8720	Sequence 8720, Ap
701	32	3.7	1734	5	US-10-007-236A-51	Sequence 51, Appl	C 774	31.6	3.6	450	5	US-10-131-831-8720	Sequence 8720, Ap
702	32	3.7	1936	3	US-09-949-016-716	Sequence 716, Appl	775	31.6	3.6	601	3	US-09-949-016-180739	Sequence 180739,
703	32	3.7	2031	3	US-09-417-251A-9	Sequence 9, Appl	776	31.6	3.6	614	3	US-09-902-540-1318	Sequence 1318, Ap
704	32	3.7	2031	3	US-09-417-251A-9	Sequence 9, Appl	777	31.6	3.6	664	3	US-09-904-615-66	Sequence 66, Appl
705	32	3.7	2065	3	US-09-370-473-5	Sequence 5, Appl	778	31.6	3.6	664	3	US-10-054-988-66	Sequence 66, Appl
706	32	3.7	2101	3	US-08-190-204-1	Sequence 1, Appl	779	31.6	3.6	801	3	US-10-039-659A-5	Sequence 5, Appl
707	32	3.7	2338	3	US-09-582-337-1	Sequence 1, Appl	780	31.6	3.6	850	3	US-09-322-409-6	Sequence 6, Appl
708	32	3.7	2434	3	US-09-489-847-67	Sequence 67, Appl	781	31.6	3.6	1013	3	US-09-322-409-6	Sequence 6, Appl
709	32	3.7	2474	3	US-10-164-230-62	Sequence 62, Appl	C 782	31.6	3.6	1013	3	US-09-322-409-8	Sequence 8, Appl
710	32	3.7	2738	4	US-08-927-939A-80	Sequence 80, Appl	783	31.6	3.6	1013	3	US-09-451-527-6	Sequence 6, Appl
711	32	3.7	3824	3	US-09-688-188B-20	Sequence 20, Appl	C 784	31.6	3.6	1013	3	US-09-451-527-8	Sequence 8, Appl
712	32	3.7	3824	3	US-09-291-417D-20	Sequence 20, Appl	785	31.6	3.6	1013	5	US-10-262-439-6	Sequence 6, Appl
713	32	3.7	4931	3	US-08-726-320-2	Sequence 2, Appl	C 786	31.6	3.6	1013	5	US-10-262-439-8	Sequence 8, Appl
714	32	3.7	4931	3	US-09-208-716-2	Sequence 2, Appl	787	31.6	3.6	1040	3	US-09-589-287B-22	Sequence 22, Appl
715	32	3.7	5000	3	US-08-836-687B-35	Sequence 35, Appl	788	31.6	3.6	1040	3	US-09-588-947A-22	Sequence 22, Appl
716	32	3.7	82612	3	US-09-949-016-16823	Sequence 16823, A	789	31.6	3.6	1040	3	US-09-589-286A-22	Sequence 22, Appl
717	32	3.7	138693	3	US-09-949-016-16724	Sequence 16724, A	790	31.6	3.6	1040	3	US-09-507-968D-22	Sequence 22, Appl
718	32	3.7	152524	3	US-09-949-016-16683	Sequence 12683, A	791	31.6	3.6	1040	3	US-09-589-285-22	Sequence 22, Appl
719	32	3.7	152524	3	US-09-834-700-13	Sequence 13, Appl	792	31.6	3.6	1117	3	US-09-148-545-54	Sequence 54, Appl
720	32	3.7	162025	3	US-09-834-700-14	Sequence 14, Appl	793	31.6	3.6	1117	3	US-09-621-011-54	Sequence 54, Appl
721	32	3.7	162025	3	US-09-834-700-17	Sequence 17, Appl	794	31.6	3.6	1146	3	US-08-596-684F-1	Sequence 1, Appl
722	32	3.7	162025	3	US-09-834-700-18	Sequence 18, Appl	795	31.6	3.6	1146	3	US-09-949-016-4186	Sequence 4186, Ap
723	32	3.7	162025	3	US-09-834-700-18	Sequence 18, Appl	796	31.6	3.6	1279	3	US-09-248-335-25	Sequence 25, Appl
724	32	3.7	200863	3	US-09-949-016-15569	Sequence 12569, A	797	31.6	3.6	1308	3	US-10-151-832-1	Sequence 1, Appl
725	32	3.7	203093	3	US-09-949-016-14445	Sequence 14445, A	798	31.6	3.6	1398	3	US-09-949-016-1132	Sequence 1132, Ap
726	32	3.7	231129	3	US-09-949-016-16110	Sequence 16110, A	799	31.6	3.6	1507	3	US-09-453-323-1	Sequence 1, Appl
727	32	3.7	266293	3	US-09-949-016-11934	Sequence 11934, A	800	31.6	3.6	1526	3	US-10-067-443-23	Sequence 23, Appl
728	32	3.7	340380	3	US-09-949-016-14179	Sequence 14179, A	801	31.6	3.6	1591	3	US-09-399-913-50	Sequence 50, Appl
729	32	3.7	640581	3	US-09-790-988-1	Sequence 1, Appl	802	31.6	3.6	1591	3	US-09-350-614-50	Sequence 50, Appl
730	31.8	3.7	351	3	US-09-621-976-16140	Sequence 16140, A	803	31.6	3.6	1636	3	US-09-578-194-6	Sequence 6, Appl
731	31.8	3.7	577	3	US-09-385-982-203	Sequence 203, Appl	804	31.6	3.6	1798	3	US-09-797-906-1	Sequence 1, Appl
732	31.8	3.7	601	3	US-09-949-016-66701	Sequence 66701, A	805	31.6	3.6	1883	3	US-09-646-561-48	Sequence 48, Appl
733	31.8	3.7	832	3	US-09-621-976-2813	Sequence 2813, Ap	C 806	31.6	3.6	1883	3	US-09-646-561-48	Sequence 48, Appl
734	31.8	3.7	1024	3	US-09-328-475C-50	Sequence 50, Appl	807	31.6	3.6	1927	3	US-09-336-536-66	Sequence 66, Appl
735	31.8	3.7	1065	3	US-09-976-594-833	Sequence 833, Appl	808	31.6	3.6	2010	2	US-07-864-475A-4	Sequence 4, Appl
736	31.8	3.7	1069	2	US-08-768-964-1	Sequence 1, Appl	809	31.6	3.6	2010	2	US-08-468-249A-4	Sequence 4, Appl
737	31.8	3.7	1069	2	US-08-768-964-3	Sequence 3, Appl	810	31.6	3.6	2106	3	US-09-856-327-1	Sequence 1, Appl
738	31.8	3.7	1069	3	US-09-005-299-1	Sequence 1, Appl	811	31.6	3.6	2197	3	US-10-067-443-1	Sequence 1, Appl
739	31.8	3.7	1069	3	US-09-005-299-3	Sequence 3, Appl	812	31.6	3.6	2218	2	US-08-985-090-4	Sequence 4, Appl
740	31.8	3.7	1069	3	US-09-515-431-1	Sequence 1, Appl	813	31.6	3.6	2218	3	US-09-165-543-31	Sequence 31, Appl
741	31.8	3.7	1069	3	US-09-515-431-3	Sequence 3, Appl	814	31.6	3.6	2285	2	US-08-967-101-136	Sequence 136, Appl
742	31.8	3.7	1191	3	US-09-459-133-3	Sequence 3, Appl	815	31.6	3.6	2285	2	US-08-592-541-136	Sequence 136, Appl
743	31.8	3.7	1454	3	US-09-372-422A-19	Sequence 19, Appl	816	31.6	3.6	2285	3	US-09-124-698-136	Sequence 136, Appl
744	31.8	3.7	1817	2	US-08-473-981A-5	Sequence 5, Appl	817	31.6	3.6	2285	3	US-09-127-480-136	Sequence 136, Appl
745	31.8	3.7	1817	2	US-08-474-087-5	Sequence 5, Appl	818	31.6	3.6	2285	3	US-09-134-523-136	Sequence 136, Appl
746	31.8	3.7	2038	3	US-09-885-723-6	Sequence 6, Appl	819	31.6	3.6	2285	3	US-09-636-796A-136	Sequence 136, Appl
747	31.8	3.7	2202	3	US-09-465-558-59	Sequence 59, Appl	820	31.6	3.6	2285	4	US-09-878-454B-25	Sequence 25, Appl
748	31.8	3.7	2246	3	US-09-363-708-3	Sequence 3, Appl	821	31.6	3.6	2285	4	US-09-689-159A-137	Sequence 137, Appl
749	31.8	3.7	2246	3	US-09-083-587-3	Sequence 3, Appl	822	31.6	3.6	2413	3	US-09-399-913-48	Sequence 48, Appl
750	31.8	3.7	7200	3	US-09-853-450-48	Sequence 48, Appl	823	31.6	3.6	2583	3	US-09-350-614-48	Sequence 9, Appl
751	31.8	3.7	7608	3	US-09-221-017B-14	Sequence 14, Appl	824	31.6	3.6	2583	3	US-09-857-556A-9	Sequence 9, Appl
752	31.8	3.7	9196	3	US-09-971-773-3	Sequence 3, Appl	825	31.6	3.6	2628	2	US-08-143-219-1	Sequence 1, Appl
753	31.8	3.7	40493	3	US-09-949-016-15453	Sequence 15453, A	826	31.6	3.6	2915	3	US-09-549-872B-4	Sequence 4, Appl

827	31.6	3.6	3244	3	US-09-165-543-4	Sequence 4, Appli	900	31.4	3.6	1969	3	US-10-012-064A-49	Sequence 49, Appl
828	31.6	3.6	5026	3	US-09-549-872B-3	Sequence 3, Appli	901	31.4	3.6	1969	4	US-10-015-392A-49	Sequence 49, Appl
829	31.6	3.6	6344	3	US-08-843-417-1	Sequence 1, Appli	902	31.4	3.6	1969	5	US-10-011-795B-49	Sequence 49, Appl
830	31.6	3.6	6344	3	US-09-527-013-1	Sequence 1, Appli	903	31.4	3.6	1969	5	US-10-015-386A-49	Sequence 49, Appl
831	31.6	3.6	6612	3	US-09-549-872B-5	Sequence 5, Appli	904	31.4	3.6	1969	5	US-10-012-121A-49	Sequence 49, Appl
832	31.6	3.6	8330	5	US-09-347-311A-3	Sequence 3, Appli	905	31.4	3.6	1969	5	US-10-006-485A-49	Sequence 49, Appl
833	31.6	3.6	9772	3	US-09-949-016-17211	Sequence 17211, A	906	31.4	3.6	1969	5	US-10-006-746A-49	Sequence 49, Appl
834	31.6	3.6	11207	3	US-09-549-872B-2	Sequence 2, Appli	907	31.4	3.6	1969	5	US-10-012-752A-49	Sequence 49, Appl
835	31.6	3.6	41578	3	US-09-949-016-15345	Sequence 15245, A	908	31.4	3.6	1969	5	US-10-017-253A-49	Sequence 49, Appl
836	31.6	3.6	45365	3	US-09-949-016-11893	Sequence 11893, A	909	31.4	3.6	1969	5	US-10-015-519A-49	Sequence 49, Appl
837	31.6	3.6	45456	3	US-09-949-016-17007	Sequence 17007, A	910	31.4	3.6	1969	5	US-10-015-715A-49	Sequence 49, Appl
838	31.6	3.6	47110	3	US-09-949-016-17609	Sequence 17609, A	911	31.4	3.6	1969	5	US-10-007-236A-49	Sequence 49, Appl
839	31.6	3.6	70770	3	US-09-949-016-16938	Sequence 16938, A	912	31.4	3.6	2263	3	US-09-399-913-69	Sequence 69, Appl
840	31.6	3.6	71387	3	US-09-949-016-16938	Sequence 16938, A	913	31.4	3.6	2263	3	US-09-350-614-69	Sequence 69, Appl
841	31.6	3.6	79835	3	US-09-949-016-16754	Sequence 16754, A	914	31.4	3.6	2327	3	US-10-066-130-20	Sequence 20, Appl
842	31.6	3.6	79835	3	US-09-949-016-16754	Sequence 16754, A	915	31.4	3.6	2327	3	US-10-066-130-20	Sequence 20, Appl
843	31.6	3.6	84761	3	US-09-949-016-16121	Sequence 16121, A	916	31.4	3.6	2634	3	US-09-463-238-3	Sequence 3, Appli
844	31.6	3.6	84761	3	US-09-949-016-11919	Sequence 11919, A	917	31.4	3.6	2674	3	US-10-066-130-19	Sequence 19, Appl
845	31.6	3.6	84763	3	US-09-949-016-13914	Sequence 13914, A	918	31.4	3.6	2771	3	US-10-066-130-18	Sequence 18, Appl
846	31.6	3.6	86585	4	US-09-531-120-198	Sequence 198, App	919	31.4	3.6	2783	3	US-09-136-282-1	Sequence 1, Appli
847	31.6	3.6	135476	3	US-09-949-016-12111	Sequence 12611, A	920	31.4	3.6	2783	3	US-09-505-744-1	Sequence 1, Appli
848	31.6	3.6	135476	3	US-09-949-016-14113	Sequence 14113, A	921	31.4	3.6	2882	3	US-09-949-016-724	Sequence 724, App
849	31.6	3.6	135667	3	US-09-949-016-15051	Sequence 15051, A	922	31.4	3.6	2889	10	5378464-1	Patent No. 5378464
850	31.6	3.6	142504	3	US-09-949-016-13693	Sequence 13693, A	923	31.4	3.6	3438	3	US-10-164-595-29	Sequence 29, Appl
851	31.6	3.6	142506	3	US-09-949-016-12474	Sequence 12474, A	924	31.4	3.6	3580	3	US-09-081-345-1	Sequence 1, Appli
852	31.6	3.6	143550	3	US-09-949-016-12474	Sequence 12474, A	925	31.4	3.6	3580	3	US-09-822-295-1	Sequence 1, Appli
853	31.6	3.6	152486	3	US-09-949-016-14143	Sequence 14143, A	926	31.4	3.6	4182	3	US-09-667-422-2	Sequence 2, Appli
854	31.6	3.6	260286	3	US-09-949-016-12869	Sequence 12869, A	927	31.4	3.6	4182	3	US-10-246-435-2	Sequence 2, Appli
855	31.6	3.6	260293	3	US-09-949-016-17037	Sequence 17037, A	928	31.4	3.6	5329	3	US-09-949-016-12252	Sequence 12252, A
856	31.4	3.6	141	3	US-09-621-976-12106	Sequence 12106, A	929	31.4	3.6	5330	3	US-09-949-016-14028	Sequence 14028, A
857	31.4	3.6	150	3	US-09-621-976-13989	Sequence 13989, A	930	31.4	3.6	5807	3	US-10-066-130-17	Sequence 17, Appl
858	31.4	3.6	169	3	US-09-621-976-11249	Sequence 11249, A	931	31.4	3.6	58407	3	US-09-949-016-11892	Sequence 1, Appli
859	31.4	3.6	179	3	US-09-621-976-9575	Sequence 9575, Ap	932	31.4	3.6	58407	3	US-09-692-570-2	Sequence 2, Appli
860	31.4	3.6	179	3	US-09-621-976-18054	Sequence 18054, A	933	31.4	3.6	59123	3	US-09-949-016-12177	Sequence 12177, A
861	31.4	3.6	347	3	US-09-621-976-16026	Sequence 16026, A	934	31.4	3.6	59123	3	US-09-949-016-13504	Sequence 13504, A
862	31.4	3.6	356	2	US-08-520-678A-22	Sequence 22, Appl	935	31.4	3.6	60376	3	US-09-949-016-15004	Sequence 15004, A
863	31.4	3.6	356	2	US-08-520-678A-22	Sequence 22, Appl	936	31.4	3.6	60376	3	US-09-949-016-15004	Sequence 15004, A
864	31.4	3.6	356	3	US-10-158-314B-22	Sequence 22, Appl	937	31.4	3.6	64309	3	US-09-949-016-14581	Sequence 14581, A
865	31.4	3.6	357	3	US-09-621-976-16058	Sequence 16058, A	938	31.4	3.6	64309	3	US-09-949-016-15773	Sequence 15773, A
866	31.4	3.6	359	3	US-09-621-976-16008	Sequence 16008, A	939	31.4	3.6	75336	3	US-09-410-551B-1	Sequence 1, Appli
867	31.4	3.6	359	3	US-09-621-976-16019	Sequence 16019, A	940	31.4	3.6	75336	3	US-09-940-318B-1	Sequence 1, Appli
868	31.4	3.6	362	3	US-09-621-976-16010	Sequence 16010, A	941	31.4	3.6	77536	3	US-09-531-120-204	Sequence 204, App
869	31.4	3.6	365	3	US-09-621-976-16042	Sequence 16042, A	942	31.4	3.6	109974	4	US-09-531-120-204	Sequence 204, App
870	31.4	3.6	449	3	US-09-621-976-15458	Sequence 15458, A	943	31.4	3.6	114139	3	US-09-949-016-16536	Sequence 16536, A
871	31.4	3.6	500	3	US-09-004-730A-126	Sequence 126, App	944	31.4	3.6	166006	3	US-09-949-016-16804	Sequence 16804, A
872	31.4	3.6	500	3	US-09-004-730A-126	Sequence 126, App	945	31.4	3.6	166006	3	US-09-949-016-16804	Sequence 16804, A
873	31.4	3.6	500	3	US-08-981-799A-128	Sequence 128, App	946	31.4	3.6	176006	3	US-09-949-016-16804	Sequence 16804, A
874	31.4	3.6	500	3	US-08-981-799A-128	Sequence 128, App	947	31.4	3.6	176006	3	US-09-949-016-16804	Sequence 16804, A
875	31.4	3.6	566	3	US-09-621-976-14817	Sequence 14817, A	948	31.4	3.6	186959	3	US-09-949-016-13125	Sequence 13125, A
876	31.4	3.6	601	3	US-09-949-016-20694	Sequence 20694, A	949	31.4	3.6	186959	3	US-09-949-016-13125	Sequence 13125, A
877	31.4	3.6	601	3	US-09-949-016-60283	Sequence 60283, A	950	31.4	3.6	235033	5	US-08-852-495C-1	Sequence 1, Appli
878	31.4	3.6	601	3	US-09-949-016-60283	Sequence 60283, A	951	31.4	3.6	235033	5	US-08-852-495C-1	Sequence 2, Appli
879	31.4	3.6	601	3	US-09-949-016-60283	Sequence 60283, A	952	31.4	3.6	237326	5	US-08-852-495C-1	Sequence 2, Appli
880	31.4	3.6	601	3	US-09-949-016-60283	Sequence 60283, A	953	31.4	3.6	246240	2	US-08-724-394A-20	Sequence 20, Appl
881	31.4	3.6	601	3	US-09-949-016-60283	Sequence 60283, A	954	31.4	3.6	246240	2	US-08-724-394A-20	Sequence 20, Appl
882	31.4	3.6	601	3	US-09-949-016-60283	Sequence 60283, A	955	31.4	3.6	246240	2	US-08-724-394A-20	Sequence 20, Appl
883	31.4	3.6	601	3	US-09-949-016-60283	Sequence 60283, A	956	31.4	3.6	246240	2	US-08-724-394A-20	Sequence 20, Appl
884	31.4	3.6	601	3	US-09-949-016-60283	Sequence 60283, A	957	31.4	3.6	246240	2	US-08-724-394A-20	Sequence 20, Appl
885	31.4	3.6	601	3	US-09-949-016-60283	Sequence 60283, A	958	31.4	3.6	246240	2	US-08-724-394A-20	Sequence 20, Appl
886	31.4	3.6	601	3	US-09-949-016-60283	Sequence 60283, A	959	31.4	3.6	246240	2	US-08-724-394A-20	Sequence 20, Appl
887	31.4	3.6	601	3	US-09-949-016-60283	Sequence 60283, A	960	31.4	3.6	246240	2	US-08-724-394A-20	Sequence 20, Appl
888	31.4	3.6	601	3	US-09-949-016-60283	Sequence 60283, A	961	31.4	3.6	246240	2	US-08-724-394A-20	Sequence 20, Appl
889	31.4	3.6	601	3	US-09-949-016-60283	Sequence 60283, A	962	31.4	3.6	246240	2	US-08-724-394A-20	Sequence 20, Appl
890	31.4	3.6	601	3	US-09-949-016-60283	Sequence 60283, A	963	31.4	3.6	246240	2	US-08-724-394A-20	Sequence 20, Appl
891	31.4	3.6	601	3	US-09-949-016-60283	Sequence 60283, A	964	31.4	3.6	246240	2	US-08-724-394A-20	Sequence 20, Appl
892	31.4	3.6	601	3	US-09-949-016-60283	Sequence 60283, A	965	31.4	3.6	246240	2	US-08-724-394A-20	Sequence 20, Appl
893	31.4	3.6	601	3	US-09-949-016-60283	Sequence 60283, A	966	31.4	3.6	246240	2	US-08-724-394A-20	Sequence 20, Appl
894	31.4	3.6	601	3	US-09-949-016-60283	Sequence 60283, A	967	31.4	3.6	246240	2	US-08-724-394A-20	Sequence 20, Appl
895	31.4	3.6	601	3	US-09-949-016-60283	Sequence 60283, A	968	31.4	3.6	246240	2	US-08-724-394A-20	Sequence 20, Appl
896	31.4	3.6	601	3	US-09-949-016-60283	Sequence 60283, A	969	31.4	3.6	246240	2	US-08-724-394A-20	Sequence 20, Appl
897	31.4	3.6	601	3	US-09-949-016-60283	Sequence 60283, A	970	31.4	3.6	246240	2	US-08-724-394A-20	Sequence 20, Appl
898	31.4	3.6	601	3	US-09-949-016-60283	Sequence 60283, A	971	31.4	3.6	246240	2	US-08-724-394A-20	Sequence 20, Appl
899	31.4	3.6	601	3	US-09-949-016-60283	Sequence 60283, A	972	31.4	3.6	246240	2	US-08-724-394A-20	Sequence 20, Appl

c 973	31.2	3.6	396	3	US-09-825-294-53	Sequence 53, Appl	1046	31.2	3.6	2406	3	US-09-594-506-37	Sequence 37, Appl
c 974	31.2	3.6	396	3	US-09-970-966-53	Sequence 53, Appl	1047	31.2	3.6	2476	3	US-10-012-231A-131	Sequence 131, App
c 975	31.2	3.6	402	3	US-10-131-827-8426	Sequence 8426, Ap	1048	31.2	3.6	2476	3	US-10-015-389A-131	Sequence 131, App
c 976	31.2	3.6	402	5	US-10-131-831-8426	Sequence 8426, Ap	1049	31.2	3.6	2476	3	US-10-006-768A-131	Sequence 131, App
c 977	31.2	3.6	548	3	US-09-036-335A-1	Sequence 1, Appli	1050	31.2	3.6	2476	3	US-10-015-671A-131	Sequence 131, App
c 978	31.2	3.6	548	3	US-09-702-647A-1	Sequence 1, Appli	1051	31.2	3.6	2476	3	US-10-015-393A-131	Sequence 131, App
c 979	31.2	3.6	548	3	US-10-218-689-1	Sequence 1, Appli	1052	31.2	3.6	2476	3	US-10-011-833A-131	Sequence 131, App
c 980	31.2	3.6	601	3	US-09-949-016-77505	Sequence 77505, A	1053	31.2	3.6	2476	3	US-10-006-041A-131	Sequence 131, App
c 981	31.2	3.6	601	3	US-09-949-016-77506	Sequence 77506, A	1054	31.2	3.6	2476	3	US-10-012-064A-131	Sequence 131, App
c 982	31.2	3.6	601	3	US-09-949-016-77507	Sequence 77507, A	1055	31.2	3.6	2476	4	US-10-015-392A-131	Sequence 131, App
c 983	31.2	3.6	601	3	US-09-949-016-119283	Sequence 119283, A	1056	31.2	3.6	2476	5	US-10-011-795B-131	Sequence 131, App
c 984	31.2	3.6	601	3	US-09-949-016-119284	Sequence 119284, A	1057	31.2	3.6	2476	5	US-10-015-386A-131	Sequence 131, App
c 985	31.2	3.6	601	3	US-09-949-016-156244	Sequence 156244, A	1058	31.2	3.6	2476	5	US-10-012-121A-131	Sequence 131, App
c 986	31.2	3.6	606	3	US-09-004-730A-100	Sequence 100, App	1059	31.2	3.6	2476	5	US-10-006-485A-131	Sequence 131, App
c 987	31.2	3.6	606	3	US-09-004-730A-102	Sequence 102, App	1060	31.2	3.6	2476	5	US-10-006-746A-131	Sequence 131, App
c 988	31.2	3.6	606	3	US-08-981-799A-100	Sequence 100, App	1061	31.2	3.6	2476	5	US-10-012-752A-131	Sequence 131, App
c 989	31.2	3.6	606	3	US-08-981-799A-102	Sequence 102, App	1062	31.2	3.6	2476	5	US-10-017-253A-131	Sequence 131, App
c 990	31.2	3.6	612	3	US-09-032-540-1357	Sequence 1357, Ap	1063	31.2	3.6	2476	5	US-10-015-519A-131	Sequence 131, App
c 991	31.2	3.6	708	4	US-09-297-648-3418	Sequence 3418, Ap	1064	31.2	3.6	2476	5	US-10-015-715A-131	Sequence 131, App
c 992	31.2	3.6	708	4	US-09-297-648-3419	Sequence 3419, Ap	1065	31.2	3.6	2476	5	US-10-007-236A-131	Sequence 131, App
c 993	31.2	3.6	763	3	US-09-743-207-3	Sequence 3, Appli	1066	31.2	3.6	2483	3	US-08-205-258-68	Sequence 68, Appl
c 994	31.2	3.6	789	3	US-09-020-956-32	Sequence 32, Appl	1067	31.2	3.6	2483	3	US-10-004-860-68	Sequence 68, Appl
c 995	31.2	3.6	789	3	US-09-030-607-32	Sequence 32, Appl	1068	31.2	3.6	2485	3	US-09-889-463A-9	Sequence 9, Appli
c 996	31.2	3.6	789	3	US-09-439-313-32	Sequence 32, Appl	1069	31.2	3.6	2608	2	US-08-160-861-1	Sequence 1, Appli
c 997	31.2	3.6	789	3	US-09-352-616A-32	Sequence 32, Appl	1070	31.2	3.6	2771	3	US-09-674-824-1	Sequence 1, Appli
c 998	31.2	3.6	789	3	US-09-232-149A-32	Sequence 32, Appl	1071	31.2	3.6	3055	3	US-10-001-887-57	Sequence 57, Appl
c 999	31.2	3.6	789	3	US-09-159-812-32	Sequence 32, Appl	1072	31.2	3.6	3152	4	US-09-880-107-3431	Sequence 3431, Ap
c 1000	31.2	3.6	789	3	US-09-636-215-32	Sequence 32, Appl	1073	31.2	3.6	3410	3	US-09-020-956-110	Sequence 110, App
c 1001	31.2	3.6	789	3	US-09-685-166A-32	Sequence 32, Appl	1074	31.2	3.6	3410	3	US-09-030-607-110	Sequence 110, App
c 1002	31.2	3.6	789	3	US-09-115-453-32	Sequence 32, Appl	1075	31.2	3.6	3410	3	US-09-439-313-110	Sequence 110, App
c 1003	31.2	3.6	789	3	US-09-688-489-32	Sequence 32, Appl	1076	31.2	3.6	3410	3	US-09-352-616A-110	Sequence 110, App
c 1004	31.2	3.6	789	3	US-09-679-426-32	Sequence 32, Appl	1077	31.2	3.6	3410	3	US-09-602-877A-100	Sequence 100, App
c 1005	31.2	3.6	789	3	US-09-759-143-32	Sequence 32, Appl	1078	31.2	3.6	3410	3	US-09-232-149A-110	Sequence 110, App
c 1006	31.2	3.6	789	3	US-09-651-236-32	Sequence 32, Appl	1079	31.2	3.6	3410	3	US-09-159-812-110	Sequence 110, App
c 1007	31.2	3.6	789	3	US-09-030-606-32	Sequence 32, Appl	1080	31.2	3.6	3410	3	US-09-636-215-110	Sequence 110, App
c 1008	31.2	3.6	789	3	US-09-657-279-32	Sequence 32, Appl	1081	31.2	3.6	3410	3	US-09-685-166A-110	Sequence 110, App
c 1009	31.2	3.6	789	3	US-10-012-896-32	Sequence 32, Appl	1082	31.2	3.6	3410	3	US-09-115-453-110	Sequence 110, App
c 1010	31.2	3.6	789	5	US-09-116-134-32	Sequence 32, Appl	1083	31.2	3.6	3410	3	US-09-688-489-110	Sequence 110, App
c 1011	31.2	3.6	796	2	US-10-144-678A-32	Sequence 32, Appl	1084	31.2	3.6	3410	3	US-09-679-426-110	Sequence 110, App
c 1012	31.2	3.6	831	3	US-09-118-554-66	Sequence 66, Appl	1085	31.2	3.6	3410	3	US-09-759-143-110	Sequence 110, App
c 1013	31.2	3.6	831	3	US-09-118-627-66	Sequence 66, Appl	1086	31.2	3.6	3410	3	US-09-651-236-110	Sequence 110, App
c 1014	31.2	3.6	831	3	US-09-602-877A-66	Sequence 66, Appl	1087	31.2	3.6	3410	3	US-09-030-606-110	Sequence 110, App
c 1015	31.2	3.6	885	3	US-09-322-409-25	Sequence 25, Appl	1088	31.2	3.6	3410	3	US-09-657-279-110	Sequence 110, App
c 1016	31.2	3.6	885	3	US-09-322-409-27	Sequence 27, Appl	1089	31.2	3.6	3410	3	US-10-012-896-110	Sequence 110, App
c 1017	31.2	3.6	885	3	US-09-451-527-25	Sequence 25, Appl	1090	31.2	3.6	3410	5	US-09-116-134-110	Sequence 110, App
c 1018	31.2	3.6	885	3	US-09-451-527-27	Sequence 27, Appl	1091	31.2	3.6	3410	5	US-10-144-678A-110	Sequence 110, App
c 1019	31.2	3.6	885	5	US-10-262-439-25	Sequence 25, Appl	1092	31.2	3.6	3556	3	US-09-270-767-10439	Sequence 10439, A
c 1020	31.2	3.6	885	5	US-10-262-439-27	Sequence 27, Appl	1093	31.2	3.6	3556	3	US-09-112-096-28	Sequence 28, Appl
c 1021	31.2	3.6	1097	3	US-09-270-767-5246	Sequence 5246, Ap	1094	31.2	3.6	3674	3	US-09-410-551B-26	Sequence 26, Appl
c 1022	31.2	3.6	1097	3	US-09-270-767-20528	Sequence 20528, A	1095	31.2	3.6	3674	3	US-09-940-316B-26	Sequence 26, Appl
c 1023	31.2	3.6	1098	3	US-09-248-335-35	Sequence 35, Appl	1096	31.2	3.6	4725	3	US-09-940-316B-24	Sequence 24, Appl
c 1024	31.2	3.6	1133	3	US-09-916-204-1	Sequence 1, Appli	1097	31.2	3.6	4725	3	US-09-940-316B-24	Sequence 24, Appl
c 1025	31.2	3.6	1133	3	US-10-282-048-1	Sequence 1, Appli	1098	31.2	3.6	4737	3	US-09-410-551B-30	Sequence 30, Appl
c 1026	31.2	3.6	1141	3	US-09-800-729-78	Sequence 78, Appl	1099	31.2	3.6	4737	3	US-09-940-316B-30	Sequence 30, Appl
c 1027	31.2	3.6	1258	3	US-09-208-258-169	Sequence 169, App	1100	31.2	3.6	4767	3	US-09-410-551B-28	Sequence 28, Appl
c 1028	31.2	3.6	1258	3	US-10-004-860-169	Sequence 169, App	1101	31.2	3.6	4767	3	US-09-940-316B-28	Sequence 28, Appl
c 1029	31.2	3.6	1512	3	US-08-909-965C-8	Sequence 8, Appli	1102	31.2	3.6	4818	3	US-09-410-551B-32	Sequence 32, Appl
c 1030	31.2	3.6	1728	3	US-08-985-950-7	Sequence 7, Appli	1103	31.2	3.6	4818	3	US-09-940-316B-32	Sequence 32, Appl
c 1031	31.2	3.6	1728	3	US-09-546-049-7	Sequence 7, Appli	1104	31.2	3.6	5668	3	US-09-112-096-14	Sequence 14, Appl
c 1032	31.2	3.6	1788	3	US-09-328-352-306	Sequence 306, App	1105	31.2	3.6	5668	3	US-09-636-215-777	Sequence 777, App
c 1033	31.2	3.6	2239	3	US-09-196-390-1	Sequence 1, Appli	1106	31.2	3.6	5668	3	US-09-685-166A-777	Sequence 777, App
c 1034	31.2	3.6	2239	3	US-09-952-677-1	Sequence 1, Appli	1107	31.2	3.6	5668	3	US-09-679-426-777	Sequence 777, App
c 1035	31.2	3.6	2264	3	US-09-126-109-9	Sequence 9, Appli	1108	31.2	3.6	5668	3	US-09-759-143-777	Sequence 777, App
c 1036	31.2	3.6	2271	3	US-10-104-047-155	Sequence 155, App	1109	31.2	3.6	5668	3	US-09-651-236-777	Sequence 777, App
c 1037	31.2	3.6	2271	3	US-09-949-016-2520	Sequence 2520, Ap	1110	31.2	3.6	5668	3	US-09-657-279-777	Sequence 777, App
c 1038	31.2	3.6	2279	3	US-09-949-016-2520	Sequence 2520, Ap	1111	31.2	3.6	5668	3	US-10-012-896-777	Sequence 777, App
c 1039	31.2	3.6	2318	3	US-09-620-312D-916	Sequence 916, App	1112	31.2	3.6	5668	5	US-10-144-678A-777	Sequence 777, App
c 1040	31.2	3.6	2318	3	US-09-949-016-2520	Sequence 2520, Ap	1113	31.2	3.6	5668	5	US-09-331-581-3	Sequence 3, Appli
c 1041	31.2	3.6	2318	3	US-09-949-016-2520	Sequence 2520, Ap	1114	31.2	3.6	7286	3	US-09-331-581-14	Sequence 14, Appl
c 1042	31.2	3.6	2318	3	US-09-949-016-2520	Sequence 2520, Ap	1115	31.2	3.6	7938	3	US-09-331-581-14	Sequence 14, Appl
c 1043	31.2	3.6	2318	3	US-09-949-016-2520	Sequence 2520, Ap	1116	31.2	3.6	7938	3	US-09-331-581-14	Sequence 14, Appl
c 1044	31.2	3.6	2318	3	US-09-949-016-2520	Sequence 2520, Ap	1117	31.2	3.6	7938	3	US-09-331-581-14	Sequence 14, Appl
c 1045	31.2	3.6	2318	3	US-09-949-016-2520	Sequence 2520, Ap	1118	31.2	3.6	7938	3	US-09-331-581-14	Sequence 14, Appl

c1119	31.2	3.6	44072	3	US-09-949-016-15757	Sequence 15757, A	1192	31	3.6	1701	3	US-09-997-333-114	Sequence 114, App
c1120	31.2	3.6	50000	3	US-09-146-053-3	Sequence 3, Appli	1193	31	3.6	1701	3	US-09-992-598-114	Sequence 114, App
c1121	31.2	3.6	64024	3	US-09-949-016-17593	Sequence 17593, A	1194	31	3.6	1701	4	US-09-989-735-114	Sequence 114, App
c1122	31.2	3.6	101011	3	US-09-949-016-16333	Sequence 16333, A	1195	31	3.6	1701	5	US-09-989-726-114	Sequence 114, App
c1123	31.2	3.6	105055	3	US-09-949-016-14001	Sequence 14001, A	1196	31	3.6	1701	5	US-09-997-514-114	Sequence 114, App
c1124	31.2	3.6	114842	3	US-09-949-016-14993	Sequence 14993, A	1197	31	3.6	1701	5	US-09-989-728-114	Sequence 114, App
c1125	31.2	3.6	147382	3	US-09-949-016-14624	Sequence 14624, A	1198	31	3.6	1701	5	US-09-997-349-114	Sequence 114, App
c1126	31.2	3.6	169998	3	US-09-676-610B-24	Sequence 24, Appl	1199	31	3.6	1701	5	US-09-997-653-114	Sequence 114, App
c1127	31.2	3.6	176373	3	US-09-128-155-17	Sequence 17, Appl	1200	31	3.6	1701	5	US-09-989-293A-114	Sequence 114, App
c1128	31.2	3.6	197496	3	US-09-877-177A-10	Sequence 10, Appl	1201	31	3.6	1746	3	US-09-485-529-57	Sequence 57, Appl
c1129	31.2	3.6	278866	3	US-09-949-016-13922	Sequence 13922, A	1202	31	3.6	1766	3	US-10-142-833-27	Sequence 27, Appl
c1130	31.2	3.6	278866	3	US-09-949-016-13923	Sequence 13923, A	1203	31	3.6	1768	3	US-09-485-529-13	Sequence 13, Appl
c1131	31.2	3.6	278866	3	US-09-949-016-13924	Sequence 13924, A	1204	31	3.6	1835	3	US-09-485-549-1	Sequence 1, Appli
c1132	31.2	3.6	278866	3	US-09-949-016-13925	Sequence 13925, A	1205	31	3.6	1843	3	US-08-718-738-1	Sequence 1, Appli
c1133	31.2	3.6	278866	3	US-09-949-016-13926	Sequence 13926, A	1206	31	3.6	1843	3	US-09-221-84-1	Sequence 1, Appli
c1134	31.2	3.6	278866	3	US-09-949-016-14699	Sequence 14699, A	1207	31	3.6	1843	3	US-09-843-846-1	Sequence 1, Appli
c1135	31.2	3.6	278866	3	US-09-949-016-14700	Sequence 14700, A	1208	31	3.6	1843	7	PCT-US95-0333A-1	Sequence 1, Appli
c1136	31.2	3.6	278866	3	US-09-949-016-14701	Sequence 14701, A	1209	31	3.6	1844	3	US-09-123-913-88	Sequence 88, Appl
c1137	31.2	3.6	278866	3	US-09-949-016-14702	Sequence 14702, A	1210	31	3.6	1844	3	US-09-643-597-88	Sequence 88, Appl
c1138	31.2	3.6	278866	3	US-09-949-016-14703	Sequence 14703, A	1211	31	3.6	1844	3	US-09-480-884A-88	Sequence 88, Appl
c1139	31.2	3.6	580073	3	US-08-545-5280-1	Sequence 1, Appli	1212	31	3.6	1844	3	US-09-542-615A-88	Sequence 88, Appl
c1140	31.2	3.6	1664976	3	US-08-916-421B-1	Sequence 1, Appli	1213	31	3.6	1844	3	US-09-606-421B-88	Sequence 88, Appl
c1141	31.2	3.6	1664976	3	US-09-692-570-1	Sequence 1, Appli	1214	31	3.6	1844	3	US-09-221-107-88	Sequence 88, Appl
c1142	31	3.6	127	3	US-10-021-338A-29	Sequence 29, Appl	1215	31	3.6	1844	3	US-09-466-396A-88	Sequence 88, Appl
c1143	31	3.6	181	3	US-09-621-976-17313	Sequence 17313, A	1216	31	3.6	1844	3	US-09-476-496A-88	Sequence 88, Appl
c1144	31	3.6	190	3	US-09-621-976-16784	Sequence 16784, A	1217	31	3.6	1844	3	US-09-630-940B-88	Sequence 88, Appl
c1145	31	3.6	191	4	US-09-880-107-525	Sequence 525, App	1218	31	3.6	1844	3	US-09-285-473-88	Sequence 88, Appl
c1146	31	3.6	195	3	US-09-621-976-18062	Sequence 18062, A	1219	31	3.6	1844	3	US-10-007-700-88	Sequence 88, Appl
c1147	31	3.6	226	3	US-10-131-827-8671	Sequence 8671, Ap	1220	31	3.6	1872	3	US-09-291-922-27	Sequence 27, Appl
c1148	31	3.6	226	5	US-10-131-831-8671	Sequence 8671, Ap	1221	31	3.6	1975	3	US-09-910-174B-3	Sequence 3, Appli
c1149	31	3.6	272	3	US-09-621-976-8353	Sequence 8353, Ap	1222	31	3.6	1975	3	US-09-620-461-3	Sequence 3, Appli
c1150	31	3.6	358	3	US-09-621-976-927	Sequence 927, App	1223	31	3.6	1985	3	US-09-907-794A-212	Sequence 212, App
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c1153	31	3.6	414	3	US-09-270-767-22225	Sequence 22225, A	1226	31	3.6	1985	3	US-09-906-700-212	Sequence 212, App
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c1165	31	3.6	601	3	US-09-949-016-117755	Sequence 117755, A	1238	31	3.6	1985	5	US-09-907-841-212	Sequence 212, App
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c1167	31	3.6	601	3	US-09-949-016-139892	Sequence 139892, A	1240	31	3.6	2198	2	US-08-755-728-2	Sequence 2, Appli
c1168	31	3.6	601	3	US-09-949-016-157902	Sequence 157902, A	1241	31	3.6	2198	2	US-08-974-653-2	Sequence 2, Appli
c1169	31	3.6	601	3	US-09-949-016-159667	Sequence 159667, A	1242	31	3.6	2198	2	US-09-283-011-2	Sequence 2, Appli
c1170	31	3.6	601	3	US-09-949-016-182741	Sequence 182741, A	1243	31	3.6	2198	3	US-09-012-135A-2	Sequence 2, Appli
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c1173	31	3.6	601	4	US-09-880-107-1421	Sequence 1421, Ap	1246	31	3.6	2218	3	US-10-329-668-7	Sequence 7, Appli
c1174	31	3.6	700	3	US-09-832-123-23	Sequence 23, Appl	1247	31	3.6	2218	4	US-09-880-107-3411	Sequence 3411, Ap
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c1176	31	3.6	774	3	US-09-105-542A-4	Sequence 4, Appli	1249	31	3.6	2229	3	US-09-620-461-1	Sequence 1, Appli
c1177	31	3.6	840	3	US-09-244-111-5	Sequence 5, Appli	1250	31	3.6	2229	3	US-09-482-273-97	Sequence 97, Appl
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c1179	31	3.6	1008	3	US-09-780-641-1	Sequence 1, Appli	1252	31	3.6	2242	3	US-09-482-273-35	Sequence 35, Appl
c1180	31	3.6	1167	2	US-08-671-320-16	Sequence 16, Appl	1253	31	3.6	2292	5	US-09-430-590B-128	Sequence 128, App
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c1184	31	3.6	1342	3	US-09-489-847-89	Sequence 89, Appl	1257	31	3.6	2407	3	US-09-921-259-7	Sequence 7, Appli
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c1186	31	3.6	1411	3	US-09-496-692-5	Sequence 5, Appli	1259	31	3.6	2805	3	US-08-892-695-4	Sequence 4, Appli
c1187	31	3.6	1411	3	US-10-000-273-5	Sequence 5, Appli	1260	31	3.6	3812	3	US-10-104-047-981	Sequence 981, App
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1271	31	3.6	26700	2	US-08-472-217-1	Sequence 1, Appli	1344	30.8	3.5	1743	3	US-10-015-671A-235	Sequence 235, App
1272	31	3.6	26700	2	US-08-488-199-5	Sequence 5, Appli	1345	30.8	3.5	1743	3	US-10-015-932A-235	Sequence 235, App
1273	31	3.6	26700	2	US-08-760-534A-1	Sequence 1, Appli	1346	30.8	3.5	1743	3	US-10-011-833A-235	Sequence 235, App
1274	31	3.6	26700	3	US-09-336-757-1	Sequence 1, Appli	1347	30.8	3.5	1743	3	US-10-006-041A-235	Sequence 235, App
1275	31	3.6	34063	3	US-09-453-702B-96	Sequence 96, Appl	1348	30.8	3.5	1743	3	US-10-012-064A-235	Sequence 235, App
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1279	31	3.6	57392	3	US-09-949-016-12070	Sequence 12070, A	1352	30.8	3.5	1743	5	US-10-012-121A-235	Sequence 235, App
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1281	31	3.6	75378	3	US-09-949-016-17140	Sequence 17140, A	1354	30.8	3.5	1743	5	US-10-006-746A-235	Sequence 235, App
1282	31	3.6	83218	3	US-09-949-016-14489	Sequence 14489, A	1355	30.8	3.5	1743	5	US-10-012-752A-235	Sequence 235, App
1283	31	3.6	85122	3	US-09-949-016-14693	Sequence 14693, A	1356	30.8	3.5	1743	5	US-10-017-253A-235	Sequence 235, App
1284	31	3.6	86857	3	US-09-949-016-14688	Sequence 14688, A	1357	30.8	3.5	1743	5	US-10-015-519A-235	Sequence 235, App
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1288	31	3.6	112132	3	US-09-741-150-3	Sequence 3, Appli	1361	30.8	3.5	1781	3	US-09-270-767-2416	Sequence 2416, Ap
1289	31	3.6	112132	3	US-10-160-187-3	Sequence 3, Appli	1362	30.8	3.5	1781	3	US-09-270-767-17698	Sequence 17698, A
1290	31	3.6	119214	3	US-09-949-016-12507	Sequence 12507, A	1363	30.8	3.5	1781	3	US-10-354-065-1	Sequence 1, Appli
1291	31	3.6	135010	3	US-09-949-016-17234	Sequence 17234, A	1364	30.8	3.5	1859	3	US-09-369-247-48	Sequence 48, Appl
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1293	31	3.6	181251	3	US-09-949-016-15970	Sequence 15970, A	1366	30.8	3.5	2034	5	US-10-426-776-19	Sequence 19, Appl
1294	31	3.6	191433	3	US-09-949-016-15144	Sequence 16144, A	1367	30.8	3.5	2055	3	US-09-023-655-1036	Sequence 1036, Ap
1295	31	3.6	212139	3	US-09-949-016-16065	Sequence 16065, A	1368	30.8	3.5	2055	3	US-09-667-365-1900	Sequence 1900, Ap
1296	31	3.6	251672	3	US-09-949-016-17296	Sequence 17296, A	1369	30.8	3.5	2062	2	US-08-073-383-5	Sequence 5, Appli
1297	31	3.6	251682	3	US-09-949-016-11973	Sequence 11973, A	1370	30.8	3.5	2062	3	US-08-328-239A-3	Sequence 3, Appli
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1300	31	3.6	264304	3	US-09-949-016-13249	Sequence 13249, A	1373	30.8	3.5	2150	5	US-10-131-831-9109	Sequence 9109, Ap
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1307	30.8	3.5	446	3	US-10-178-213-241	Sequence 241, App	1380	30.8	3.5	2707	3	US-09-870-956-55	Sequence 55, Appl
1308	30.8	3.5	450	3	US-09-270-767-12394	Sequence 12394, A	1381	30.8	3.5	2843	3	US-10-028-952A-7	Sequence 7, Appli
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1313	30.8	3.5	601	3	US-09-949-016-58349	Sequence 58349, A	1386	30.8	3.5	4767	3	US-09-644-947A-21	Sequence 21, Appl
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1315	30.8	3.5	601	3	US-09-949-016-176085	Sequence 176085, A	1388	30.8	3.5	5075	4	US-09-422-999B-7	Sequence 7, Appli
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1318	30.8	3.5	601	3	US-09-949-016-201402	Sequence 201402, A	1391	30.8	3.5	9281	3	US-09-949-016-14660	Sequence 14660, A
1319	30.8	3.5	601	3	US-09-949-016-206788	Sequence 206788, A	1392	30.8	3.5	11874	3	US-09-949-016-16309	Sequence 16309, A
1320	30.8	3.5	601	3	US-09-949-003-7984	Sequence 7984, Ap	1393	30.8	3.5	13011	2	US-08-731-849A-14	Sequence 14, Appl
1321	30.8	3.5	601	3	US-09-949-003-7985	Sequence 7985, Ap	1394	30.8	3.5	15252	3	US-09-949-016-13584	Sequence 13584, A
1322	30.8	3.5	674	3	US-09-620-405B-465	Sequence 465, App	1395	30.8	3.5	15418	3	US-09-783-203-1	Sequence 1, Appli
1323	30.8	3.5	674	3	US-09-433-826B-465	Sequence 465, App	1396	30.8	3.5	15418	3	US-09-994-427A-1	Sequence 1, Appli
1324	30.8	3.5	674	3	US-09-604-287A-465	Sequence 465, App	1397	30.8	3.5	15418	3	US-09-244-438-1	Sequence 1, Appli
1325	30.8	3.5	674	3	US-09-834-759-465	Sequence 465, App	1398	30.8	3.5	15418	3	US-09-995-419A-1	Sequence 1, Appli
1326	30.8	3.5	674	3	US-09-590-751A-465	Sequence 465, App	1399	30.8	3.5	18466	3	US-09-949-016-17279	Sequence 17279, A
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1330	30.8	3.5	674	4	US-10-124-805-465	Sequence 465, App	1403	30.8	3.5	27009	3	US-09-949-016-11848	Sequence 11848, A
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ALIGNMENTS

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; Sequence 164, Application US/09991181
; Patent No. 6913919
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
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; APPLICANT: Gerber, Hanspeter
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; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kijavini, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730P1C53
; CURRENT FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
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; PRIOR FILING DATE: 1997-10-17
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; PRIOR FILING DATE: 1998-07-09

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Best Local Similarity 100.0%; Pred. No. 5.2e-265;
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; Patent No. 6930170
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
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; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C19
; CURRENT APPLICATION NUMBER: US/09/990,444
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/049787
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; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 870; DB 3; Length 870;

Best Local Similarity 100.0%; Pred. No. 5.2e-265;

Matches 870; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTCGCCCTCAAAATGGGAACGCTGGCTGGGACTAAAGCATAGACACCCAGGCTGAGTATC 60
Db 1 CTCGCCCTCAAAATGGGAACGCTGGCTGGGACTAAAGCATAGACACCCAGGCTGAGTATC 60
Qy 61 CTGACCTGAGTCATCCCGAGGATCAGGAGCTCCAGCAGGAACTTCCATTATATCT 120
Db 61 CTGACCTGAGTCATCCCGAGGATCAGGAGCTCCAGCAGGAACTTCCATTATATCT 120
Qy 121 TCAAGCAACTTACAGCTGCACCGCAGTTGCGATGAAAGTTCTAATCTCTTCCCTCCTCC 180
Db 121 TCAAGCAACTTACAGCTGCACCGCAGTTGCGATGAAAGTTCTAATCTCTTCCCTCCTCC 180
Qy 181 TGTTCCTGCCACTAATGCTGATGCCATGGTCTCTAGCAGCTGAATCCAGGGTCGCCA 240
Db 181 TGTTCCTGCCACTAATGCTGATGCCATGGTCTCTAGCAGCTGAATCCAGGGTCGCCA 240

Db 181 TGTGCTGCCACTAATGCTGATGTCCATGGTCTCTAGCAGCCTGAATCCAGGGGTCCGCA 240
QY 241 GAGGCCACAGGACCGAGGCCAGGCTTCTAGGATGGCTCCAGGAAGCGGCCAAGAT 300
Db 241 GAGGCCACAGGACCGAGGCCAGGCTTCTAGGATGGCTCCAGGAAGCGGCCAAGAT 300
QY 301 GTGAGTGCAAGATGTTGTTCTTGAGAGCCCCGAGAGAAATTCATGACAGTGTCTGGGC 360
Db 301 GTGAGTGCAAGATGTTGTTCTTGAGAGCCCCGAGAGAAATTCATGACAGTGTCTGGGC 360
QY 361 TGCCAAAGAGCGAGTCCCTGTGATCATTTCAAGGGCAATGTGAAGAAAAACAAGACCC 420
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QY 421 AAAGGCACACAGAGAACCAACAGCATTTCCAGAGCCTGCCAGCAATTTCTCAACAAT 480
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QY 481 GTCAGCTAAGAAGCTTTGCTCTGCTTGTAGGAGCTCTGAGCGCCCACTTTTCCAATTA 540
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QY 541 AACATTCTCAGCCAAAGACAGTGAAGACACCTACAGACACTCTTCTTCCACCTC 600
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QY 601 ACTCTCCCACTGACCCACCCCTTAATCATTTCCAGTGCTCTCAAAAGCATGTTTTTCAA 660
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QY 661 GATCATTTTGTGTTGCTCTCTAGTGTCTTCTTCTCTCGTCACTTTAGCTGTGCC 720
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QY 841 TTTTAAATGTCAAAAAAATCAAAAAAATCAAAAAAATCAAAAAAATCAAAAAAAT 870
Db 841 TTTTAAATGTCAAAAAAATCAAAAAAATCAAAAAAATCAAAAAAATCAAAAAAAT 870

RESULT 3

US-09-997-333-164
; Sequence 164, Application US/09997333
; Patent No. 6953836
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J..
; APPLICANT: Baker, Kevin P..
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L..
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerlitsen, Mary E..
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J..
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L..
; APPLICANT: Kljavin, Ivar J..
; APPLICANT: Napier, Mary A..
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F..
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A..
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K..
; APPLICANT:

; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I..
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730PIC27
; CURRENT APPLICATION NUMBER: US/09/997,333
; CURRENT FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: 60/049787
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; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 870; DB 3; Length 870;

Best Local Similarity 100.0%; Pred. No. 5.2e-265; Indels 0; Gaps 0;
Matches 870; Conservative 0; Mismatches 0;

Qy	1	CTCGCCCTCAAAATGGGAACGCTGGCGCTGGGACTAAAGCATAGACACACAGGCTGAGTATC	60
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Qy	61	CTGACCTGAGTCATCCCGAGGGATCAGAGGCTCAGCAGGGAACCTTCATTATTTCT	120
Db	61	CTGACCTGAGTCATCCCGAGGGATCAGAGGCTCAGCAGGGAACCTTCATTATTTCT	120
Qy	121	TCAAGCAACTTACAGCTGCACCGACAGTTGGAGTGAAGTTCTAATCTCTTCCCTCCTCC	180
Db	121	TCAAGCAACTTACAGCTGCACCGACAGTTGGAGTGAAGTTCTAATCTCTTCCCTCCTCC	180
Qy	181	TGTTGCTGCCACTAATGCTGATGTCCATGGTCTCTAGCAGCCTGAATCCAGGGTCCGCA	240
Db	181	TGTTGCTGCCACTAATGCTGATGTCCATGGTCTCTAGCAGCCTGAATCCAGGGTCCGCA	240
Qy	241	GAGGCCACAGGACCGAGGCCAGGCTTCTAGAGATGGCTCCAGGAAGCGGCCAAGAT	300
Db	241	GAGGCCACAGGACCGAGGCCAGGCTTCTAGAGATGGCTCCAGGAAGCGGCCAAGAT	300
Qy	301	GTGAGTGCAAGATTGGTTCTCTGAGGCCCGAGAGAAATTCATGACGTCTGGGC	360
Db	301	GTGAGTGCAAGATTGGTTCTCTGAGGCCCGAGAGAAATTCATGACGTCTGGGC	360
Qy	361	TGCCAAAGAACGAGTGGCCCTGTGATCATTTCAAGGGCAATGTGAAGAAAACAAGACACC	420
Db	361	TGCCAAAGAACGAGTGGCCCTGTGATCATTTCAAGGGCAATGTGAAGAAAACAAGACACC	420
Qy	421	AAAGGCACACAGAAAGCCAAACAGCATTTCCAGAGCTGCCAGCAATTTCTCAACAAAT	480
Db	421	AAAGGCACACAGAAAGCCAAACAGCATTTCCAGAGCTGCCAGCAATTTCTCAACAAAT	480
Qy	481	GTGAGCTAAGAGCTTTGCTCTGCTTTGTAGGAGCTCTGAGCGCCCACTCTTCCAATTA	540
Db	481	GTGAGCTAAGAGCTTTGCTCTGCTTTGTAGGAGCTCTGAGCGCCCACTCTTCCAATTA	540
Qy	541	AACATTCTCAGCAAGAGACAGTGAGCACACCTACCAGACACTCTTCTTCCCACTTC	600

Db	541	AA	CA	TTTCTAGCCAGAGACAGTGGACACCTACGACACACTCTTCTTCTCCACCTC	600
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Db	661	GAT	CATTTTGT	TGTTGCTCTCTCTAGTGTCTTCTCTCTCAGTCTTAGCCGTGTGCC	720
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Qy	721	CT	CCCTTACC	CAGGCTTAGGCTTAATTAACCTGAAAGATTCCAGGAAACTGTAGCTTCT	780
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Qy	781	AG	CTAGTGT	CAATTAACCTTAAATGCAATCAGGAAAGTAGCAAAACAGAGTCAATAAATA	840
				PRIOR APPLICATION NUMBER: 60/088025	
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Db	781	AG	CTAGTGT	CAATTAACCTTAAATGCAATCAGGAAAGTAGCAAAACAGAGTCAATAAATA	840
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				PRIOR FILING DATE: 1998-06-04	
Qy	841	TTTT	TAATGT	CAAAAAA	870
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				PRIOR FILING DATE: 1998-06-04	
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				PRIOR FILING DATE: 1998-06-04	
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US-09-392-598-164					
Sequence 164, Application US/09992598					
Patent No: 6956108					
GENERAL INFORMATION:					
APPLICANT: Ashkenazi, Avi J.					
APPLICANT: Baker, Kevin P.					
APPLICANT: Botstein, David					
APPLICANT: Deenoyers, Luc					
APPLICANT: Eaton, Dan L.					
APPLICANT: Ferrara, Napoleone					
APPLICANT: Fong, Sherman					
APPLICANT: Gerber, Hanspeter					
APPLICANT: Gerritsen, Mary E.					
APPLICANT: Goddard, Audrey					
APPLICANT: Godowski, Paul J.					
APPLICANT: Grimaldi, J. Christopher					
APPLICANT: Gurney, Austin L.					
APPLICANT: Kljavin, Ivar J.					
APPLICANT: Napier, Mary A.					
APPLICANT: Pan, James					
APPLICANT: Paoni, Nicholas P.					
APPLICANT: Roy, Margaret Ann					
APPLICANT: Stewart, Timothy A.					
APPLICANT: Tumas, Daniel					
APPLICANT: Watanabe, Colin K.					
APPLICANT: Williams, P. Mickey					
APPLICANT: Wood, William I.					
APPLICANT: Zhang, Zemin					
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic					
TITLE OF INVENTION: Acids Encoding the Same					
FILE REFERENCE: P2730P1C20					
CURRENT APPLICATION NUMBER: US/09/992,598					
CURRENT FILING DATE: 2001-11-14					
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; PRIOR FILING DATE: 1998-06-17
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; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 870; DB 3; Length 870;
Best Local Similarity 100.0%; Pred. No. 5.2e-265; Mismatches 0; Indels 0; Gaps 0;
Matches 870; Conservative 0;

Qy 1 CTCGCCCTCAAAATGGGAACGCTGGCCTGGGACTAAAGCATAGACCAACAGGCTGAGTATC 60
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Db 61 CTGACCTGAGTCATCCCCAGGGATCAGGAGCCTCCAGCAGGAACTTTCCATATATTTCT 120

Qy 121 TCAAGCAACTTACAGCTGCACCGACAGTTGGATGGAAGTTCTAATCTTTCCCTCCCTCC 180
Db 121 TCAAGCAACTTACAGCTGCACCGACAGTTGGATGGAAGTTCTAATCTTTCCCTCCCTCC 180

Qy 181 TGTTCCTGCCACTAATGCTGATGTCATGCTCTCTAGCAGCCTGAATCCAGGGGTGCGCA 240
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Qy 841 TTTTAAATGTCAAAAAAAAAAAAAAAAAAAAA 870
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RESULT 5

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; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
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; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730PIC61
; CURRENT APPLICATION NUMBER: US/09/989,735
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/049787
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; PRIOR FILING DATE: 1998-07-09

Query Match      100.0%; Score 870; DB 4; Length 870;
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Db 121 TCAAGCAACTTACAGCTGCACCGACAGTTGGGATGAAAGTTCTTAATCTCTCCCTCCCTCC 180
Qy 181 TGTGCTGCCACTAATGCTGATGCTCAATGCTCTTAGCAGGCTGNAATCCAGGGGTGCGCA 240
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; Patent No. 7018811
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
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; APPLICANT: Gerritsen, Mary E.
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; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
```


APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730PIC60
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CURRENT FILING DATE: 2001-11-19
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;	PRIOR APPLICATION NUMBER: 60/091519	;
;	PRIOR FILING DATE: 1998-07-02	;
;	PRIOR APPLICATION NUMBER: 60/091626	;
;	PRIOR FILING DATE: 1998-07-02	;
;	PRIOR APPLICATION NUMBER: 60/091633	;

; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 870; DB 5; Length 870;
Best Local Similarity 100.0%; Pred. No. 5.2e-265;
Matches 870; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	CTCGCCCTCAATGGGAAGCGCTGGCTGGGACTAAGCATAGACACCAAGGCTGAGTATC	60
Db	1	CTCGCCCTCAATGGGAAGCGCTGGCTGGGACTAAGCATAGACACCAAGGCTGAGTATC	60
Qy	61	CTGACCTGAGTCATCCCAAGGATCAGGAGCTCAGCAGGGAAGCTTCCATTATATCT	120
Db	61	CTGACCTGAGTCATCCCAAGGATCAGGAGCTCAGCAGGGAAGCTTCCATTATATCT	120
Qy	121	TCAAGCAACTTACAGCTGCACGACAGTTGGATGAAAGTTCTAATCTTCCCTCCCTCC	180
Db	121	TCAAGCAACTTACAGCTGCACGACAGTTGGATGAAAGTTCTAATCTTCCCTCCCTCC	180
Qy	181	TGTTGCTGCACTAATGCTGATGTCATGTTCTTAGCAGCTGAATCCAGGGTGGCCA	240
Db	181	TGTTGCTGCACTAATGCTGATGTCATGTTCTTAGCAGCTGAATCCAGGGTGGCCA	240
Qy	241	GAGGCCACAGGACCGAGGCGAGGCTTCTAGGAGATGCTCCAGGAAGCGGCCAAGAT	300
Db	241	GAGGCCACAGGACCGAGGCGAGGCTTCTAGGAGATGCTCCAGGAAGCGGCCAAGAT	300
Qy	301	GTGAGTGCAAGATTTGGTTCTCTGAGAGCCCGAGAGAAAATTCATGACAGTGTCTGGGC	360
Db	301	GTGAGTGCAAGATTTGGTTCTCTGAGAGCCCGAGAGAAAATTCATGACAGTGTCTGGGC	360
Qy	361	TGCCAAGAGCAGTGCCTCTGTATCATTTCAAGGGCAATGTGAAGAAAACAGACACC	420
Db	361	TGCCAAGAGCAGTGCCTCTGTATCATTTCAAGGGCAATGTGAAGAAAACAGACACC	420
Qy	421	AAAGSCACACAGAAAGCCAAACAGATTCAGAGCCTGCCAGCAATTTCTCAAAAT	480
Db	421	AAAGSCACACAGAAAGCCAAACAGATTCAGAGCCTGCCAGCAATTTCTCAAAAT	480
Qy	481	GTGAGTAAAGAGCTTTGCTCTGCTGCTTTGTAGGAGCTCTGAGCGCCCACTCTTCCAATTA	540
Db	481	GTGAGTAAAGAGCTTTGCTCTGCTGCTTTGTAGGAGCTCTGAGCGCCCACTCTTCCAATTA	540
Qy	541	AACATTCTCAGCAAGAGAGAGTGAAGCACTTACAGACACTCTTCTTCCCACTTC	600
Db	541	AACATTCTCAGCAAGAGAGAGTGAAGCACTTACAGACACTCTTCTTCCCACTTC	600
Qy	601	ACTCTCCCACTGTACCCACCTTAATCATTCAGTGTCTCAAAAGCATGTTTTTCAA	660
Db	601	ACTCTCCCACTGTACCCACCTTAATCATTCAGTGTCTCAAAAGCATGTTTTTCAA	660
Qy	661	GATCAATTTGTTGTTGCTCTCTAGTGTCTTCTCTCTGTCAGTCTTACGCTTGTGC	720
Db	661	GATCAATTTGTTGTTGCTCTCTAGTGTCTTCTCTCTGTCAGTCTTACGCTTGTGC	720
Qy	721	CTCCCTTACCAAGCTTAGGCTTAATTAACCTGAAGATTCAGGAACCTGAGCTTCT	780
Db	721	CTCCCTTACCAAGCTTAGGCTTAATTAACCTGAAGATTCAGGAACCTGAGCTTCT	780
Qy	781	AGCTAGTGTCTTAATTAACCTTAATCAATCAGGAAGTAGCAACAGAGTCAATAATA	840
Db	781	AGCTAGTGTCTTAATTAACCTTAATCAATCAGGAAGTAGCAACAGAGTCAATAATA	840
Qy	841	TTTTTAAATGTCAAAAAAATTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	870
Db	841	TTTTTAAATGTCAAAAAAATTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	870

RESULT 8
US-09-989-728-164
; Sequence 164, Application US/09989728
; Patent No. 7029873
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Deenoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C72
; CURRENT APPLICATION NUMBER: US/09/989,728
; CURRENT FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
; PRIOR FILING DATE: 1997-11-12
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; PRIOR FILING DATE: 1998-06-03
; PRIOR APPLICATION NUMBER: 60/088021
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088025
; PRIOR FILING DATE: 1998-06-04
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; PRIOR APPLICATION NUMBER: 60/088028
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088029
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088030

35	PRIOR APPLICATION NUMBER: 60/090355	
36	PRIOR FILING DATE: 1998-06-23	
37	PRIOR APPLICATION NUMBER: 60/090429	
38	PRIOR FILING DATE: 1998-06-24	
39	PRIOR APPLICATION NUMBER: 60/090431	
40	PRIOR FILING DATE: 1998-06-24	
41	PRIOR APPLICATION NUMBER: 60/090435	
42	PRIOR FILING DATE: 1998-06-24	
43	PRIOR APPLICATION NUMBER: 60/090444	
44	PRIOR FILING DATE: 1998-06-24	
45	PRIOR APPLICATION NUMBER: 60/090445	
46	PRIOR FILING DATE: 1998-06-24	
47	PRIOR APPLICATION NUMBER: 60/090472	
48	PRIOR FILING DATE: 1998-06-24	
49	PRIOR APPLICATION NUMBER: 60/090535	
50	PRIOR FILING DATE: 1998-06-24	
51	PRIOR APPLICATION NUMBER: 60/090540	
52	PRIOR FILING DATE: 1998-06-24	
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55	PRIOR APPLICATION NUMBER: 60/090557	
56	PRIOR FILING DATE: 1998-06-24	
57	PRIOR APPLICATION NUMBER: 60/090676	
58	PRIOR FILING DATE: 1998-06-25	
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63	PRIOR APPLICATION NUMBER: 60/090694	
64	PRIOR FILING DATE: 1998-06-25	
65	PRIOR APPLICATION NUMBER: 60/090695	
66	PRIOR FILING DATE: 1998-06-25	
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68	PRIOR FILING DATE: 1998-06-25	
69	PRIOR APPLICATION NUMBER: 60/090862	
70	PRIOR FILING DATE: 1998-06-26	
71	PRIOR APPLICATION NUMBER: 60/090863	
72	PRIOR FILING DATE: 1998-06-26	
73	PRIOR APPLICATION NUMBER: 60/091360	
74	PRIOR FILING DATE: 1998-07-01	
75	PRIOR APPLICATION NUMBER: 60/091478	
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77	PRIOR APPLICATION NUMBER: 60/091544	
78	PRIOR FILING DATE: 1998-07-01	
79	PRIOR APPLICATION NUMBER: 60/091519	
80	PRIOR FILING DATE: 1998-07-02	
81	PRIOR APPLICATION NUMBER: 60/091626	
82	PRIOR FILING DATE: 1998-07-02	
83	PRIOR APPLICATION NUMBER: 60/091633	
84	PRIOR FILING DATE: 1998-07-02	
85	PRIOR APPLICATION NUMBER: 60/091978	
86	PRIOR FILING DATE: 1998-07-07	
87	PRIOR APPLICATION NUMBER: 60/091982	
88	PRIOR FILING DATE: 1998-07-07	
89	PRIOR APPLICATION NUMBER: 60/092182	
90	PRIOR FILING DATE: 1998-07-09	

Query Match 100.0%; Score 870; DB 5; Length 870;
Best Local Similarity 100.0%; Pred. No. 5.2e-265;

181	Qy	TGTTGCTGCCACTAATGCTGATGTCCATGGTCTCTAGCAGCCTGAATCCAGGGGTGCGCA	240
181	Db	TGTTGCTGCCACTAATGCTGATGTCCATGGTCTCTAGCAGCCTGAATCCAGGGGTGCGCA	240
241	Qy	GAGGCCACAGGGACCGAGGCCAGGGCTTCTAGGAGATGGCTCCAGGAAGCGGCCCAAGAAT	300
241	Db	GAGGCCACAGGGACCGAGGCCAGGGCTTCTAGGAGATGGCTCCAGGAAGCGGCCCAAGAAT	300
301	Qy	GTGAGTGCAAAAGATTGGTTTCTGAGAGCCCGAGAAAGAAAATCATGACAGTGTCTGGGC	360
301	Db	GTGAGTGCAAAAGATTGGTTTCTGAGAGCCCGAGAAAGAAAATCATGACAGTGTCTGGGC	360
361	Qy	TGCCAAAGAAGCAGTGGCCCTGTGTATCATTTCAAGGGCAATCTGAAGGAAAAACAAGACACC	420
361	Db	TGCCAAAGAAGCAGTGGCCCTGTGTATCATTTCAAGGGCAATCTGAAGGAAAAACAAGACACC	420
421	Qy	AAAGGCCACACAGAAAGCCAAACAAGCATTTCCAGAGCCTGCCAGCAATTTCTCAAAACAAT	480
421	Db	AAAGGCCACACAGAAAGCCAAACAAGCATTTCCAGAGCCTGCCAGCAATTTCTCAAAACAAT	480
481	Qy	GTGAGCTTAAGAAGCTTTTGCTCTGGCTTTGTAGGAGCTCTGAGCGCCCACTCTTCCAAATTA	540
481	Db	GTGAGCTTAAGAAGCTTTTGCTCTGGCTTTGTAGGAGCTCTGAGCGCCCACTCTTCCAAATTA	540
541	Qy	AACATTTCTCAGCCAAAGAAAGACAGTGAAGCACACTACCAGACACTCTTCTTCTCCACCTC	600
541	Db	AACATTTCTCAGCCAAAGAAAGACAGTGAAGCACACTACCAGACACTCTTCTTCTCCACCTC	600
601	Qy	ACTCTCCACATGTACCCACCCCTAAATCATTTCCAGTGTCTCTCAAAAGCATGTTTTCAA	660
601	Db	ACTCTCCACATGTACCCACCCCTAAATCATTTCCAGTGTCTCTCAAAAGCATGTTTTCAA	660
661	Qy	GATCATTTTGTGTGTGCTCTCTAGTGTCTTCTTCTCTCGTCAAGTCTTACGCTGTGGC	720
661	Db	GATCATTTTGTGTGTGCTCTCTAGTGTCTTCTTCTCTCGTCAAGTCTTACGCTGTGGC	720
721	Qy	CTCCCTTTACCGAGCTTAGGCTTAATTAAGTCTGAAAGATTTCCAGGAAACTGTAGCTTCT	780
721	Db	CTCCCTTTACCGAGCTTAGGCTTAATTAAGTCTGAAAGATTTCCAGGAAACTGTAGCTTCT	780
781	Qy	AGCTAGTGTGATTTAACCTTTAAATGCAATCAGGAAAGTAGCAAAACAGAAGTCAATAAATA	840
781	Db	AGCTAGTGTGATTTAACCTTTAAATGCAATCAGGAAAGTAGCAAAACAGAAGTCAATAAATA	840
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841	Db	TTTTTAAATGTCAAAAAATAAAAAAAAAAAAAA	870

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RESULT 9
US-09-997-349-164
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; Patent No. 7034106
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Borstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.

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; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088826
; PRIOR FILING DATE: 1998-06-10
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; PRIOR FILING DATE: 1998-06-25
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; PRIOR FILING DATE: 1998-06-25
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; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091626
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091633
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 870; DB 5; Length 870;
Best Local Similarity 100.0%; Pred. No. 5.2e-265;
Matches 870; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	CTCGCCCTCAAAATGGGAACGCTGGGCTAAAGCATAGACACCAAGGCTGAGTATC	60
Db	1	CTCGCCCTCAAAATGGGAACGCTGGGCTAAAGCATAGACACCAAGGCTGAGTATC	60
QY	61	CTGACCTGAGTCATCCCAAGGATCAGGAGCTCCAGCAGGGAACCTTCCATTATTTCT	120
Db	61	CTGACCTGAGTCATCCCAAGGATCAGGAGCTCCAGCAGGGAACCTTCCATTATTTCT	120
QY	121	TCAAGCAACTTACAGCTGACCGACAGTTGCGATGAAAGTTCTTAATCTCTTCCCTCTCC	180
Db	121	TCAAGCAACTTACAGCTGACCGACAGTTGCGATGAAAGTTCTTAATCTCTTCCCTCTCC	180
QY	181	TGTTGCTGCCACTAATGCTGATGTCATGGTCTCTAGCAGCCTGAATCCAGGGTCCCA	240
Db	181	TGTTGCTGCCACTAATGCTGATGTCATGGTCTCTAGCAGCCTGAATCCAGGGTCCCA	240
QY	241	GAGGCCACAGGACCGAGGCCAGGCTTCTAGGAGATGGCTCCAGGAAGCGGCAAGAAT	300
Db	241	GAGGCCACAGGACCGAGGCCAGGCTTCTAGGAGATGGCTCCAGGAAGCGGCAAGAAT	300
QY	301	GTGAGTGCAAAAGATTGGTTCTTGAGAGCCCCGAGAGAAAAATTCATGACAGTCTCTGGGC	360
Db	301	GTGAGTGCAAAAGATTGGTTCTTGAGAGCCCCGAGAGAAAAATTCATGACAGTCTCTGGGC	360
QY	361	TGCCAAGNAGCAGTGCCCTCTGATCATTTCAAGGGCAATCTGAGAAAAACAAGACCC	420
Db	361	TGCCAAGNAGCAGTGCCCTCTGATCATTTCAAGGGCAATCTGAGAAAAACAAGACCC	420
QY	421	AAAGGCACCAAGAAAGCCAAACAAAGCATTCCAGAGCCTGCCAGCAATTTCTCAACAAT	480
Db	421	AAAGGCACCAAGAAAGCCAAACAAAGCATTCCAGAGCCTGCCAGCAATTTCTCAACAAT	480
QY	481	GTGAGCTAAGAAAGCTTTGCTCTGCTCTTTGTAGAGCTCTGAGCGCCACTCTTCCAATTA	540
Db	481	GTGAGCTAAGAAAGCTTTGCTCTGCTCTTTGTAGAGCTCTGAGCGCCACTCTTCCAATTA	540

[illegible][illegible]

RESULT 11
US-09-989-293A-164
; Sequence 164, Application US/09989293A
; Patent No. 7034136
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730PIC66
; CURRENT APPLICATION NUMBER: US/09/989,293A
; CURRENT FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
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; PRIOR APPLICATION NUMBER: 60/065311
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; PRIOR APPLICATION NUMBER: 60/089532
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089538
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089598
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; PRIOR FILING DATE: 1998-06-23
; PRIOR APPLICATION NUMBER: 60/090355
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; PRIOR FILING DATE: 1998-07-02
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; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
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; PRIOR FILING DATE: 1998-07-09

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Best Local Similarity 100.0%; Pred. No. 5.2e-265;
Matches 870; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 121 TCAAGCAACTTACAGCTGCACCGACAGTTGCGATGAAAGTTCTTAATCTCTTCCCTCCTCC 180

181 TGTGTGCTGCCACTAATGCTGATGTCCATGGTCTCTAGCAGCCTGAATCCAGGGGTGCGCA 240
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QY 241 GAGGCCACAGGGACCGAGGCCAGGCTTCTAGGAGATGGCTCCAGGAAGGGCGGCAAGAAT 300
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QY 841 TTTTAAATGTCAAAAAA 870
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RESULT 12
US-09-702-705-113
; Sequence 113, Application US/09702705
; Patent No. 6504010
; GENERAL INFORMATION:
; APPLICANT: Wang, TongLong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Darrick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; APPLICANT: Fan, Liqun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.478C14
; CURRENT APPLICATION NUMBER: US/09/702,705
; CURRENT FILING DATE: 2000-10-30
; NUMBER OF SEQ ID NOS: 1833
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 113
; LENGTH: 533
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; TYPE: DNA
; ORGANISM: Homo sapien
US-09-702-705-113

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Best Local Similarity 99.6%; Pred. No. 4.7e-156;
Matches 527; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY 196 TGTCTATGTCATGTCCTTAGCAGCCTTAATCCAGGGGTGCGCAGAGGCCACAGGGACC 255
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QY 256 GAGGCCAGGCTTCTAGGAGATGGCTCCAGGAAGGGCGCAAGAAATGTGAGTGCAAAAGATT 315
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QY 556 GAAGACAGTGAGCAGACCTTACAGACACTCTTCTTCCGACCTCCTCCCTGCTGAC 615
Db 421 GAAGACAGTGAGCAGACCTTACAGACACTCTTCTTCCGACCTCCTCCCTGCTGAC 480

QY 616 CCACCCCTAAATCATTTCCAGTGCTCTCAAAAAGCATGTTTTTCAAGATC 664
Db 481 CCACCCCTAAATCATTTCCAGTGCTCTCAAAAAGCATGTTTTTCAAGATC 529

RESULT 13
US-09-736-457-113
; Sequence 113, Application US/09736457
; Patent No. 6509448
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Darick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.478C15
; CURRENT APPLICATION NUMBER: US/09/736,457
; CURRENT FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 1864
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 113
; LENGTH: 533
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-736-457-113

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Best Local Similarity 99.6%; Pred. No. 4.7e-156;
Matches 527; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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RESULT 14
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; Sequence 113, Application US/09614124B
; Patent No. 6830574
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Darick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; FILE REFERENCE: 210121.478C9
; CURRENT APPLICATION NUMBER: US/09/614,124B
; CURRENT FILING DATE: 2001-07-11
; NUMBER OF SEQ ID NOS: 1668
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 113
; LENGTH: 533
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-614-124B-113

Query Match      60.4%; Score 525.8; DB 3; Length 533;
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Matches 527; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Db 421 GGTTCCTGAGAGCCCGGAGAGAAATTCATGACAGTGTCTGGGCTGCCAAAGAGCAGT 480
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RESULT 15
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; Sequence 113, Application US/09671325
; Patent No. 6667154
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Darick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; APPLICANT: Fan, Liqun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.478C12
; CURRENT APPLICATION NUMBER: US/09/671,325
; CURRENT FILING DATE: 2000-09-26
; NUMBER OF SEQ ID NOS: 1825
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 113
; LENGTH: 533
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-671-325-113

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Best Local Similarity 99.6%; Pred. No. 4.7e-156;
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Db 1 CTGCACCGACAGTTGGATGAAGAATCTTAATCTCTTCCCTCTCTCTGTTGCTGCCACTAA 60
QY 196 TGCTGATGTCCATGGTCTCTAGCAGGCTGAATCTCAGGGGTGCGCAGAGGCCACAGGGACC 255
Db 61 TGCTGATGTCCATGGTCTCTAGCAGGCTGAATCTCAGGGGTGCGCAGAGGCCACAGGGACC 120

QY 256 GAGGCCAGGCTTCTAGGAGATGCTCCAGGAAGGCCCAAGAATGTGAGTGCAGAAAGATT 315
Db 121 GAGGCCAGGCTTCTAGGAGATGCTCCAGGAAGGCCCAAGAATGTGAGTGCAGAAAGATT 180
QY 316 GGTTCCTGAGAGCCCGGAGAGAAATTCATGACAGTGTCTGGGCTGCCAAAGAGCAGT 375
Db 181 GGTTCCTGAGAGCCCGGAGAGAAATTCATGACAGTGTCTGGGCTGCCAAAGAGCAGT 240
QY 376 GGTTCCTGAGAGCCCGGAGAGAAATTCATGACAGTGTCTGGGCTGCCAAAGAGCAGT 435
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Db 301 GGTTCCTGAGAGCCCGGAGAGAAATTCATGACAGTGTCTGGGCTGCCAAAGAGCAGT 360
QY 496 GGTTCCTGAGAGCCCGGAGAGAAATTCATGACAGTGTCTGGGCTGCCAAAGAGCAGT 555
Db 361 GGTTCCTGAGAGCCCGGAGAGAAATTCATGACAGTGTCTGGGCTGCCAAAGAGCAGT 420
QY 556 GGTTCCTGAGAGCCCGGAGAGAAATTCATGACAGTGTCTGGGCTGCCAAAGAGCAGT 615
Db 421 GGTTCCTGAGAGCCCGGAGAGAAATTCATGACAGTGTCTGGGCTGCCAAAGAGCAGT 480
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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5	870	100.0	870	8	US-11-266-748A-161169
6	870	100.0	870	8	US-11-266-748A-406176
7	870	100.0	870	8	US-11-266-748A-477222
8	856.6	98.5	1172	6	US-10-525-116-1107
9	832.2	95.7	920	8	US-11-266-748A-185141
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C 105	35.6	4.1	1000	8	US-11-266-748A-401156	Sequence 401156,	C 179	35	4.0	31483	8	US-11-266-748A-58439	Sequence 58439, A
C 106	35.6	4.1	1000	8	US-11-266-748A-470396	Sequence 470396,	C 180	35	4.0	523643	6	US-10-540-898-308	Sequence 308, App
C 107	35.6	4.1	1000	8	US-11-266-748A-471514	Sequence 471514,	C 181	34.8	4.0	754	8	US-11-266-748A-214622	Sequence 214622,
C 108	35.6	4.1	1000	8	US-11-266-748A-471819	Sequence 471819,	182	34.8	4.0	754	8	US-11-266-748A-237158	Sequence 237158,
C 109	35.6	4.1	1000	8	US-11-266-748A-471819	Sequence 471819,	183	34.8	4.0	1000	8	US-11-266-748A-115421	Sequence 115421,
C 110	35.6	4.1	7364	6	US-10-486-020-33	Sequence 33,	184	34.8	4.0	1000	8	US-11-266-748A-115494	Sequence 115494,
C 111	35.6	4.1	114854	6	US-10-486-020-33	Sequence 33, App1	185	34.8	4.0	1000	8	US-11-266-748A-115494	Sequence 115494,
C 112	35.6	4.1	203132	6	US-10-539-228-459	Sequence 850, App	186	34.8	4.0	1000	8	US-11-266-748A-119027	Sequence 119027,
C 113	35.4	4.1	249	8	US-11-266-748A-411248	Sequence 459, App	C 187	34.8	4.0	1000	8	US-11-266-748A-157585	Sequence 157585,
C 114	35.4	4.1	856	8	US-11-266-748A-50143	Sequence 50143, A	C 188	34.8	4.0	1000	8	US-11-266-748A-161191	Sequence 161191,
C 115	35.4	4.1	1000	8	US-11-266-748A-284969	Sequence 284969,	189	34.8	4.0	1000	8	US-11-266-748A-206574	Sequence 206574,
C 116	35.4	4.1	1000	8	US-11-266-748A-290799	Sequence 290799,	190	34.8	4.0	1000	8	US-11-266-748A-284640	Sequence 284640,
C 117	35.4	4.1	1000	8	US-11-266-748A-294060	Sequence 294060,	191	34.8	4.0	1000	8	US-11-266-748A-284832	Sequence 284832,
C 118	35.4	4.1	1000	8	US-11-266-748A-336398	Sequence 336398,	192	34.8	4.0	1000	8	US-11-266-748A-284900	Sequence 284900,
C 119	35.4	4.1	1000	8	US-11-266-748A-342228	Sequence 342228,	193	34.8	4.0	1000	8	US-11-266-748A-286693	Sequence 286693,
C 120	35.4	4.1	1000	8	US-11-266-748A-345489	Sequence 345489,	194	34.8	4.0	1000	8	US-11-266-748A-293177	Sequence 293177,
C 121	35.4	4.1	1234	7	US-11-376-673-63	Sequence 63, App1	195	34.8	4.0	1000	8	US-11-266-748A-293237	Sequence 293237,
C 122	35.4	4.1	1234	7	US-11-376-673-63	Sequence 63, App1	196	34.8	4.0	1000	8	US-11-266-748A-294057	Sequence 294057,
C 123	35.4	4.1	1234	7	US-11-376-673-63	Sequence 63, App1	197	34.8	4.0	1000	8	US-11-266-748A-336069	Sequence 336069,
C 124	35.4	4.1	1498	7	US-11-218-305-18404	Sequence 18404, A	C 198	34.8	4.0	1000	8	US-11-266-748A-336261	Sequence 336261,
C 125	35.2	4.0	743	8	US-11-266-748A-34474	Sequence 34474, A	C 199	34.8	4.0	1000	8	US-11-266-748A-336329	Sequence 336329,
C 126	35.2	4.0	746	8	US-11-266-748A-45798	Sequence 45798, A	C 200	34.8	4.0	1000	8	US-11-266-748A-338322	Sequence 338322,
C 127	35.2	4.0	969	8	US-11-217-529-293	Sequence 293, App	C 201	34.8	4.0	1000	8	US-11-266-748A-344606	Sequence 344606,
C 128	35.2	4.0	1000	8	US-11-266-748A-116732	Sequence 116732,	C 202	34.8	4.0	1000	8	US-11-266-748A-344666	Sequence 344666,
C 129	35.2	4.0	1000	8	US-11-266-748A-158896	Sequence 158896,	C 203	34.8	4.0	1000	8	US-11-266-748A-345486	Sequence 345486,
C 130	35.2	4.0	1000	8	US-11-266-748A-288232	Sequence 288232,	C 204	34.8	4.0	1000	8	US-11-266-748A-393988	Sequence 393988,
C 131	35.2	4.0	1000	8	US-11-266-748A-288232	Sequence 288232,	205	34.8	4.0	1000	8	US-11-266-748A-394942	Sequence 394942,
C 132	35.2	4.0	1000	8	US-11-266-748A-339661	Sequence 339661,	206	34.8	4.0	1000	8	US-11-266-748A-397460	Sequence 397460,
C 133	35.2	4.0	1000	8	US-11-266-748A-340255	Sequence 340255,	207	34.8	4.0	1000	8	US-11-266-748A-397843	Sequence 397843,
C 134	35.2	4.0	1000	8	US-11-266-748A-398471	Sequence 398471,	208	34.8	4.0	1000	8	US-11-266-748A-405090	Sequence 405090,
C 135	35.2	4.0	1000	8	US-11-266-748A-399073	Sequence 399073,	209	34.8	4.0	1000	8	US-11-266-748A-405183	Sequence 405183,
C 136	35.2	4.0	1000	8	US-11-266-748A-399747	Sequence 399747,	210	34.8	4.0	1000	8	US-11-266-748A-406259	Sequence 406259,
C 137	35.2	4.0	1000	8	US-11-266-748A-469517	Sequence 469517,	C 211	34.8	4.0	1000	8	US-11-266-748A-465034	Sequence 465034,
C 138	35.2	4.0	1000	8	US-11-266-748A-470119	Sequence 470119,	C 212	34.8	4.0	1000	8	US-11-266-748A-465988	Sequence 465988,
C 139	35.2	4.0	1000	8	US-11-266-748A-470193	Sequence 470193,	C 213	34.8	4.0	1000	8	US-11-266-748A-468506	Sequence 468506,
C 140	35.2	4.0	1110	7	US-11-218-305-3740	Sequence 3740, App	C 214	34.8	4.0	1000	8	US-11-266-748A-468889	Sequence 468889,
C 141	35.2	4.0	1151	8	US-11-216-545-7947	Sequence 7947, App	C 215	34.8	4.0	1000	8	US-11-266-748A-476136	Sequence 476136,
C 142	35.2	4.0	1270	8	US-11-216-545-1128	Sequence 1128, App	C 216	34.8	4.0	1000	8	US-11-266-748A-476229	Sequence 476229,
C 143	35.2	4.0	1459	7	US-11-218-305-1862	Sequence 1862, App	C 217	34.8	4.0	1000	8	US-11-266-748A-477305	Sequence 477305,
C 144	35.2	4.0	1966	8	US-11-216-545-7823	Sequence 7823, App	C 218	34.8	4.0	1133	7	US-11-056-355B-62113	Sequence 62113, A
C 145	35.2	4.0	2317	8	US-11-266-748A-29972	Sequence 29972, A	219	34.8	4.0	1275	7	US-11-218-305-12535	Sequence 12535, A
C 146	35.2	4.0	2380	8	US-11-266-748A-29972	Sequence 29972, A	220	34.8	4.0	1607	8	US-11-216-545-1884	Sequence 1884, App
C 147	35.2	4.0	2522	7	US-11-218-305-24510	Sequence 24510, A	221	34.8	4.0	1926	7	US-11-218-305-16080	Sequence 16080, A
C 148	35.2	4.0	2630	8	US-11-266-748A-27342	Sequence 27342, A	222	34.8	4.0	1998	7	US-11-218-305-17499	Sequence 17499, A
C 149	35.2	4.0	4596	8	US-11-266-748A-30159	Sequence 30159, A	223	34.8	4.0	2434	8	US-11-266-748A-23037	Sequence 23037, A
C 150	35.2	4.0	4670	8	US-11-145-307A-29	Sequence 29, App1	224	34.8	4.0	2435	8	US-11-266-748A-27697	Sequence 27697, A
C 151	35.2	4.0	6001	6	US-10-517-441-344	Sequence 344, App	C 225	34.8	4.0	2501	6	US-10-517-441-286	Sequence 286, App
C 152	35.2	4.0	17897	6	US-10-517-441-344	Sequence 344, App	C 226	34.8	4.0	2501	6	US-10-517-441-560	Sequence 560, App
C 153	35.2	4.0	17897	6	US-10-517-441-618	Sequence 618, App	C 227	34.8	4.0	2614	8	US-11-266-748A-23126	Sequence 23126, A
C 154	35	4.0	719	8	US-11-216-545-855	Sequence 855, App	228	34.8	4.0	3976	8	US-11-266-748A-27299	Sequence 27299, A
C 155	35	4.0	869	8	US-11-266-748A-44784	Sequence 44784, A	229	34.8	4.0	4437	8	US-11-266-748A-28422	Sequence 28422, A
C 156	35	4.0	1000	8	US-11-266-748A-119068	Sequence 119068,	230	34.8	4.0	5261	8	US-11-266-748A-24343	Sequence 24343, A
C 157	35	4.0	1000	8	US-11-266-748A-161232	Sequence 161232,	231	34.8	4.0	5297	8	US-11-266-748A-29617	Sequence 29617, A
C 158	35	4.0	1000	8	US-11-266-748A-221950	Sequence 221950,	232	34.8	4.0	5493	6	US-10-517-441-417	Sequence 417, App
C 159	35	4.0	1000	8	US-11-266-748A-287551	Sequence 287551,	C 233	34.8	4.0	10865	6	US-10-517-441-464	Sequence 464, App
C 160	35	4.0	1000	8	US-11-266-748A-294371	Sequence 294371,	C 234	34.8	4.0	10865	6	US-10-517-441-738	Sequence 738, App
C 161	35	4.0	1000	8	US-11-266-748A-338980	Sequence 338980,	C 235	34.8	4.0	176928	8	US-11-266-748A-60803	Sequence 60803, A
C 162	35	4.0	1000	8	US-11-266-748A-345800	Sequence 345800,	C 236	34.6	4.0	390	8	US-11-266-748A-101792	Sequence 101792,
C 163	35	4.0	1000	8	US-11-266-748A-398275	Sequence 398275,	237	34.6	4.0	390	8	US-11-266-748A-154603	Sequence 154603,
C 164	35	4.0	1000	8	US-11-266-748A-405845	Sequence 405845,	238	34.6	4.0	647	7	US-11-218-305-21341	Sequence 21341, A
C 165	35	4.0	1000	8	US-11-266-748A-406404	Sequence 406404,	239	34.6	4.0	1000	8	US-11-266-748A-118863	Sequence 118863,
C 166	35	4.0	1000	8	US-11-266-748A-406628	Sequence 406628,	240	34.6	4.0	1000	8	US-11-266-748A-161027	Sequence 161027,
C 167	35	4.0	1000	8	US-11-266-748A-469321	Sequence 469321,	241	34.6	4.0	1000	8	US-11-266-748A-206499	Sequence 206499,
C 168	35	4.0	1000	8	US-11-266-748A-476891	Sequence 476891,	242	34.6	4.0	1000	8	US-11-266-748A-206829	Sequence 206829,
C 169	35	4.0	1000	8	US-11-266-748A-477450	Sequence 477450,	C 243	34.6	4.0	1000	8	US-11-266-748A-209393	Sequence 209393,
C 170	35	4.0	1000	8	US-11-266-748A-477674	Sequence 477674,	C 244	34.6	4.0	1000	8	US-11-266-748A-233969	Sequence 233969,
C 171	35	4.0	1195	6	US-10-374-780A-722	Sequence 722, App	245	34.6	4.0	1000	8	US-11-266-748A-285941	Sequence 285941,
C 172	35	4.0	1545	8	US-11-216-545-1120	Sequence 1120, App	246	34.6	4.0	1000	8	US-11-266-748A-285941	Sequence 285941,

247	34.6	4.0	1000	8	US-11-266-748A-293457	Sequence 293457,	c 320	34.2	3.9	1152	7	US-11-218-305-21291	Sequence 21291, A
C 248	34.6	4.0	1000	8	US-11-266-748A-337370	Sequence 337370,	321	34.2	3.9	1153	8	US-11-216-545-1113	Sequence 1113, Ap
C 249	34.6	4.0	1000	8	US-11-266-748A-344886	Sequence 344886,	322	34.2	3.9	1305	8	US-11-216-545-4873	Sequence 4873, Ap
250	34.6	4.0	1000	8	US-11-266-748A-396292	Sequence 396292,	323	34.2	3.9	1370	7	US-11-266-748A-26242	Sequence 26242, A
251	34.6	4.0	1000	8	US-11-266-748A-405486	Sequence 405486,	324	34.2	3.9	1432	7	US-11-218-305-1986	Sequence 1986, Ap
C 252	34.6	4.0	1000	8	US-11-266-748A-467338	Sequence 467338,	c 325	34.2	3.9	1591	8	US-11-216-545-2432	Sequence 2432, Ap
C 253	34.6	4.0	1020	7	US-11-266-748A-476532	Sequence 476532,	326	34.2	3.9	1723	8	US-11-266-748A-31403	Sequence 31403, A
C 254	34.6	4.0	1020	7	US-11-305-666-132	Sequence 132, App	327	34.2	3.9	2017	7	US-11-366-001-45	Sequence 45, Appl
C 255	34.6	4.0	1020	7	US-11-317-789A-39	Sequence 39, Appl	328	34.2	3.9	2057	8	US-11-266-748A-26180	Sequence 26180, A
C 256	34.6	4.0	1314	8	US-11-216-545-3174	Sequence 3174, Ap	329	34.2	3.9	2084	8	US-11-266-748A-26502	Sequence 26502, A
257	34.6	4.0	1386	7	US-11-218-305-14787	Sequence 14787, A	330	34.2	3.9	2708	8	US-11-266-748A-27992	Sequence 27992, A
258	34.6	4.0	1467	8	US-11-266-748A-24319	Sequence 24319, A	331	34.2	3.9	2781	6	US-10-511-937-470	Sequence 470, App
259	34.6	4.0	1480	8	US-11-216-545-7639	Sequence 7639, Ap	332	34.2	3.9	2781	8	US-11-266-748A-27281	Sequence 27281, A
260	34.6	4.0	1591	8	US-11-266-748A-57969	Sequence 57969, A	333	34.2	3.9	2781	8	US-11-266-748A-31492	Sequence 31492, A
261	34.6	4.0	1651	8	US-11-266-748A-178609	Sequence 178609, A	334	34.2	3.9	2781	8	US-11-266-748A-56756	Sequence 56756, A
262	34.6	4.0	2005	6	US-11-266-748A-25450	Sequence 25450, A	335	34.2	3.9	5993	6	US-10-564-311-2	Sequence 2, Appl
263	34.6	4.0	2205	6	US-10-953-349-9921	Sequence 9921, Ap	336	34.2	3.9	5993	6	US-10-517-441-308	Sequence 308, App
264	34.6	4.0	2205	7	US-11-056-355B-45587	Sequence 45587, A	C 337	34.2	3.9	8093	6	US-10-517-441-582	Sequence 582, App
265	34.6	4.0	3021	8	US-11-181-115-9	Sequence 9, Appl	338	34	3.9	691	8	US-11-266-748A-217675	Sequence 217675,
C 266	34.6	4.0	3294	8	US-11-266-748A-31414	Sequence 31414, A	C 339	34	3.9	691	8	US-11-266-748A-238689	Sequence 238689,
C 267	34.4	4.0	419	8	US-11-266-748A-302966	Sequence 302966,	340	34	3.9	807	6	US-10-953-349-36144	Sequence 36144, A
C 268	34.4	4.0	489	8	US-11-266-748A-44601	Sequence 44601, A	341	34	3.9	812	7	US-11-218-305-15354	Sequence 15354, A
269	34.4	4.0	598	8	US-11-266-748A-54876	Sequence 54876, A	342	34	3.9	950	7	US-11-218-305-18511	Sequence 18511, A
270	34.4	4.0	751	8	US-11-266-748A-42650	Sequence 42650, A	C 343	34	3.9	1000	8	US-11-266-748A-206408	Sequence 206408,
C 271	34.4	4.0	972	7	US-11-218-305-17390	Sequence 17390, A	C 344	34	3.9	1000	8	US-11-266-748A-210626	Sequence 210626,
C 272	34.4	4.0	1000	8	US-11-266-748A-160120	Sequence 160120,	345	34	3.9	1000	8	US-11-266-748A-223811	Sequence 223811,
273	34.4	4.0	1000	8	US-11-266-748A-17956	Sequence 17956,	346	34	3.9	1000	8	US-11-266-748A-287489	Sequence 287489,
274	34.4	4.0	1000	8	US-11-266-748A-224490	Sequence 224490,	C 347	34	3.9	1000	8	US-11-266-748A-288276	Sequence 288276,
275	34.4	4.0	1000	8	US-11-266-748A-286087	Sequence 286087,	348	34	3.9	1000	8	US-11-266-748A-232535	Sequence 232535,
276	34.4	4.0	1000	8	US-11-266-748A-290633	Sequence 290633,	C 349	34	3.9	1000	8	US-11-266-748A-338918	Sequence 338918,
277	34.4	4.0	1000	8	US-11-266-748A-290862	Sequence 290862,	C 350	34	3.9	1000	8	US-11-266-748A-339705	Sequence 339705,
278	34.4	4.0	1000	8	US-11-266-748A-293570	Sequence 293570,	C 351	34	3.9	1000	8	US-11-266-748A-343964	Sequence 343964,
C 279	34.4	4.0	1000	8	US-11-266-748A-337516	Sequence 337516,	C 352	34	3.9	1000	8	US-11-266-748A-399124	Sequence 399124,
C 280	34.4	4.0	1000	8	US-11-266-748A-342062	Sequence 342062,	353	34	3.9	1000	8	US-11-266-748A-400211	Sequence 400211,
C 281	34.4	4.0	1000	8	US-11-266-748A-342291	Sequence 342291,	354	34	3.9	1000	8	US-11-266-748A-403532	Sequence 403532,
C 282	34.4	4.0	1000	8	US-11-266-748A-344999	Sequence 344999,	355	34	3.9	1000	8	US-11-266-748A-404254	Sequence 404254,
283	34.4	4.0	1000	8	US-11-266-748A-401593	Sequence 401593,	356	34	3.9	1000	8	US-11-266-748A-404282	Sequence 404282,
284	34.4	4.0	1000	8	US-11-266-748A-401953	Sequence 401953,	357	34	3.9	1000	8	US-11-266-748A-470170	Sequence 470170,
285	34.4	4.0	1000	8	US-11-266-748A-402225	Sequence 402225,	C 358	34	3.9	1000	8	US-11-266-748A-471257	Sequence 471257,
286	34.4	4.0	1000	8	US-11-266-748A-402225	Sequence 402225,	C 359	34	3.9	1000	8	US-11-266-748A-474578	Sequence 474578,
C 287	34.4	4.0	1000	8	US-11-266-748A-405640	Sequence 405640,	C 360	34	3.9	1000	8	US-11-266-748A-475300	Sequence 475300,
C 288	34.4	4.0	1000	8	US-11-266-748A-472639	Sequence 472639,	C 361	34	3.9	1000	8	US-11-266-748A-475328	Sequence 475328,
C 289	34.4	4.0	1000	8	US-11-266-748A-472999	Sequence 472999,	362	34	3.9	1051	7	US-11-218-305-17914	Sequence 17914, A
C 290	34.4	4.0	1000	8	US-11-266-748A-473271	Sequence 473271,	363	34	3.9	1149	8	US-11-266-748A-23108	Sequence 23108, A
C 291	34.4	4.0	1899	7	US-11-218-305-2730	Sequence 2730, Ap	364	34	3.9	1149	8	US-11-266-748A-58461	Sequence 58461, A
292	34.4	4.0	1327	6	US-10-374-780A-732	Sequence 732, App	365	34	3.9	1312	8	US-11-266-748A-25591	Sequence 25591, A
293	34.4	4.0	1448	7	US-11-218-305-1185	Sequence 1185, Ap	366	34	3.9	1581	7	US-11-056-355B-66051	Sequence 66051, A
C 294	34.4	4.0	1591	7	US-11-218-305-24586	Sequence 24586, A	367	34	3.9	1630	7	US-11-218-305-15787	Sequence 15787, A
C 295	34.4	4.0	1843	6	US-10-511-937-620	Sequence 620, App	368	34	3.9	1700	6	US-10-953-349-21788	Sequence 21788, A
296	34.4	4.0	1989	8	US-11-216-545-5413	Sequence 5413, Ap	369	34	3.9	1700	7	US-11-056-355B-57271	Sequence 57271, A
297	34.4	4.0	2213	8	US-11-216-545-3411	Sequence 3411, Ap	370	34	3.9	2446	8	US-11-266-748A-23513	Sequence 23513, A
298	34.4	4.0	2708	8	US-11-266-748A-27840	Sequence 27840, A	371	34	3.9	2979	8	US-11-266-748A-23702	Sequence 23702, A
299	34.4	4.0	3883	8	US-11-266-748A-27939	Sequence 27939, A	372	34	3.9	3345	8	US-11-266-748A-27340	Sequence 27340, A
300	34.4	4.0	4089	8	US-11-266-748A-27497	Sequence 27497, A	373	34	3.9	3411	8	US-11-266-748A-27212	Sequence 27212, A
301	34.2	3.9	390	8	US-11-266-748A-58049	Sequence 58049, A	C 374	34	3.9	4894	6	US-10-511-937-566	Sequence 566, App
302	34.2	3.9	653	8	US-11-266-748A-410282	Sequence 410282,	C 375	34	3.9	14147	6	US-10-517-441-265	Sequence 265, App
C 303	34.2	3.9	736	8	US-11-266-748A-212952	Sequence 212952,	C 376	33.8	3.9	693	8	US-11-266-748A-211768	Sequence 211768,
304	34.2	3.9	736	8	US-11-266-748A-236207	Sequence 236207,	377	33.8	3.9	693	8	US-11-266-748A-235371	Sequence 235371,
305	34.2	3.9	893	7	US-11-218-305-1005	Sequence 1005, Ap	378	33.8	3.9	813	8	US-11-216-545-7334	Sequence 7324, Ap
306	34.2	3.9	924	8	US-11-266-748A-45588	Sequence 45588, A	C 379	33.8	3.9	899	7	US-11-218-305-10455	Sequence 10455, A
307	34.2	3.9	931	8	US-11-266-748A-40946	Sequence 40946, A	C 380	33.8	3.9	1000	8	US-11-266-748A-115665	Sequence 115665,
308	34.2	3.9	1000	8	US-11-266-748A-118848	Sequence 118848,	381	33.8	3.9	1000	8	US-11-266-748A-116660	Sequence 116660,
C 309	34.2	3.9	1000	8	US-11-266-748A-161012	Sequence 161012,	C 382	33.8	3.9	1000	8	US-11-266-748A-157829	Sequence 157829,
310	34.2	3.9	1000	8	US-11-266-748A-206477	Sequence 206477,	C 383	33.8	3.9	1000	8	US-11-266-748A-158824	Sequence 158824,
311	34.2	3.9	1000	8	US-11-266-748A-209665	Sequence 209665,	384	33.8	3.9	1000	8	US-11-266-748A-224245	Sequence 224245,
312	34.2	3.9	1000	8	US-11-266-748A-287498	Sequence 287498,	385	33.8	3.9	1000	8	US-11-266-748A-224579	Sequence 224579,
313	34.2	3.9	1000	8	US-11-266-748A-288969	Sequence 288969,	386	33.8	3.9	1000	8	US-11-266-748A-287427	Sequence 287427,
314	34.2	3.9	1000	8	US-11-266-748A-293408	Sequence 293408,	387	33.8	3.9	1000	8	US-11-266-748A-291640	Sequence 291640,
C 315	34.2	3.9	1000	8	US-11-266-748A-338927	Sequence 338927,	388	33.8	3.9	1000	8	US-11-266-748A-232902	Sequence 232902,
C 316	34.2	3.9	1000	8	US-11-266-748A-340398	Sequence 340398,	C 389	33.8	3.9	1000	8	US-11-266-748A-338856	Sequence 338856,
C 317	34.2	3.9	1000	8	US-11-266-748A-344837	Sequence 344837,	C 390	33.8	3.9	1000	8	US-11-266-748A-343069	Sequence 343069,
318	34.2	3.9	1000	8	US-11-266-748A-398211	Sequence 398211,	C 391	33.8	3.9	1000	8	US-11-266-748A-344331	Sequence 344331,
C 319	34.2	3.9	1000	8	US-11-266-748A-469257	Sequence 469257,	392	33.8	3.9	1000	8	US-11-266-748A-395395	Sequence 395395,

393	33.8	3.9	1000	8	US-11-266-748A-398108	Sequence 398108,	c 467	33.6	3.9	1121	7	US-11-218-305-22972	Sequence 22972, A
394	33.8	3.9	1000	8	US-11-266-748A-398448	Sequence 398448,	468	33.6	3.9	1124	7	US-11-218-305-19059	Sequence 19059, A
395	33.8	3.9	1000	8	US-11-266-748A-403132	Sequence 403132,	469	33.6	3.9	1334	7	US-11-218-305-7319	Sequence 7319, Ap
396	33.8	3.9	1000	8	US-11-266-748A-404754	Sequence 404754,	470	33.6	3.9	1351	7	US-11-266-748A-56863	Sequence 56863, A
397	33.8	3.9	1000	8	US-11-266-748A-405042	Sequence 405042,	471	33.6	3.9	1368	8	US-11-266-748A-32768	Sequence 32768, A
398	33.8	3.9	1000	8	US-11-266-748A-405973	Sequence 405973,	c 472	33.6	3.9	1415	7	US-11-218-305-21764	Sequence 21764, A
399	33.8	3.9	1000	8	US-11-266-748A-466441	Sequence 466441,	c 473	33.6	3.9	1630	6	US-10-517-441-552	Sequence 552, App
400	33.8	3.9	1000	8	US-11-266-748A-469154	Sequence 469154,	c 474	33.6	3.9	1678	8	US-11-216-545-1613	Sequence 1613, Ap
401	33.8	3.9	1000	8	US-11-266-748A-469494	Sequence 469494,	c 475	33.6	3.9	1753	8	US-11-216-545-1680	Sequence 1680, Ap
402	33.8	3.9	1000	8	US-11-266-748A-474178	Sequence 474178,	476	33.6	3.9	1783	8	US-11-216-545-5349	Sequence 5349, Ap
403	33.8	3.9	1000	8	US-11-266-748A-475800	Sequence 475800,	477	33.6	3.9	2036	7	US-11-218-305-3322	Sequence 3322, Ap
404	33.8	3.9	1000	8	US-11-266-748A-476088	Sequence 476088,	478	33.6	3.9	2286	7	US-11-266-748A-30211	Sequence 30211, A
405	33.8	3.9	1000	8	US-11-266-748A-477019	Sequence 477019,	c 479	33.6	3.9	2303	7	US-11-218-305-15401	Sequence 15401, A
406	33.8	3.9	1023	6	US-10-374-780A-1317	Sequence 1317, Ap	480	33.6	3.9	2315	7	US-11-218-305-15574	Sequence 15574, A
407	33.8	3.9	1316	6	US-10-953-349-14397	Sequence 14397, A	481	33.6	3.9	2419	8	US-11-266-748A-27485	Sequence 27485, A
408	33.8	3.9	1316	6	US-11-216-545-7178	Sequence 7178, Ap	482	33.6	3.9	2566	8	US-11-216-545-5967	Sequence 5967, Ap
409	33.8	3.9	1428	7	US-11-218-305-10458	Sequence 10458, A	483	33.6	3.9	2627	8	US-11-266-748A-26574	Sequence 26574, Ap
410	33.8	3.9	1621	8	US-11-266-748A-26773	Sequence 26773, A	c 484	33.6	3.9	2679	8	US-11-216-545-1918	Sequence 1918, Ap
411	33.8	3.9	1685	8	US-11-266-748A-57523	Sequence 57523, A	485	33.6	3.9	2714	8	US-11-266-748A-23931	Sequence 23931, Ap
412	33.8	3.9	1777	7	US-11-218-305-10457	Sequence 10457, A	486	33.6	3.9	3575	8	US-11-266-748A-24461	Sequence 24461, A
413	33.8	3.9	1857	8	US-11-216-545-8563	Sequence 8563, Ap	487	33.6	3.9	3930	8	US-11-266-748A-26576	Sequence 26576, A
414	33.8	3.9	1874	7	US-11-218-305-20059	Sequence 20059, A	488	33.6	3.9	4496	7	US-11-317-330A-16	Sequence 16, Appl
415	33.8	3.9	2117	7	US-11-218-305-18284	Sequence 18284, A	489	33.6	3.9	4731	8	US-11-266-748A-21774	Sequence 21774, A
416	33.8	3.9	2181	8	US-11-216-545-4687	Sequence 4687, Ap	490	33.6	3.9	5895	7	US-11-218-305-8517	Sequence 8517, Ap
417	33.8	3.9	2261	6	US-10-511-937-415	Sequence 415, App	491	33.6	3.9	9747	8	US-11-266-748A-28362	Sequence 28362, A
418	33.8	3.9	2261	7	US-11-346-759-99	Sequence 99, Appl	492	33.6	3.9	15964	8	US-11-266-748A-22815	Sequence 22815, A
419	33.8	3.9	2270	8	US-11-266-748A-26193	Sequence 26193, A	c 493	33.6	3.9	15964	8	US-11-540-898-868	Sequence 868, App
420	33.8	3.9	2379	8	US-11-266-748A-25071	Sequence 25071, A	494	33.4	3.8	617	7	US-11-218-305-12814	Sequence 12814, A
421	33.8	3.9	2414	6	US-10-374-780A-1604	Sequence 1604, Ap	c 495	33.4	3.8	627	8	US-11-266-748A-212396	Sequence 212396, A
422	33.8	3.9	4081	8	US-11-266-748A-23051	Sequence 23051, A	496	33.4	3.8	627	8	US-11-266-748A-235835	Sequence 235835, A
423	33.8	3.9	7132	8	US-11-266-748A-28498	Sequence 28498, A	c 497	33.4	3.8	697	8	US-11-266-748A-44345	Sequence 44345, A
424	33.8	3.9	138754	8	US-11-266-748A-23615	Sequence 23615, A	c 498	33.4	3.8	714	8	US-11-266-748A-17742	Sequence 17742, A
425	33.8	3.9	286	6	US-10-488-619-2977	Sequence 2977, Ap	499	33.4	3.8	958	8	US-11-266-748A-118706	Sequence 118706, A
426	33.6	3.9	626	8	US-11-266-748A-211275	Sequence 211275,	c 500	33.4	3.8	958	8	US-11-266-748A-160870	Sequence 160870, A
427	33.6	3.9	626	8	US-11-266-748A-234983	Sequence 234983,	501	33.4	3.8	958	8	US-11-266-748A-404762	Sequence 404762, A
428	33.6	3.9	705	8	US-11-266-748A-58294	Sequence 58294, A	c 502	33.4	3.8	958	8	US-11-266-748A-475808	Sequence 475808, A
429	33.6	3.9	932	8	US-11-266-748A-27640	Sequence 27640, A	503	33.4	3.8	960	8	US-11-266-748A-284744	Sequence 284744, A
430	33.6	3.9	1000	8	US-11-266-748A-118509	Sequence 118509,	c 504	33.4	3.8	960	8	US-11-266-748A-336173	Sequence 336173, A
431	33.6	3.9	1000	8	US-11-266-748A-160673	Sequence 160673,	505	33.4	3.8	1000	8	US-11-266-748A-222773	Sequence 222773, A
432	33.6	3.9	1000	8	US-11-266-748A-221596	Sequence 221596,	506	33.4	3.8	1000	8	US-11-266-748A-224499	Sequence 224499, A
433	33.6	3.9	1000	8	US-11-266-748A-223510	Sequence 223510,	507	33.4	3.8	1000	8	US-11-266-748A-289874	Sequence 289874, A
434	33.6	3.9	1000	8	US-11-266-748A-286954	Sequence 286954,	508	33.4	3.8	1000	8	US-11-266-748A-290880	Sequence 290880, A
435	33.6	3.9	1000	8	US-11-266-748A-289020	Sequence 289020,	509	33.4	3.8	1000	8	US-11-266-748A-291206	Sequence 291206, A
436	33.6	3.9	1000	8	US-11-266-748A-289939	Sequence 289939,	510	33.4	3.8	1000	8	US-11-266-748A-293531	Sequence 293531, A
437	33.6	3.9	1000	8	US-11-266-748A-291166	Sequence 291166,	511	33.4	3.8	1000	8	US-11-266-748A-293595	Sequence 293595, A
438	33.6	3.9	1000	8	US-11-266-748A-291187	Sequence 291187,	c 512	33.4	3.8	1000	8	US-11-266-748A-341303	Sequence 341303, A
439	33.6	3.9	1000	8	US-11-266-748A-292342	Sequence 292342,	513	33.4	3.8	1000	8	US-11-266-748A-342309	Sequence 342309, A
440	33.6	3.9	1000	8	US-11-266-748A-292318	Sequence 292318,	c 514	33.4	3.8	1000	8	US-11-266-748A-343635	Sequence 343635, A
441	33.6	3.9	1000	8	US-11-266-748A-292918	Sequence 292918,	c 515	33.4	3.8	1000	8	US-11-266-748A-343960	Sequence 343960, A
442	33.6	3.9	1000	8	US-11-266-748A-338383	Sequence 338383,	c 516	33.4	3.8	1000	8	US-11-266-748A-345024	Sequence 345024, A
443	33.6	3.9	1000	8	US-11-266-748A-344347	Sequence 344347,	517	33.4	3.8	1000	8	US-11-266-748A-394052	Sequence 394052, A
444	33.6	3.9	1000	8	US-11-266-748A-344623	Sequence 344623,	518	33.4	3.8	1000	8	US-11-266-748A-402244	Sequence 402244, A
445	33.6	3.9	1000	8	US-11-266-748A-340449	Sequence 340449,	519	33.4	3.8	1000	8	US-11-266-748A-403604	Sequence 403604, A
446	33.6	3.9	1000	8	US-11-266-748A-341368	Sequence 341368,	520	33.4	3.8	1000	8	US-11-266-748A-403917	Sequence 403917, A
447	33.6	3.9	1000	8	US-11-266-748A-342593	Sequence 342593,	521	33.4	3.8	1000	8	US-11-266-748A-404276	Sequence 404276, A
448	33.6	3.9	1000	8	US-11-266-748A-342616	Sequence 342616,	522	33.4	3.8	1000	8	US-11-266-748A-405674	Sequence 405674, A
449	33.6	3.9	1000	8	US-11-266-748A-343771	Sequence 343771,	523	33.4	3.8	1000	8	US-11-266-748A-405698	Sequence 405698, A
450	33.6	3.9	1000	8	US-11-266-748A-344347	Sequence 344347,	c 524	33.4	3.8	1000	8	US-11-266-748A-465098	Sequence 465098, A
451	33.6	3.9	1000	8	US-11-266-748A-344623	Sequence 344623,	c 525	33.4	3.8	1000	8	US-11-266-748A-473290	Sequence 473290, A
452	33.6	3.9	1000	8	US-11-266-748A-399964	Sequence 399964,	526	33.4	3.8	1000	8	US-11-266-748A-473650	Sequence 473650, A
453	33.6	3.9	1000	8	US-11-266-748A-402555	Sequence 402555,	c 527	33.4	3.8	1000	8	US-11-266-748A-474963	Sequence 474963, A
454	33.6	3.9	1000	8	US-11-266-748A-403977	Sequence 403977,	c 528	33.4	3.8	1000	8	US-11-266-748A-475322	Sequence 475322, A
455	33.6	3.9	1000	8	US-11-266-748A-404781	Sequence 404781,	529	33.4	3.8	1000	8	US-11-266-748A-476720	Sequence 476720, A
456	33.6	3.9	1000	8	US-11-266-748A-405112	Sequence 405112,	530	33.4	3.8	1047	7	US-11-218-305-7255	Sequence 7255, Ap
457	33.6	3.9	1000	8	US-11-266-748A-405655	Sequence 405655,	c 531	33.4	3.8	1106	7	US-11-218-305-20472	Sequence 20472, A
458	33.6	3.9	1000	8	US-11-266-748A-405629	Sequence 405629,	532	33.4	3.8	1178	8	US-11-216-545-991	Sequence 991, App
459	33.6	3.9	1000	8	US-11-266-748A-465328	Sequence 465328,	c 533	33.4	3.8	1214	8	US-11-266-748A-31148	Sequence 31148, A
460	33.6	3.9	1000	8	US-11-266-748A-471010	Sequence 471010,	534	33.4	3.8	1234	7	US-11-218-305-23945	Sequence 23945, A
461	33.6	3.9	1000	8	US-11-266-748A-473601	Sequence 473601,	535	33.4	3.8	1629	8	US-11-266-748A-28193	Sequence 28193, A
462	33.6	3.9	1000	8	US-11-266-748A-474943	Sequence 474943,	536	33.4	3.8	1661	8	US-11-266-748A-26508	Sequence 26508, A
463	33.6	3.9	1000	8	US-11-266-748A-475827	Sequence 475827,	537	33.4	3.8	1750	8	US-11-266-748A-31545	Sequence 31545, A
464	33.6	3.9	1000	8	US-11-266-748A-476158	Sequence 476158,	538	33.4	3.8	1885	8	US-11-266-748A-28499	Sequence 28499, A
465	33.6	3.9	1000	8	US-11-266-748A-476701	Sequence 476701,	539	33.4	3.8	1958	7	US-11-218-305-16733	Sequence 16733, A
466	33.6	3.9	1000	8	US-11-266-748A-477575	Sequence 477575,	540	33.4	3.8	2059	8	US-11-266-748A-57711	Sequence 57711, A

540	33.4	3.8	2408	8	US-11-266-748A-26410	Sequence 26410, A	613	33.2	3.8	1344	7	US-11-218-305-3321	Sequence 3321, Ap
541	33.4	3.8	2735	8	US-11-266-748A-27563	Sequence 27563, A	614	33.2	3.8	1350	8	US-11-266-748A-58384	Sequence 58384, A
542	33.4	3.8	2909	8	US-11-216-545-5695	Sequence 5695, Ap	615	33.2	3.8	1370	7	US-11-218-305-15856	Sequence 15856, A
543	33.4	3.8	3098	6	US-10-539-228-716	Sequence 716, App	616	33.2	3.8	1596	8	US-11-266-748A-20200	Sequence 20200, A
544	33.4	3.8	3551	8	US-11-266-748A-24371	Sequence 24371, A	617	33.2	3.8	1646	8	US-11-266-748A-27752	Sequence 27752, A
545	33.4	3.8	3593	7	US-11-340-429-10	Sequence 10, Appl	618	33.2	3.8	1758	8	US-11-266-748A-57522	Sequence 57522, A
546	33.4	3.8	4023	8	US-11-266-748A-30712	Sequence 30712, A	619	33.2	3.8	1828	8	US-11-216-545-8656	Sequence 8656, Ap
547	33.4	3.8	4023	8	US-11-266-748A-57006	Sequence 57006, A	620	33.2	3.8	1843	8	US-11-266-748A-53276	Sequence 53276, A
548	33.4	3.8	4384	8	US-11-266-748A-22846	Sequence 22846, A	621	33.2	3.8	1850	7	US-11-056-355B-53395	Sequence 53395, A
549	33.4	3.8	4930	6	US-10-517-441-6287	Sequence 627, App	622	33.2	3.8	1983	7	US-11-218-305-23832	Sequence 23832, A
550	33.4	3.8	6001	6	US-10-517-441-786	Sequence 786, App	623	33.2	3.8	2110	8	US-11-216-545-2569	Sequence 2569, Ap
551	33.4	3.8	7833	6	US-10-517-441-623	Sequence 623, App	624	33.2	3.8	2339	8	US-11-216-545-4350	Sequence 4350, Ap
552	33.4	3.8	47322	6	US-10-539-228-507	Sequence 507, App	625	33.2	3.8	2955	8	US-11-266-748A-28001	Sequence 28001, A
553	33.4	3.8	48643	6	US-10-539-228-715	Sequence 715, App	626	33.2	3.8	3315	8	US-11-266-748A-27139	Sequence 27139, A
554	33.4	3.8	70019	6	US-10-539-228-823	Sequence 823, App	627	33.2	3.8	3844	8	US-11-266-748A-27661	Sequence 27661, A
555	33.4	3.8	113539	8	US-11-266-748A-60002	Sequence 60002, A	628	33.2	3.8	4365	8	US-11-266-748A-28358	Sequence 28358, A
556	33.2	3.8	342	8	US-11-266-748A-61402	Sequence 61402, A	629	33.2	3.8	4382	8	US-11-266-748A-27432	Sequence 27432, A
557	33.2	3.8	574	7	US-11-056-355B-62259	Sequence 62259, A	630	33.2	3.8	5133	8	US-11-266-748A-29007	Sequence 29007, A
558	33.2	3.8	808	8	US-11-266-748A-46111	Sequence 46111, A	631	33.2	3.8	75217	6	US-10-517-441-526	Sequence 526, App
559	33.2	3.8	1000	8	US-11-266-748A-115981	Sequence 115981, A	632	33.2	3.8	75217	8	US-11-266-748A-29045	Sequence 29045, A
560	33.2	3.8	1000	8	US-11-266-748A-117802	Sequence 117802, A	633	33	3.8	434	8	US-11-266-748A-36150	Sequence 36150, A
561	33.2	3.8	1000	8	US-11-266-748A-158145	Sequence 158145, A	634	33	3.8	434	8	US-11-266-748A-148961	Sequence 148961, A
562	33.2	3.8	1000	8	US-11-266-748A-159966	Sequence 159966, A	635	33	3.8	502	8	US-11-266-748A-57937	Sequence 57937, A
563	33.2	3.8	1000	8	US-11-266-748A-206836	Sequence 206836, A	636	33	3.8	588	8	US-11-266-748A-50474	Sequence 50474, A
564	33.2	3.8	1000	8	US-11-266-748A-223110	Sequence 223110, A	637	33	3.8	651	8	US-11-266-748A-50145	Sequence 50145, A
565	33.2	3.8	1000	8	US-11-266-748A-223198	Sequence 223198, A	638	33	3.8	687	8	US-11-266-748A-213934	Sequence 213934, A
566	33.2	3.8	1000	8	US-11-266-748A-224355	Sequence 224355, A	639	33	3.8	687	8	US-11-266-748A-236725	Sequence 236725, A
567	33.2	3.8	1000	8	US-11-266-748A-284621	Sequence 284621, A	640	33	3.8	688	8	US-11-266-748A-57859	Sequence 57859, A
568	33.2	3.8	1000	8	US-11-266-748A-285972	Sequence 285972, A	641	33	3.8	688	8	US-11-266-748A-21144	Sequence 21144, A
569	33.2	3.8	1000	8	US-11-266-748A-286670	Sequence 286670, A	642	33	3.8	688	8	US-11-266-748A-234874	Sequence 234874, A
570	33.2	3.8	1000	8	US-11-266-748A-288892	Sequence 288892, A	643	33	3.8	698	8	US-11-266-748A-207686	Sequence 207686, A
571	33.2	3.8	1000	8	US-11-266-748A-289534	Sequence 289534, A	644	33	3.8	892	8	US-11-216-545-56	Sequence 56, Appl
572	33.2	3.8	1000	8	US-11-266-748A-289689	Sequence 289689, A	645	33	3.8	1000	8	US-11-266-748A-116386	Sequence 116386, A
573	33.2	3.8	1000	8	US-11-266-748A-290205	Sequence 290205, A	646	33	3.8	1000	8	US-11-266-748A-158550	Sequence 158550, A
574	33.2	3.8	1000	8	US-11-266-748A-292998	Sequence 292998, A	647	33	3.8	1000	8	US-11-266-748A-220618	Sequence 220618, A
575	33.2	3.8	1000	8	US-11-266-748A-293191	Sequence 293191, A	648	33	3.8	1000	8	US-11-266-748A-222188	Sequence 222188, A
576	33.2	3.8	1000	8	US-11-266-748A-303222	Sequence 303222, A	649	33	3.8	1000	8	US-11-266-748A-222655	Sequence 222655, A
577	33.2	3.8	1000	8	US-11-266-748A-303605	Sequence 303605, A	650	33	3.8	1000	8	US-11-266-748A-285076	Sequence 285076, A
578	33.2	3.8	1000	8	US-11-266-748A-337301	Sequence 337301, A	651	33	3.8	1000	8	US-11-266-748A-285121	Sequence 285121, A
579	33.2	3.8	1000	8	US-11-266-748A-338099	Sequence 338099, A	652	33	3.8	1000	8	US-11-266-748A-289196	Sequence 289196, A
580	33.2	3.8	1000	8	US-11-266-748A-340321	Sequence 340321, A	653	33	3.8	1000	8	US-11-266-748A-289639	Sequence 289639, A
581	33.2	3.8	1000	8	US-11-266-748A-340963	Sequence 340963, A	654	33	3.8	1000	8	US-11-266-748A-293355	Sequence 293355, A
582	33.2	3.8	1000	8	US-11-266-748A-341118	Sequence 341118, A	655	33	3.8	1000	8	US-11-266-748A-336505	Sequence 336505, A
583	33.2	3.8	1000	8	US-11-266-748A-341634	Sequence 341634, A	656	33	3.8	1000	8	US-11-266-748A-336550	Sequence 336550, A
584	33.2	3.8	1000	8	US-11-266-748A-344427	Sequence 344427, A	657	33	3.8	1000	8	US-11-266-748A-340625	Sequence 340625, A
585	33.2	3.8	1000	8	US-11-266-748A-344620	Sequence 344620, A	658	33	3.8	1000	8	US-11-266-748A-341068	Sequence 341068, A
586	33.2	3.8	1000	8	US-11-266-748A-344651	Sequence 344651, A	659	33	3.8	1000	8	US-11-266-748A-344784	Sequence 344784, A
587	33.2	3.8	1000	8	US-11-266-748A-393007	Sequence 393007, A	660	33	3.8	1000	8	US-11-266-748A-393751	Sequence 393751, A
588	33.2	3.8	1000	8	US-11-266-748A-397198	Sequence 397198, A	661	33	3.8	1000	8	US-11-266-748A-395310	Sequence 395310, A
589	33.2	3.8	1000	8	US-11-266-748A-400583	Sequence 400583, A	662	33	3.8	1000	8	US-11-266-748A-397358	Sequence 397358, A
590	33.2	3.8	1000	8	US-11-266-748A-400752	Sequence 400752, A	663	33	3.8	1000	8	US-11-266-748A-397994	Sequence 397994, A
591	33.2	3.8	1000	8	US-11-266-748A-401393	Sequence 401393, A	664	33	3.8	1000	8	US-11-266-748A-398971	Sequence 398971, A
592	33.2	3.8	1000	8	US-11-266-748A-404882	Sequence 404882, A	665	33	3.8	1000	8	US-11-266-748A-400181	Sequence 400181, A
593	33.2	3.8	1000	8	US-11-266-748A-405110	Sequence 405110, A	666	33	3.8	1000	8	US-11-266-748A-400533	Sequence 400533, A
594	33.2	3.8	1000	8	US-11-266-748A-405159	Sequence 405159, A	667	33	3.8	1000	8	US-11-266-748A-400695	Sequence 400695, A
595	33.2	3.8	1000	8	US-11-266-748A-406650	Sequence 406650, A	668	33	3.8	1000	8	US-11-266-748A-402856	Sequence 402856, A
596	33.2	3.8	1000	8	US-11-266-748A-468244	Sequence 468244, A	669	33	3.8	1000	8	US-11-266-748A-404496	Sequence 404496, A
597	33.2	3.8	1000	8	US-11-266-748A-471629	Sequence 471629, A	670	33	3.8	1000	8	US-11-266-748A-404497	Sequence 404497, A
598	33.2	3.8	1000	8	US-11-266-748A-471798	Sequence 471798, A	671	33	3.8	1000	8	US-11-266-748A-464797	Sequence 464797, A
599	33.2	3.8	1000	8	US-11-266-748A-472439	Sequence 472439, A	672	33	3.8	1000	8	US-11-266-748A-466356	Sequence 466356, A
600	33.2	3.8	1000	8	US-11-266-748A-475928	Sequence 475928, A	673	33	3.8	1000	8	US-11-266-748A-468404	Sequence 468404, A
601	33.2	3.8	1000	8	US-11-266-748A-476156	Sequence 476156, A	674	33	3.8	1000	8	US-11-266-748A-469040	Sequence 469040, A
602	33.2	3.8	1000	8	US-11-266-748A-476205	Sequence 476205, A	675	33	3.8	1000	8	US-11-266-748A-470017	Sequence 470017, A
603	33.2	3.8	1000	8	US-11-266-748A-477696	Sequence 477696, A	676	33	3.8	1000	8	US-11-266-748A-471227	Sequence 471227, A
604	33.2	3.8	1000	8	US-11-266-748A-483725	Sequence 483725, A	677	33	3.8	1000	8	US-11-266-748A-471579	Sequence 471579, A
605	33.2	3.8	1018	8	US-11-266-748A-427350	Sequence 427350, A	678	33	3.8	1000	8	US-11-266-748A-471741	Sequence 471741, A
606	33.2	3.8	1038	7	US-11-218-305-17388	Sequence 17388, A	679	33	3.8	1000	8	US-11-266-748A-473902	Sequence 473902, A
607	33.2	3.8	1155	8	US-11-266-748A-259577	Sequence 259577, A	680	33	3.8	1000	8	US-11-266-748A-475542	Sequence 475542, A
608	33.2	3.8	1155	8	US-11-266-748A-320094	Sequence 320094, A	681	33	3.8	1000	8	US-11-266-748A-475543	Sequence 475543, A
609	33.2	3.8	1226	8	US-11-266-748A-193829	Sequence 193829, A	682	33	3.8	1174	8	US-11-266-748A-25800	Sequence 25800, A
610	33.2	3.8	1226	8	US-11-266-748A-227351	Sequence 227351, A	683	33	3.8	1190	7	US-11-218-305-11533	Sequence 11533, A
611	33.2	3.8	1229	8	US-11-266-748A-172863	Sequence 172863, A	684	33	3.8	1283	7	US-11-218-305-18128	Sequence 18128, A
612	33.2	3.8	1318	7	US-11-218-305-12279	Sequence 12279, A	685	33	3.8	1352	8	US-11-216-545-23	Sequence 23, Appl

686	33	3.8	1459	6	US-10-953-349-27966	Sequence 27966, A	c 759	32.8	3.8	1000	8	US-11-266-748A-159905	Sequence 159905, A
687	33	3.8	1459	7	US-11-056-355B-64482	Sequence 64482, A	c 760	32.8	3.8	1000	8	US-11-266-748A-160717	Sequence 160717, A
688	33	3.8	1517	8	US-11-216-545-1233	Sequence 1233, Ap	761	32.8	3.8	1000	8	US-11-266-748A-205673	Sequence 205673, A
689	33	3.8	1589	8	US-11-266-748A-25642	Sequence 25642, A	762	32.8	3.8	1000	8	US-11-266-748A-221139	Sequence 221139, A
690	33	3.8	1641	8	US-11-266-748A-25642	Sequence 25642, A	763	32.8	3.8	1000	8	US-11-266-748A-221753	Sequence 221753, A
691	33	3.8	1645	8	US-11-266-748A-27204	Sequence 27204, A	764	32.8	3.8	1000	8	US-11-266-748A-223853	Sequence 223853, A
692	33	3.8	1685	6	US-10-533-868-25	Sequence 25, Appl	765	32.8	3.8	1000	8	US-11-266-748A-287052	Sequence 287052, A
693	33	3.8	1751	8	US-11-216-545-212	Sequence 212, Appl	766	32.8	3.8	1000	8	US-11-266-748A-289331	Sequence 289331, A
694	33	3.8	1825	8	US-11-216-545-8590	Sequence 8590, Ap	767	32.8	3.8	1000	8	US-11-266-748A-289425	Sequence 289425, A
695	33	3.8	1842	7	US-11-218-305-9077	Sequence 9077, Ap	768	32.8	3.8	1000	8	US-11-266-748A-290020	Sequence 290020, A
696	33	3.8	1858	7	US-11-218-305-234	Sequence 234, Ap	769	32.8	3.8	1000	8	US-11-266-748A-290653	Sequence 290653, A
697	33	3.8	1922	7	US-11-218-305-5933	Sequence 5933, Ap	770	32.8	3.8	1000	8	US-11-266-748A-292069	Sequence 292069, A
698	33	3.8	2005	8	US-11-266-748A-27282	Sequence 27282, A	771	32.8	3.8	1000	8	US-11-266-748A-292374	Sequence 292374, A
699	33	3.8	2037	8	US-11-266-748A-26997	Sequence 26997, A	772	32.8	3.8	1000	8	US-11-266-748A-293044	Sequence 293044, A
700	33	3.8	2051	8	US-11-266-748A-31300	Sequence 31300, A	773	32.8	3.8	1000	8	US-11-266-748A-338481	Sequence 338481, A
701	33	3.8	2133	8	US-11-266-748A-29684	Sequence 29684, A	774	32.8	3.8	1000	8	US-11-266-748A-340760	Sequence 340760, A
702	33	3.8	2247	8	US-11-266-748A-25703	Sequence 25703, A	775	32.8	3.8	1000	8	US-11-266-748A-340854	Sequence 340854, A
703	33	3.8	2494	8	US-11-266-748A-23443	Sequence 23443, A	776	32.8	3.8	1000	8	US-11-266-748A-341449	Sequence 341449, A
704	33	3.8	2510	8	US-11-266-748A-27211	Sequence 27211, A	777	32.8	3.8	1000	8	US-11-266-748A-342082	Sequence 342082, A
705	33	3.8	2608	7	US-11-218-305-22500	Sequence 22500, A	778	32.8	3.8	1000	8	US-11-266-748A-343498	Sequence 343498, A
706	33	3.8	2618	8	US-11-266-748A-27744	Sequence 27744, A	779	32.8	3.8	1000	8	US-11-266-748A-343803	Sequence 343803, A
707	33	3.8	2668	8	US-11-266-748A-27838	Sequence 27838, A	780	32.8	3.8	1000	8	US-11-266-748A-344473	Sequence 344473, A
708	33	3.8	2942	7	US-11-218-305-15147	Sequence 15147, A	781	32.8	3.8	1000	8	US-11-266-748A-395719	Sequence 395719, A
709	33	3.8	3298	8	US-11-266-748A-26098	Sequence 26098, A	782	32.8	3.8	1000	8	US-11-266-748A-396553	Sequence 396553, A
710	33	3.8	3440	8	US-11-266-748A-25944	Sequence 25944, A	783	32.8	3.8	1000	8	US-11-266-748A-397645	Sequence 397645, A
711	33	3.8	3658	8	US-11-266-748A-27744	Sequence 27744, A	784	32.8	3.8	1000	8	US-11-266-748A-400460	Sequence 400460, A
712	33	3.8	3883	8	US-11-266-748A-28593	Sequence 28593, A	785	32.8	3.8	1000	8	US-11-266-748A-401175	Sequence 401175, A
713	33	3.8	5027	7	US-11-218-305-24326	Sequence 24326, A	786	32.8	3.8	1000	8	US-11-266-748A-401976	Sequence 401976, A
714	33	3.8	5155	8	US-11-266-748A-28283	Sequence 28283, A	787	32.8	3.8	1000	8	US-11-266-748A-403664	Sequence 403664, A
715	33	3.8	5976	6	US-10-517-441-554	Sequence 554, Appl	788	32.8	3.8	1000	8	US-11-266-748A-404057	Sequence 404057, A
716	33	3.8	6181	8	US-11-266-748A-24504	Sequence 24504, A	789	32.8	3.8	1000	8	US-11-266-748A-404760	Sequence 404760, A
717	33	3.8	7001	6	US-10-517-441-513	Sequence 513, Appl	790	32.8	3.8	1000	8	US-11-266-748A-404931	Sequence 404931, A
718	33	3.8	7001	6	US-10-517-441-787	Sequence 787, Appl	791	32.8	3.8	1000	8	US-11-266-748A-466765	Sequence 466765, A
719	33	3.8	8900	6	US-10-517-441-428	Sequence 428, Appl	792	32.8	3.8	1000	8	US-11-266-748A-467599	Sequence 467599, A
720	33	3.8	11429	6	US-10-517-441-479	Sequence 479, Appl	793	32.8	3.8	1000	8	US-11-266-748A-468691	Sequence 468691, A
721	33	3.8	11429	6	US-10-517-441-753	Sequence 753, Appl	794	32.8	3.8	1000	8	US-11-266-748A-471506	Sequence 471506, A
722	33	3.8	14147	6	US-10-517-441-539	Sequence 539, Appl	795	32.8	3.8	1000	8	US-11-266-748A-472221	Sequence 472221, A
723	33	3.8	261789	8	US-11-260-842-1	Sequence 1, Appl	796	32.8	3.8	1000	8	US-11-266-748A-473022	Sequence 473022, A
724	32.8	3.8	417	8	US-11-266-748A-293090	Sequence 293090, A	797	32.8	3.8	1000	8	US-11-266-748A-473022	Sequence 473022, A
725	32.8	3.8	417	8	US-11-266-748A-344519	Sequence 344519, A	798	32.8	3.8	1000	8	US-11-266-748A-474710	Sequence 474710, A
726	32.8	3.8	459	8	US-11-266-748A-7608	Sequence 7608, Ap	799	32.8	3.8	1000	8	US-11-266-748A-475103	Sequence 475103, A
727	32.8	3.8	459	8	US-11-266-748A-81577	Sequence 81577, A	800	32.8	3.8	1000	8	US-11-266-748A-475806	Sequence 475806, A
728	32.8	3.8	459	8	US-11-266-748A-111081	Sequence 111081, A	801	32.8	3.8	1118	7	US-11-218-305-12485	Sequence 12485, A
729	32.8	3.8	459	8	US-11-266-748A-134388	Sequence 134388, A	802	32.8	3.8	1163	8	US-11-105-233-108	Sequence 108, Appl
730	32.8	3.8	459	8	US-11-266-748A-177744	Sequence 177744, A	803	32.8	3.8	1175	8	US-11-266-748A-27680	Sequence 27680, A
731	32.8	3.8	459	8	US-11-266-748A-251094	Sequence 251094, A	804	32.8	3.8	1306	8	US-11-216-545-2259	Sequence 2259, Ap
732	32.8	3.8	459	8	US-11-266-748A-311611	Sequence 311611, A	805	32.8	3.8	1425	8	US-11-266-748A-58244	Sequence 58244, A
733	32.8	3.8	459	8	US-11-266-748A-358300	Sequence 358300, A	806	32.8	3.8	1448	8	US-11-266-748A-27177	Sequence 27177, A
734	32.8	3.8	459	8	US-11-266-748A-41679	Sequence 41679, A	807	32.8	3.8	1607	7	US-11-218-305-22253	Sequence 22253, A
735	32.8	3.8	459	8	US-11-266-748A-400949	Sequence 400949, A	808	32.8	3.8	1658	8	US-11-216-545-3140	Sequence 3140, Ap
736	32.8	3.8	532	8	US-11-266-748A-471995	Sequence 471995, A	809	32.8	3.8	1741	8	US-11-266-748A-26965	Sequence 26965, A
737	32.8	3.8	580	8	US-11-266-748A-53319	Sequence 53319, A	810	32.8	3.8	1886	6	US-10-449-902-548	Sequence 548, Appl
738	32.8	3.8	581	8	US-11-266-748A-371855	Sequence 371855, A	811	32.8	3.8	1914	7	US-11-366-001-34	Sequence 34, Appl
739	32.8	3.8	581	8	US-11-266-748A-455234	Sequence 455234, A	812	32.8	3.8	1946	7	US-11-218-305-2525	Sequence 2525, Ap
740	32.8	3.8	678	8	US-11-266-748A-209877	Sequence 209877, A	813	32.8	3.8	1952	7	US-11-218-305-18680	Sequence 18680, A
741	32.8	3.8	678	8	US-11-266-748A-234234	Sequence 234234, A	814	32.8	3.8	1990	8	US-11-266-748A-76	Sequence 76, Appl
742	32.8	3.8	702	8	US-11-266-748A-20926	Sequence 20926, A	815	32.8	3.8	2057	8	US-11-266-748A-28575	Sequence 28575, A
743	32.8	3.8	721	8	US-11-266-748A-42254	Sequence 42254, A	816	32.8	3.8	2105	8	US-11-266-748A-6720	Sequence 6720, Ap
744	32.8	3.8	764	8	US-11-216-545-4622	Sequence 4622, Ap	817	32.8	3.8	2307	8	US-11-216-545-1611	Sequence 1611, Ap
745	32.8	3.8	788	7	US-11-056-355B-60582	Sequence 60582, A	818	32.8	3.8	2442	6	US-10-953-349-35802	Sequence 35802, A
746	32.8	3.8	807	7	US-11-218-305-21335	Sequence 21335, A	819	32.8	3.8	2442	7	US-11-218-305-18102	Sequence 18102, A
747	32.8	3.8	883	6	US-10-953-349-15521	Sequence 15521, A	820	32.8	3.8	2530	8	US-11-145-307A-70	Sequence 70, Appl
748	32.8	3.8	931	8	US-11-266-748A-25720	Sequence 25720, A	821	32.8	3.8	2530	8	US-11-266-748A-56717	Sequence 56717, A
749	32.8	3.8	944	8	US-11-216-545-7493	Sequence 7493, Ap	822	32.8	3.8	2572	8	US-11-266-748A-24373	Sequence 24373, A
750	32.8	3.8	976	8	US-11-266-748A-81578	Sequence 81578, A	823	32.8	3.8	2745	7	US-11-218-305-18483	Sequence 18483, A
751	32.8	3.8	976	8	US-11-266-748A-111082	Sequence 111082, A	824	32.8	3.8	2848	6	US-10-449-902-16718	Sequence 16718, A
752	32.8	3.8	976	8	US-11-266-748A-134389	Sequence 134389, A	825	32.8	3.8	3158	6	US-10-504-973-76	Sequence 76, Appl
753	32.8	3.8	1000	8	US-11-266-748A-116497	Sequence 116497, A	826	32.8	3.8	3183	8	US-11-266-748A-27495	Sequence 27495, A
754	32.8	3.8	1000	8	US-11-266-748A-117511	Sequence 117511, A	827	32.8	3.8	3183	8	US-11-266-748A-57723	Sequence 57723, A
755	32.8	3.8	1000	8	US-11-266-748A-117741	Sequence 117741, A	828	32.8	3.8	3189	8	US-11-266-748A-25316	Sequence 25316, A
756	32.8	3.8	1000	8	US-11-266-748A-118553	Sequence 118553, A	829	32.8	3.8	3189	8	US-10-449-902-17285	Sequence 17285, A
757	32.8	3.8	1000	8	US-11-266-748A-158661	Sequence 158661, A	830	32.8	3.8	3606	6	US-11-266-748A-26097	Sequence 26097, A
758	32.8	3.8	1000	8	US-11-266-748A-159675	Sequence 159675, A	831	32.8	3.8	3666	7	US-11-218-305-18860	Sequence 18860, A

832	32.8	3.8	3741	8	US-11-266-748A-31177	Sequence 31177, A	C 905	32.6	3.7	1000	8	US-11-266-748A-469819	Sequence 469819, A
833	32.8	3.8	3898	8	US-11-266-748A-24597	Sequence 24597, A	C 906	32.6	3.7	1000	8	US-11-266-748A-47013	Sequence 47013, A
C 834	32.8	3.8	4039	6	US-10-449-902-25532	Sequence 25532, A	C 907	32.6	3.7	1000	8	US-11-266-748A-470167	Sequence 470167, A
835	32.8	3.8	4086	8	US-11-301-554-1801	Sequence 1801, Ap	C 908	32.6	3.7	1000	8	US-11-266-748A-471981	Sequence 471981, A
836	32.8	3.8	4538	8	US-11-266-748A-30642	Sequence 30642, A	C 909	32.6	3.7	1000	8	US-11-266-748A-472868	Sequence 472868, A
C 837	32.8	3.8	5376	6	US-10-517-441-280	Sequence 280, App	C 910	32.6	3.7	1000	8	US-11-266-748A-473266	Sequence 473266, A
C 838	32.8	3.8	11021	6	US-10-517-441-450	Sequence 450, App	C 911	32.6	3.7	1000	8	US-11-266-748A-474525	Sequence 474525, A
C 839	32.8	3.8	11021	6	US-10-517-441-450	Sequence 450, App	C 912	32.6	3.7	1000	8	US-11-266-748A-475047	Sequence 475047, A
C 840	32.8	3.8	81463	6	US-10-540-898-559	Sequence 659, App	C 913	32.6	3.7	1000	8	US-11-266-748A-475679	Sequence 475679, A
C 841	32.8	3.8	115233	6	US-10-539-228-773	Sequence 773, App	C 914	32.6	3.7	1000	8	US-11-266-748A-475969	Sequence 475969, A
C 842	32.8	3.8	152331	8	US-11-175-714-86	Sequence 86, Appl	C 915	32.6	3.7	1000	8	US-11-266-748A-477571	Sequence 477571, A
C 843	32.8	3.8	197526	6	US-10-538-228-498	Sequence 498, App	C 916	32.6	3.7	1035	8	US-11-216-545-1996	Sequence 1996, Ap
C 844	32.6	3.7	586	8	US-11-145-307A-187	Sequence 187, App	C 917	32.6	3.7	1041	7	US-11-218-305-16933	Sequence 16933, A
C 845	32.6	3.7	658	8	US-11-266-748A-52927	Sequence 52927, A	C 918	32.6	3.7	1045	7	US-11-218-305-20430	Sequence 20430, A
C 846	32.6	3.7	755	8	US-11-266-748A-41499	Sequence 41499, A	C 919	32.6	3.7	1072	8	US-11-216-545-4808	Sequence 4808, Ap
C 847	32.6	3.7	762	6	US-10-953-349-30826	Sequence 30826, A	C 920	32.6	3.7	1154	7	US-11-266-748A-26212	Sequence 26212, A
C 848	32.6	3.7	844	8	US-11-216-545-1182	Sequence 1182, Ap	C 921	32.6	3.7	1196	7	US-11-218-305-18365	Sequence 18365, A
C 849	32.6	3.7	919	6	US-10-374-780A-1356	Sequence 1356, Ap	C 922	32.6	3.7	1214	8	US-11-216-545-1287	Sequence 1287, Ap
C 850	32.6	3.7	922	8	US-11-216-545-3692	Sequence 3692, Ap	C 923	32.6	3.7	1225	8	US-11-216-545-3858	Sequence 3858, Ap
C 851	32.6	3.7	960	8	US-11-266-748A-57978	Sequence 57978, A	C 924	32.6	3.7	1225	8	US-11-216-545-4292	Sequence 4292, Ap
C 852	32.6	3.7	1000	8	US-11-266-748A-116866	Sequence 116866, A	C 925	32.6	3.7	1230	7	US-11-174-307B-2729	Sequence 2729, Ap
C 853	32.6	3.7	1000	8	US-11-266-748A-117261	Sequence 116892, A	C 926	32.6	3.7	1237	7	US-11-184-982-29	Sequence 29, Appl
C 854	32.6	3.7	1000	8	US-11-266-748A-117321	Sequence 117261, A	C 927	32.6	3.7	1309	8	US-11-134-445-29	Sequence 29, Appl
C 855	32.6	3.7	1000	8	US-11-266-748A-117521	Sequence 117921, A	C 928	32.6	3.7	1309	8	US-11-216-545-3759	Sequence 3759, Ap
C 856	32.6	3.7	1000	8	US-11-266-748A-118579	Sequence 118579, A	C 929	32.6	3.7	1326	8	US-11-216-545-3452	Sequence 3452, Ap
C 857	32.6	3.7	1000	8	US-11-266-748A-159030	Sequence 159030, A	C 930	32.6	3.7	1327	8	US-11-216-545-3518	Sequence 3518, Ap
C 858	32.6	3.7	1000	8	US-11-266-748A-159056	Sequence 159056, A	C 931	32.6	3.7	1361	8	US-11-216-545-6682	Sequence 6682, Ap
C 859	32.6	3.7	1000	8	US-11-266-748A-159425	Sequence 159425, A	C 932	32.6	3.7	1416	7	US-11-218-305-17282	Sequence 17282, A
C 860	32.6	3.7	1000	8	US-11-266-748A-160085	Sequence 160085, A	C 933	32.6	3.7	1429	8	US-11-216-545-3534	Sequence 3534, Ap
C 861	32.6	3.7	1000	8	US-11-266-748A-160743	Sequence 160743, A	C 934	32.6	3.7	1543	8	US-11-266-748A-24728	Sequence 24728, A
C 862	32.6	3.7	1000	8	US-11-266-748A-222123	Sequence 222123, A	C 935	32.6	3.7	1783	8	US-11-266-748A-27762	Sequence 27762, A
C 863	32.6	3.7	1000	8	US-11-266-748A-222476	Sequence 222476, A	C 936	32.6	3.7	1802	7	US-11-056-3558-106553	Sequence 106553, A
C 864	32.6	3.7	1000	8	US-11-266-748A-222520	Sequence 222520, A	C 937	32.6	3.7	1802	7	US-11-056-3558-117792	Sequence 117792, A
C 865	32.6	3.7	1000	8	US-11-266-748A-222796	Sequence 222796, A	C 938	32.6	3.7	1859	8	US-11-266-748A-27709	Sequence 27709, A
C 866	32.6	3.7	1000	8	US-11-266-748A-223380	Sequence 223380, A	C 939	32.6	3.7	1878	8	US-11-216-545-5428	Sequence 5428, Ap
C 867	32.6	3.7	1000	8	US-11-266-748A-223976	Sequence 223976, A	C 940	32.6	3.7	1914	8	US-11-216-545-1817	Sequence 1817, Ap
C 868	32.6	3.7	1000	8	US-11-266-748A-224299	Sequence 224299, A	C 941	32.6	3.7	1937	7	US-11-218-305-14872	Sequence 14872, A
C 869	32.6	3.7	1000	8	US-11-266-748A-224736	Sequence 224736, A	C 942	32.6	3.7	2026	7	US-11-366-001-30	Sequence 30, Appl
C 870	32.6	3.7	1000	8	US-11-266-748A-287053	Sequence 287053, A	C 943	32.6	3.7	2026	8	US-11-266-748A-27048	Sequence 27048, A
C 871	32.6	3.7	1000	8	US-11-266-748A-289831	Sequence 289831, A	C 944	32.6	3.7	2080	8	US-11-216-545-5037	Sequence 5037, Ap
C 872	32.6	3.7	1000	8	US-11-266-748A-291204	Sequence 291204, A	C 945	32.6	3.7	2166	8	US-11-266-748A-25894	Sequence 25894, A
C 873	32.6	3.7	1000	8	US-11-266-748A-291919	Sequence 291919, A	C 946	32.6	3.7	2204	6	US-10-540-898-724	Sequence 724, App
C 874	32.6	3.7	1000	8	US-11-266-748A-292335	Sequence 292335, A	C 947	32.6	3.7	2245	8	US-11-218-305-44584	Sequence 44584, A
C 875	32.6	3.7	1000	8	US-11-266-748A-292457	Sequence 292457, A	C 948	32.6	3.7	2258	8	US-11-266-748A-59040	Sequence 59040, A
C 876	32.6	3.7	1000	8	US-11-266-748A-293089	Sequence 293089, A	C 949	32.6	3.7	2327	8	US-11-216-545-99	Sequence 99, Appl
C 877	32.6	3.7	1000	8	US-11-266-748A-293648	Sequence 293648, A	C 950	32.6	3.7	2460	8	US-11-266-748A-57404	Sequence 57404, A
C 878	32.6	3.7	1000	8	US-11-266-748A-293849	Sequence 293849, A	C 951	32.6	3.7	2618	8	US-11-266-748A-25961	Sequence 25961, A
C 879	32.6	3.7	1000	8	US-11-266-748A-294287	Sequence 294287, A	C 952	32.6	3.7	2747	8	US-11-266-748A-29880	Sequence 29880, A
C 880	32.6	3.7	1000	8	US-11-266-748A-338482	Sequence 338482, A	C 953	32.6	3.7	2784	8	US-11-266-748A-29880	Sequence 29880, A
C 881	32.6	3.7	1000	8	US-11-266-748A-341260	Sequence 341260, A	C 954	32.6	3.7	3053	8	US-11-266-748A-23618	Sequence 23618, A
C 882	32.6	3.7	1000	8	US-11-266-748A-342633	Sequence 342633, A	C 955	32.6	3.7	3240	8	US-11-247-437-1	Sequence 1, Appl1
C 883	32.6	3.7	1000	8	US-11-266-748A-343348	Sequence 343348, A	C 956	32.6	3.7	3420	8	US-11-266-748A-30143	Sequence 30143, A
C 884	32.6	3.7	1000	8	US-11-266-748A-343764	Sequence 343764, A	C 957	32.6	3.7	3561	7	US-11-218-305-9070	Sequence 9070, Ap
C 885	32.6	3.7	1000	8	US-11-266-748A-343886	Sequence 343886, A	C 958	32.6	3.7	3740	8	US-11-216-545-2121	Sequence 2121, Ap
C 886	32.6	3.7	1000	8	US-11-266-748A-344518	Sequence 344518, A	C 959	32.6	3.7	3861	8	US-11-216-545-9070	Sequence 9070, Ap
C 887	32.6	3.7	1000	8	US-11-266-748A-345077	Sequence 345077, A	C 960	32.6	3.7	4133	8	US-11-218-305-21828	Sequence 21828, A
C 888	32.6	3.7	1000	8	US-11-266-748A-345078	Sequence 345078, A	C 961	32.6	3.7	4241	7	US-11-218-305-21828	Sequence 21828, A
C 889	32.6	3.7	1000	8	US-11-266-748A-345716	Sequence 345716, A	C 962	32.6	3.7	4860	8	US-11-266-748A-24733	Sequence 24733, A
C 890	32.6	3.7	1000	8	US-11-266-748A-397646	Sequence 397646, A	C 963	32.6	3.7	5203	6	US-10-517-441-318	Sequence 318, App
C 891	32.6	3.7	1000	8	US-11-266-748A-398693	Sequence 398693, A	C 964	32.6	3.7	5203	6	US-10-517-441-592	Sequence 592, App
C 892	32.6	3.7	1000	8	US-11-266-748A-398773	Sequence 398773, A	C 965	32.6	3.7	5388	8	US-11-266-748A-57364	Sequence 57364, A
C 893	32.6	3.7	1000	8	US-11-266-748A-399667	Sequence 399667, A	C 966	32.6	3.7	6035	8	US-11-266-748A-32592	Sequence 32592, A
C 894	32.6	3.7	1000	8	US-11-266-748A-400521	Sequence 400521, A	C 967	32.6	3.7	15355	6	US-10-517-441-416	Sequence 416, App
C 895	32.6	3.7	1000	8	US-11-266-748A-400935	Sequence 400935, A	C 968	32.6	3.7	15355	6	US-10-517-441-690	Sequence 690, App
C 896	32.6	3.7	1000	8	US-11-266-748A-401822	Sequence 401822, A	C 969	32.6	3.7	68732	6	US-10-539-228-560	Sequence 560, App
C 897	32.6	3.7	1000	8	US-11-266-748A-402220	Sequence 402220, A	C 970	32.6	3.7	313287	6	US-10-539-228-48	Sequence 48, Appl
C 898	32.6	3.7	1000	8	US-11-266-748A-403479	Sequence 403479, A	C 971	32.4	3.7	634	8	US-10-517-441-318	Sequence 318, App
C 899	32.6	3.7	1000	8	US-11-266-748A-404001	Sequence 404001, A	C 972	32.4	3.7	635	8	US-11-218-305-9070	Sequence 9070, Ap
C 900	32.6	3.7	1000	8	US-11-266-748A-404633	Sequence 404633, A	C 973	32.4	3.7	651	8	US-11-216-545-2121	Sequence 2121, Ap
C 901	32.6	3.7	1000	8	US-11-266-748A-404923	Sequence 404923, A	C 974	32.4	3.7	651	8	US-11-266-748A-23598	Sequence 23598, A
C 902	32.6	3.7	1000	8	US-11-266-748A-405625	Sequence 405625, A	C 975	32.4	3.7	680	8	US-11-266-748A-211895	Sequence 211895, A
C 903	32.6	3.7	1000	8	US-11-266-748A-468692	Sequence 468692, A	C 976	32.4	3.7	798	7	US-11-266-748A-235440	Sequence 235440, A
C 904	32.6	3.7	1000	8	US-11-266-748A-469739	Sequence 469739, A	C 977	32.4	3.7	827	8	US-11-218-305-14209	Sequence 14209, A
C 905	32.6	3.7	1000	8	US-11-266-748A-469739	Sequence 469739, A	C 978	32.4	3.7	827	8	US-11-266-748A-83798	Sequence 83798, A

c 978	32.4	3.7	827	8	US-11-266-748A-111685	Sequence 111685,	1051	32.4	3.7	6707	8	US-11-266-748A-24508	Sequence 24508, A
c 979	32.4	3.7	827	8	US-11-266-748A-136609	Sequence 136609,	c1052	32.4	3.7	7833	6	US-10-517-441-349	Sequence 349, App
c 980	32.4	3.7	886	8	US-11-266-748A-186709	Sequence 186709,	c1053	32.4	3.7	8900	6	US-10-517-441-701	Sequence 701, App
c 981	32.4	3.7	985	8	US-11-266-748A-356904	Sequence 356904,	c1054	32.4	3.7	146733	6	US-10-540-898-387	Sequence 387, App
c 982	32.4	3.7	985	8	US-11-266-748A-386138	Sequence 386138,	c1055	32.4	3.7	390183	6	US-10-540-898-937	Sequence 937, App
c 983	32.4	3.7	985	8	US-11-266-748A-440283	Sequence 440283,	c1056	32.4	3.7	1421559	8	US-11-266-748A-28208	Sequence 28208, A
c 984	32.4	3.7	1000	8	US-11-266-748A-206699	Sequence 206699,	1057	32.2	3.7	263	8	US-11-266-748A-273348	Sequence 273348,
c 985	32.4	3.7	1000	8	US-11-266-748A-207140	Sequence 207140,	c1058	32.2	3.7	263	8	US-11-266-748A-333865	Sequence 333865,
c 986	32.4	3.7	1000	8	US-11-266-748A-209380	Sequence 209380,	c1059	32.2	3.7	425	6	US-10-953-349-14130	Sequence 14130, A
c 987	32.4	3.7	1000	8	US-11-266-748A-224360	Sequence 224360,	1060	32.2	3.7	461	8	US-11-266-748A-55654	Sequence 55654, A
c 988	32.4	3.7	1000	8	US-11-266-748A-281705	Sequence 281705,	1061	32.2	3.7	515	8	US-11-266-748A-40037	Sequence 40037, A
c 989	32.4	3.7	1000	8	US-11-266-748A-286326	Sequence 286326,	1062	32.2	3.7	687	8	US-11-242-317-38	Sequence 38, App1
c 990	32.4	3.7	1000	8	US-11-266-748A-289245	Sequence 289245,	1063	32.2	3.7	715	8	US-11-266-748A-76767	Sequence 76767, A
c 991	32.4	3.7	1000	8	US-11-266-748A-291280	Sequence 291280,	1064	32.2	3.7	715	8	US-11-266-748A-109550	Sequence 109550,
c 992	32.4	3.7	1000	8	US-11-266-748A-293235	Sequence 293235,	c1065	32.2	3.7	715	8	US-11-266-748A-129578	Sequence 129578,
c 993	32.4	3.7	1000	8	US-11-266-748A-294340	Sequence 294340,	c1066	32.2	3.7	727	8	US-11-266-748A-21264	Sequence 21264,
c 994	32.4	3.7	1000	8	US-11-266-748A-308345	Sequence 308345,	1067	32.2	3.7	727	8	US-11-266-748A-234974	Sequence 234974,
c 995	32.4	3.7	1000	8	US-11-266-748A-337755	Sequence 337755,	1068	32.2	3.7	743	7	US-11-218-305-21197	Sequence 21197, A
c 996	32.4	3.7	1000	8	US-11-266-748A-340674	Sequence 340674,	1069	32.2	3.7	790	8	US-11-266-748A-54836	Sequence 54836, A
c 997	32.4	3.7	1000	8	US-11-266-748A-342709	Sequence 342709,	1070	32.2	3.7	880	8	US-11-216-545-5474	Sequence 5474, Ap
c 998	32.4	3.7	1000	8	US-11-266-748A-344664	Sequence 344664,	1071	32.2	3.7	880	8	US-11-216-545-7492	Sequence 7492, Ap
c 999	32.4	3.7	1000	8	US-11-266-748A-345769	Sequence 345769,	1072	32.2	3.7	921	8	US-11-266-748A-43946	Sequence 43946, A
c1000	32.4	3.7	1000	8	US-11-266-748A-390767	Sequence 390767,	1073	32.2	3.7	1000	8	US-11-266-748A-117348	Sequence 117348
c1001	32.4	3.7	1000	8	US-11-266-748A-395550	Sequence 395550,	1074	32.2	3.7	1000	8	US-11-266-748A-117619	Sequence 117619
c1002	32.4	3.7	1000	8	US-11-266-748A-396751	Sequence 396751,	1075	32.2	3.7	1000	8	US-11-266-748A-117648	Sequence 117648
c1003	32.4	3.7	1000	8	US-11-266-748A-401198	Sequence 401198,	1076	32.2	3.7	1000	8	US-11-266-748A-117715	Sequence 117715
c1004	32.4	3.7	1000	8	US-11-266-748A-402705	Sequence 402705,	1077	32.2	3.7	1000	8	US-11-266-748A-118133	Sequence 118133
c1005	32.4	3.7	1000	8	US-11-266-748A-405176	Sequence 405176,	1078	32.2	3.7	1000	8	US-11-266-748A-118312	Sequence 118312
c1006	32.4	3.7	1000	8	US-11-266-748A-406596	Sequence 406596,	1079	32.2	3.7	1000	8	US-11-266-748A-118652	Sequence 118652
c1007	32.4	3.7	1000	8	US-11-266-748A-465696	Sequence 465696,	1080	32.2	3.7	1000	8	US-11-266-748A-118824	Sequence 118824
c1008	32.4	3.7	1000	8	US-11-266-748A-467797	Sequence 467797,	1081	32.2	3.7	1000	8	US-11-266-748A-119105	Sequence 119105
c1009	32.4	3.7	1000	8	US-11-266-748A-472244	Sequence 472244,	c1082	32.2	3.7	1000	8	US-11-266-748A-159512	Sequence 159512
c1010	32.4	3.7	1000	8	US-11-266-748A-473751	Sequence 473751,	c1083	32.2	3.7	1000	8	US-11-266-748A-159783	Sequence 159783
c1011	32.4	3.7	1000	8	US-11-266-748A-476222	Sequence 476222,	c1084	32.2	3.7	1000	8	US-11-266-748A-159812	Sequence 159812
c1012	32.4	3.7	1000	8	US-11-266-748A-477642	Sequence 477642,	c1085	32.2	3.7	1000	8	US-11-266-748A-159879	Sequence 159879
c1013	32.4	3.7	1000	8	US-11-266-748A-481485	Sequence 481485,	c1086	32.2	3.7	1000	8	US-11-266-748A-160297	Sequence 160297
c1014	32.4	3.7	1123	8	US-11-216-545-2723	Sequence 2723, Ap	c1087	32.2	3.7	1000	8	US-11-266-748A-160476	Sequence 160476
c1015	32.4	3.7	1181	8	US-11-266-748A-27693	Sequence 27693, A	c1088	32.2	3.7	1000	8	US-11-266-748A-160816	Sequence 160816
c1016	32.4	3.7	1238	7	US-11-218-305-11544	Sequence 11544, A	c1089	32.2	3.7	1000	8	US-11-266-748A-160988	Sequence 160988
c1017	32.4	3.7	1245	8	US-11-216-545-953	Sequence 953, App	c1090	32.2	3.7	1000	8	US-11-266-748A-161269	Sequence 161269
c1018	32.4	3.7	1488	7	US-11-056-355B-7215	Sequence 7215, Ap	1091	32.2	3.7	1000	8	US-11-266-748A-209775	Sequence 209775
c1019	32.4	3.7	1558	8	US-11-266-748A-28194	Sequence 28194, A	1092	32.2	3.7	1000	8	US-11-266-748A-221109	Sequence 221109
c1020	32.4	3.7	1640	8	US-11-216-545-6359	Sequence 6359, Ap	1093	32.2	3.7	1000	8	US-11-266-748A-222920	Sequence 222920
c1021	32.4	3.7	2078	8	US-11-266-748A-27633	Sequence 27633, A	1094	32.2	3.7	1000	8	US-11-266-748A-223013	Sequence 223013
c1022	32.4	3.7	2158	8	US-11-266-748A-31443	Sequence 31443, A	1095	32.2	3.7	1000	8	US-11-266-748A-223791	Sequence 223791
c1023	32.4	3.7	2264	8	US-11-266-748A-26575	Sequence 26575, A	1096	32.2	3.7	1000	8	US-11-266-748A-224743	Sequence 224743
c1024	32.4	3.7	2265	8	US-11-266-748A-26265	Sequence 26265, A	1097	32.2	3.7	1000	8	US-11-266-748A-285381	Sequence 285381
c1025	32.4	3.7	2275	8	US-11-266-748A-27117	Sequence 27117, A	1098	32.2	3.7	1000	8	US-11-266-748A-289027	Sequence 289027
c1026	32.4	3.7	2314	7	US-11-218-305-13396	Sequence 13396, A	1099	32.2	3.7	1000	8	US-11-266-748A-289760	Sequence 289760
c1027	32.4	3.7	2445	8	US-11-266-748A-23326	Sequence 23326, A	1100	32.2	3.7	1000	8	US-11-266-748A-289813	Sequence 289813
c1028	32.4	3.7	2494	8	US-11-266-748A-27412	Sequence 27412, A	1101	32.2	3.7	1000	8	US-11-266-748A-289950	Sequence 289950
c1029	32.4	3.7	2515	7	US-11-218-305-22550	Sequence 22550, A	1102	32.2	3.7	1000	8	US-11-266-748A-289968	Sequence 289968
c1030	32.4	3.7	2658	8	US-11-266-748A-26570	Sequence 26570, A	1103	32.2	3.7	1000	8	US-11-266-748A-291139	Sequence 291139
c1031	32.4	3.7	2702	6	US-10-449-902-25385	Sequence 25385, A	1104	32.2	3.7	1000	8	US-11-266-748A-291629	Sequence 291629
c1032	32.4	3.7	2718	7	US-11-218-305-12773	Sequence 12773, A	1105	32.2	3.7	1000	8	US-11-266-748A-291912	Sequence 291912
c1033	32.4	3.7	2729	8	US-11-293-697-755	Sequence 755, App	1106	32.2	3.7	1000	8	US-11-266-748A-292164	Sequence 292164
c1034	32.4	3.7	2729	8	US-11-266-748A-24135	Sequence 24135, A	1107	32.2	3.7	1000	8	US-11-266-748A-292675	Sequence 292675
c1035	32.4	3.7	2825	8	US-11-266-748A-27334	Sequence 27334, A	1108	32.2	3.7	1000	8	US-11-266-748A-294313	Sequence 294313
c1036	32.4	3.7	2990	8	US-11-266-748A-29313	Sequence 29313, A	c1109	32.2	3.7	1000	8	US-11-266-748A-336810	Sequence 336810
c1037	32.4	3.7	3163	8	US-11-266-748A-27609	Sequence 27609, A	c1110	32.2	3.7	1000	8	US-11-266-748A-340456	Sequence 340456
c1038	32.4	3.7	3227	8	US-11-266-748A-24367	Sequence 24367, A	c1111	32.2	3.7	1000	8	US-11-266-748A-341189	Sequence 341189
c1039	32.4	3.7	3413	8	US-11-266-748A-31777	Sequence 31777, A	c1112	32.2	3.7	1000	8	US-11-266-748A-341242	Sequence 341242
c1040	32.4	3.7	3532	8	US-11-266-748A-28445	Sequence 28445, A	c1113	32.2	3.7	1000	8	US-11-266-748A-341379	Sequence 341379
c1041	32.4	3.7	3830	8	US-11-266-748A-30484	Sequence 30484, A	c1114	32.2	3.7	1000	8	US-11-266-748A-341397	Sequence 341397
c1042	32.4	3.7	3930	8	US-11-266-748A-56192	Sequence 56192, A	c1115	32.2	3.7	1000	8	US-11-266-748A-342568	Sequence 342568
c1043	32.4	3.7	4184	8	US-11-266-748A-30162	Sequence 30162, A	c1116	32.2	3.7	1000	8	US-11-266-748A-343058	Sequence 343058
c1044	32.4	3.7	4187	8	US-11-266-748A-27596	Sequence 27596, A	c1117	32.2	3.7	1000	8	US-11-266-748A-343341	Sequence 343341
c1045	32.4	3.7	4187	8	US-11-266-748A-27597	Sequence 27597, A	c1118	32.2	3.7	1000	8	US-11-266-748A-343593	Sequence 343593
c1046	32.4	3.7	4228	8	US-11-266-748A-29485	Sequence 29485, A	c1119	32.2	3.7	1000	8	US-11-266-748A-344104	Sequence 344104
c1047	32.4	3.7	4930	6	US-10-517-441-353	Sequence 353, App	c1120	32.2	3.7	1000	8	US-11-266-748A-345742	Sequence 345742
c1048	32.4	3.7	5277	8	US-11-266-748A-28394	Sequence 28394, A	1121	32.2	3.7	1000	8	US-11-266-748A-394480	Sequence 394480
c1049	32.4	3.7	6001	6	US-10-517-441-512	Sequence 512, App	1122	32.2	3.7	1000	8	US-11-266-748A-396895	Sequence 396895
c1050	32.4	3.7	6299	7	US-11-218-305-12285	Sequence 12285, A	1123	32.2	3.7	1000	8	US-11-266-748A-397609	Sequence 397609

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1134	32.2	3.7	1000	8	US-11-266-748A-403782	Sequence 403782,	1207	32.2	3.7	9859	6	US-10-517-441-729	Sequence 729, App
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1162	32.2	3.7	1247	8	US-11-216-545-6930	Sequence 6930, Ap	1235	32	3.7	1000	8	US-11-266-748A-118743	Sequence 118743,
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1167	32.2	3.7	1590	7	US-11-056-355B-73602	Sequence 73602, A	1240	32	3.7	1000	8	US-11-266-748A-159949	Sequence 159949,
1168	32.2	3.7	1593	7	US-11-218-305-13999	Sequence 13999, A	1241	32	3.7	1000	8	US-11-266-748A-160594	Sequence 160594,
1169	32.2	3.7	1624	8	US-11-266-748A-24423	Sequence 24423, A	1242	32	3.7	1000	8	US-11-266-748A-160907	Sequence 160907,
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1172	32.2	3.7	1698	7	US-11-056-355B-73744	Sequence 73744, A	1245	32	3.7	1000	8	US-11-266-748A-220955	Sequence 220955,
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1174	32.2	3.7	1781	8	US-11-266-748A-120283	Sequence 120283,	1247	32	3.7	1000	8	US-11-266-748A-222803	Sequence 222803,
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1177	32.2	3.7	1801	8	US-11-216-545-3756	Sequence 3756, Ap	1250	32	3.7	1000	8	US-11-266-748A-285194	Sequence 285194,
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1182	32.2	3.7	1974	8	US-11-266-748A-59911	Sequence 59911, A	1255	32	3.7	1000	8	US-11-266-748A-289500	Sequence 289500,
1183	32.2	3.7	1993	8	US-11-266-748A-57024	Sequence 57024, A	1256	32	3.7	1000	8	US-11-266-748A-290170	Sequence 290170,
1184	32.2	3.7	2022	8	US-11-216-545-4236	Sequence 4236, Ap	1257	32	3.7	1000	8	US-11-266-748A-291728	Sequence 291728,
1185	32.2	3.7	2302	8	US-11-266-748A-56596	Sequence 56596, A	1258	32	3.7	1000	8	US-11-266-748A-291960	Sequence 291960,
1186	32.2	3.7	2314	8	US-11-266-748A-27714	Sequence 27714, A	1259	32	3.7	1000	8	US-11-266-748A-292425	Sequence 292425,
1187	32.2	3.7	2640	8	US-11-266-748A-23654	Sequence 23654, A	1260	32	3.7	1000	8	US-11-266-748A-233116	Sequence 233116,
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1196	32.2	3.7	3720	8	US-11-266-748A-26582	Sequence 26582, A	1269	32	3.7	1000	8	US-11-266-748A-340929	Sequence 340929,

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1277	32	3.7	1000	8	US-11-266-748A-394445	Sequence 394445,	1353	32	3.7	2106	7	US-11-320-422-48	Sequence 48, Appl
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